

9/30/26

CURRICULUM VITAE

NAME: Chloé Sarnowski, Ph.D.

PRESENT TITLE: Assistant Professor
Department of Epidemiology
UTHealth Houston
School of Public Health

WORK ADDRESS: 931.03
1930 Old Spanish Trail
Houston, TX 77054

CITIZENSHIP: FRANCE

UNDERGRADUATE EDUCATION: Evry Val d'Essonne University, Evry, France
October 2008 – June 2009
Degree: Bachelor of Science

GRADUATE EDUCATION: Evry Val d'Essonne University, Evry, France
October 2009 – June 2011
Degree: Master of Science, Genomics and Statistical Genetics
UMR946, Inserm - Paris Diderot University, Paris, France
October 2011 – December 2015
Degree: Doctorate of Philosophy, Statistical Genetics
Thesis: "Association studies considering complex mechanisms: application to asthma"

POSTGRADUATE TRAINING: Department of Biostatistics
Boston University School of Public Health
February 2016 – November 2019

ACADEMIC APPOINTMENTS: February 2016 – November 2019
Postdoctoral Associate
Mentor: Dr. Josée Dupuis
Department of Biostatistics
Boston University School of Public Health
Boston, MA

December 2019 – December 2020
Instructor
Department of Biostatistics
Boston University School of Public Health
Boston, MA

January 2021 – November 2022
Faculty Associate
Department of Epidemiology, Human Genetics & Environmental Sciences, School of Public Health

UTHealth Houston SPH
Houston, Texas

December 2022 – Present
Assistant Professor
Department of Epidemiology
UTHealth Houston SPH
Houston, Texas

**PROFESSIONAL
ORGANIZATIONS:**

International Genetic Epidemiology Society (IGES)
American Society of Human Genetics (ASHG)

HONORS AND AWARDS:

Best abstract from a young investigator
Assembly 6 "Occupation and Epidemiology Assembly"
The European Respiratory Society (London, Sept 03-07 2016)

Oral presentation and financial prize
The Genome Science Institute Research Symposium (Boston, 16
Nov 2016)

Travel award
The Cohorts for Heart and Aging Research in Genomic
Epidemiology (CHARGE) consortium conference (New York,
March 23-24, 2017)

Travel award
The Alzheimer's Association Internal Conference (AAIC) (London,
July 16-20 2017)

Finalist of the James V. Neel Award at the International Genetic
Epidemiology Society (IGES) conference (Cambridge, Sept 09-11
2017)

Best poster and financial prize
The Genome Science Institute Research Symposium (Boston, 15
Nov 2018)

Tiger Award for the contribution to the Cohorts for Heart and
Aging Research in Genomic Epidemiology (CHARGE) consortium
(CHARGE conference, St Louis, June 27-28 2019)

Travel award
The Alzheimer's Association Internal Conference (AAIC) (Los
Angeles, July 14-18 2019)

Travel award
The Cohorts for Heart and Aging Research in Genomic
Epidemiology (CHARGE) consortium conference (Houston,
January 30-31, 2020)

Finalist of the Robert C Elston Best Paper Award at the International Genetic Epidemiology Society (IGES) conference (Paris, Sept 07-09 2022)

Travel award

The Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium conference (Boston, May 09-11, 2023)

Travel award

The Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium conference (San Antonio, Oct 10-12, 2023)

Travel award

The Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium conference (Durham, December 2-4, 2025)

Tiger Award for early career achievement from the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium (CHARGE conference, Durham, December 2-4, 2025)

Finalist for the 2026 Award for Excellence in Academic Advising, UTHHealth Houston SPH

**SERVICE – THE
UNIVERSITY OF TEXAS
HEALTH SCIENCE
CENTER AT HOUSTON:**

Member of the Human Genetic Center faculty search committee
Member of the Advising & Mentoring subcommittee for PhD students

Faculty Judge for SPH Research Day 2025

Faculty Judge for SPH Research Day 2026

PhD Dissertation Committee Member

EXTERNAL SERVICE:

A. Service on National Grant Review Panels, Study Sections, Committees

1. Early Career Reviewer (ECR) in the Kidney, Endocrine, and Digestive Disorders (KEDD) NIH study section (Feb 2023)
2. Reviewer for grant application for the Wellcome Trust for Discovery award (July 2023)
3. Reviewer in the Analytics and Statistics for Population Research Panel A (ASPA) NIH study section (March 2026)

B. Journal Reviewer

1. Reviewer in 2025/2026 for: *Communications Biology, Epigenomics, Plos Genetics, Circulation: Genomic and Precision Medicine*
2. Reviewer in 2024/2025 for: *Alzheimer's & Dementia, Clinical Epigenetics, Respiratory Research, Communications Biology, Epigenomics, Plos Genetics, Circulation: Genomic and Precision Medicine*

3. Reviewer in 2023/2024 for: *Diabetes Care, Clinical Epigenetics, Alzheimer's & Dementia, Respiratory Research*
4. Reviewer in 2022/2023 for: *Diabetes Care, Diabetes, Molecular Genetics and Genomics Medicine, Clinical Epigenetics*
5. Reviewer in 2021/2022 for: *Diabetes Care, American Journal of Human Genetics, Nature Communications, Genetic Epidemiology, Journal of Clinical Medicine, Journal of Gerontology*:
6. Past Reviewer for *PLOS Genetics, Annals of Human Genetics, Scientific Reports, Human Molecular Genetics, Journal of Internal Medicine, Alzheimer's & Dementia, Journals of the American College of Cardiology*

C. Professional Service

1. Work in genetics organizations or society:

- Elected Member of the International Genetic Epidemiology Society (IGES) Board of Directors (2024-2026)
- Member and past Elected Chair (2022-2024) of the International Genetic Epidemiology Society (IGES) Young Investigators Committee
- Co-moderator of platform session at the American Society of Human Genetics (ASHG) 2023 conference (November 01-05, Washington DC): Advancing understanding of mechanism in Alzheimer's Disease [11/02/23 10:45-12:15].
- Member of the planning committee for the TOPMed Annual Meeting (February 14-16, 2024, Bethesda, MD).
- Member of the planning committee for the TOPMed Annual Meeting (February 18-20, 2026, Bethesda, MD).
- Co-chair of the planning committee for the TOPMed Annual Meeting (February 17-19, 2027, Bethesda, MD).

2. Consortium work:

- Research collaborator: The Trans-Omics for Precision Medicine (TOPMed) Program
- Research collaborator: The Alzheimer's Disease Sequencing Project (ADSP)
- Research collaborator: The Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium
- Co-convenor of TOPMed working groups: Neurocognitive, Longevity and Healthy Aging, and Reproductive Health

TEACHING ACTIVITIES:

Invited Speaker
23-26 September 2016
Neurepiomics Course, Boston, MA

A practical Introduction to the analysis of sequence data with
EPACTS

Teacher Assistant
January – May 2017
Introduction to statistical computing
Boston University School of Public Health

Invited Speaker
1st May 2017
Genomics workshop, Boston University
A practical Introduction to the analysis of sequence data with
EPACTS

Course Co-instructor
January – May 2018
Introduction to statistical computing
Boston University School of Public Health

Instructor and Research Mentor
June – July 2018
Summer Institute for Research Education in Biostatistics
Boston University School of Public Health

Invited Speaker
17-20 September 2018
Neurepiomics Course, Bordeaux, France
A practical Introduction to the analysis of sequence data with
EPACTS

Invited Speaker
18-22 October 2019
Neurepiomics Course, San Antonio, TX
A practical Introduction to the analysis of sequence data with
EPACTS

Invited Speaker
11-15 October 2021
Neurepiomics Course, remote
Introduction to genomics of complex disorders: a short primer of
GWAS and NGS

Course Co-instructor
January – May 2023
Quantitative Analysis for Public Health Research and Practice
The University of Texas Health Science Center

Invited Speaker
07-09 October 2023
Neurepiomics Course, San Antonio, TX
Association Analyses of Sequence Data

Course Co-instructor
January – May 2024
Quantitative Analysis for Public Health Research and Practice
The University of Texas Health Science Center

Invited Speaker
02-04 December 2025
The Cohorts for Heart and Aging Research in Genomic
Epidemiology (CHARGE) consortium conference (Durham, NC)
Leveraging sequencing data to study the contribution of rare
genetic variation to plasma proteomic levels

Course Co-instructor
January – May 2025
Quantitative Analysis for Public Health Research and Practice
The University of Texas Health Science Center

Course Instructor
January – May 2026
Quantitative Analysis for Public Health Research and Practice
The University of Texas Health Science Center

Course Guest Lecturer
15 July 2026
Course: Epidemiological Approaches to Neurological and Mental
Health Disorders
Lecture: Recent advances in genetic analyses of AD/HD &
cognitive impairment
The University of Texas Health Science Center

Invited Speaker
04-07 October 2026
Neurepiomics Course, San Antonio, TX
Analyses of Whole Genome Sequencing Data and Introduction to
TOPMed

Course Instructor
January – May 2027
Quantitative Analysis for Public Health Research and Practice
The University of Texas Health Science Center

Course Co-Instructor
January – May 2027
Introduction to Applied Omics for Epidemiology and Public Health
Research
The University of Texas Health Science Center

MENTORING ACTIVITIES: Research Mentor
June – July 2018
Summer Institute for Research Education in Biostatistics

Boston University School of Public Health

Supervisor

Fall 2020-Oct 2022

Yixin Zhang, PhD student in Biostatistics

Boston University School of Public Health

Supervisor

May 2020-May 2023

Lincoln Shade, PhD student in Epidemiology and Biostatistics

University of Kentucky College of Medicine

Faculty Academic Advisor for MPH students in Epidemiology

Fall 2021-Present

The University of Texas Health Science Center

Supervisor

August 2022-August 2023

Jiyuan Tang, GRA

The University of Texas Health Science Center

Supervisor

March 2023-Present

Jeewoen Shin, Biostatistician

The University of Texas Health Science Center

Supervisor

January 2024-August 2024

Hari Kishan Indupuru, GRA

The University of Texas Health Science Center

Co-Supervisor

September 2024-June 2025

Zaheer Bhojani, Research Associate

The University of Texas Health Science Center

List of MPH Epidemiology Advisees:

Student	Years	Graduation
Kameron Corrothers	Fall 2021 -	Spring 2023
Joseph Dang	Fall 2021 -	Spring 2025
Sydney Petty	Fall 2021 -	Spring 2024
Jaafar Salim	Fall 2021 -	Spring 2023
William Azadi	Fall 2022 -	Spring 2023
Hyo Jeong Jeong	Fall 2022 -	Fall 2026
Vivian Molokwu	Summer 2023 -	Spring 2024
Brianna Burzynski	Fall 2023 -	Summer 2025
Matthew Lee	Fall 2023 -	Spring 2025
Vyoma Soni	Fall 2023 -	Spring 2025
Ratnasree Vaddepalli	Fall 2023 -	Fall 2025
Haley Lu	Spring 2024 -	Spring 2027 intended

Parisa Fallah	Fall 2024 -	Spring 2026
David Palmer	Fall 2024 -	Spring 2025
Maheshwari Chauhan	Fall 2024 -	Fall 2026 intended
Thu Huynh Minh Le	Fall 2024 -	Fall 2026 intended
Mohammed Zakir	Spring 2025 -	Fall 2026 intended
Brissa Aranda	Fall 2025 -	Spring 2027 intended
Casandra Argento-Bird	Fall 2025 -	Spring 2027 intended
Diksha Ravindra Pagare	Fall 2025 -	Spring 2027 intended

ACTIVE FUNDING

RESEARCH SUPPORT:

Agency: NHLBI
 Type of grant: R01
 Title: Molecular Determinants of Atherosclerotic Cardiovascular Disease in Multi-ethnic Populations
 PD/PI: Yu, Bing
 Role: Co-Investigator
 Dates: 04/2023 – 03/2027

Agency: NIA
 Type of grant: R01
 Title: Using polygenic risk scores and omics to study how suboptimal sleep accelerates cognitive aging in diverse populations
 PD/PI: Sofer, Tamar
 Role: Co-Investigator, Subcontract
 Dates: 09/2023 – 05/2028

Agency: NHLBI
 Title: Trans-Omics for Precision Medicine (TOPMed) Informatics Research Center (IRC)
 PD/PI: Smith, Albert
 Role: Co-Investigator, Subcontract
 Dates: 04/2024 – 03/2029

Agency: NIA
 Type of grant: R01
 Title: Efficient IBD mapping for Alzheimer's Disease and related brain imaging phenotypes
 PD/PI: Chen, Han/Zhi, Degui
 Role: Co-Investigator
 Dates: 09/2024 – 06/2029

PAST FUNDING

RESEARCH SUPPORT:

Agency: NIA
 Type of grant: K99/R00
 Title: Exploring Common Biological Pathways Underlying Insulin Resistance and Alzheimer Disease using Genetics and Omic Tools
 Role: PI
 Dates: 08/2022 – 07/2026

CONFERENCE ABSTRACTS AND PUBLICATIONS:

A. Selected Conference Abstracts

1. Shin J, Chen H, Dupuis J, **Sarnowski C**. Multi-Omic Integration Reveals Rare Variant Effects on Blood DNA Methylation and Gene Expression in Alzheimer's Disease Loci. [International Genetic Epidemiology Society \(IGES\)](#), Esterel (Canada), Oct 18-20 2026 – Poster presentation.
2. **Sarnowski C**, Shin J, Blamer J, Walker K, Sweeney MD, Wang Q, TOPMed Proteomics Analysis Group, Doddapaneni H, Smith AV, Kang HM. Cross-platform comparison of cis-pQTL associations using Olink proteomic data in the Trans-Omics for Precision Medicine (TOPMed) Program. [American Society of Human Genetics \(ASHG\)](#), Montréal (Canada), Oct 20-24 2026 – Poster presentation.
3. Guo B, Naseri A, Xie Z, Zhang M, Salehi Nasab S, **Sarnowski C**, Zhi D*, Chen H*. Multi-phenotype high-resolution fast identity-by-descent mapping test. [American Society of Human Genetics \(ASHG\)](#), Montréal (Canada), Oct 20-24 2026 – Platform presentation.
4. Debban CL, Pratte KA, Nisterenko W, **Sarnowski C**, [...], Yu B, Hu X, Raffield LM, Bowler RP, Manichaikul A. Multi-ancestry cis- and trans-pQTL mapping identifies disease-relevant putative causal variants. [American Society of Human Genetics \(ASHG\)](#), Montréal (Canada), Oct 20-24 2026 – Poster presentation.
5. **Sarnowski C**, Shin J, Bressler J, Grove ML, Mosley TH, Coresh J, Morrison AC, Yu B, Fornage M. Epigenetic associations of dementia proteins in the Atherosclerosis Risk in Communities (ARIC) Study. [Cohorts for Heart and Aging Research in Genomic Epidemiology \(CHARGE\) meeting](#), Durham (NC), December 2-4 2025.
6. Shin J, **Sarnowski C**. Peripheral blood transcriptomic signatures of insulin resistance and their association in blood and brain tissues with neurological traits. [American Society of Human Genetics \(ASHG\)](#), Boston (USA), Oct 14-18 2025 – Poster presentation.
7. **Sarnowski C**, Dutta D, Zhang J, Ma J, Boerwinkle E, Coresh J, Yu B, Chatterjee N. Rare variant association analyses of plasma protein levels in a multi-ancestry cohort. [American Society of Human Genetics \(ASHG\)](#), Washington (DC), November 01-05 2023 – Poster presentation.
8. Shin J, Bressler J, Fornage M, Pankow JS, Morrison AC, Selvin E, **Sarnowski C**. Epigenetic Markers of Insulin Resistance in the Atherosclerosis Risk in Communities (ARIC) Study. [Cohorts for Heart and Aging Research in Genomic Epidemiology \(CHARGE\) meeting](#), San Antonio (TX), October 10-12 2023 - Poster presentation.
9. **Sarnowski C**, Ma J, Nguyen Q, Tin A, Ballantyne CM, Coresh J, Morrison AC, Boerwinkle E, Chatterjee N, Yu B. Ancestrally diverse genome-wide association analysis highlights population-specific differences in the genetic regulation of plasma protein levels. [Cohorts for Heart and Aging Research in Genomic Epidemiology \(CHARGE\) meeting](#), San Antonio (TX), October 10-12 2023 - Poster presentation.

10. **Sarnowski C**, Zhang Y, Ammous F, Shade L, Jian X, Dupuis J, Hivert M-F, Florez JC, Seshadri S, Morrison AC, on behalf of the TOPMed Neurocognitive and Diabetes working groups. Association analysis of genetic clusters related to insulin resistance with neurological traits in diverse populations from the Trans-Omics for Precision Medicine Program. [Cohorts for Heart and Aging Research in Genomic Epidemiology \(CHARGE\) meeting](#), Boston (MA), May 9-11 2023 – Poster presentation.
11. **Sarnowski C**, Zhang Y, Ammous F, Shade L, Jian X, Dupuis J, Hivert M-F, Florez JC, Seshadri S, Morrison AC, on behalf of the TOPMed Neurocognitive and Diabetes working groups. Effect of genetic clusters related to insulin resistance on neurological traits in diverse populations from the Trans-Omics for Precision Medicine (TOPMed) Program. [Alzheimer's Association International Conference \(AAIC\)](#), Amsterdam (Netherlands), July 16-20 2023 – Poster presentation.
12. **Sarnowski C**, Gaynor S, Jian X, Ammous F, Mosley TH, Heckbert S, Fitzpatrick AL, Longstreth WT, Bis JC, Launer LJ, Dupuis J, Florez JC, Hivert MF, Smith JA, Yanek LR, Nyquist P, Glahn DC, Curran JE, Blangero J, Mathias RA, Arnett DK, Psaty B, Ling H, Manning A, Fornage M, Rotter JI, Rich SS, Meigs JB, Seshadri S, Morrison AC, on behalf of the TOPMed Diabetes and Neurocognitive working groups. Polygenic scores for insulin resistance are associated with brain volumes in the NHLBI Trans-Omics for Precision Medicine (TOPMed) Program. [American Society of Human Genetics \(ASHG\)](#), Los Angeles (USA), Oct 25-29 2022 – Poster presentation.
13. **Sarnowski C**, Manning A, Fornage M, Rotter JI, Rich SS, Meigs JB, Seshadri S, Morrison AC. Polygenic scores for insulin resistance are associated with brain volumes in the NHLBI Trans-Omics for Precision Medicine (TOPMed) Program. [Cohorts for Heart and Aging Research in Genomic Epidemiology \(CHARGE\) meeting](#), Seattle (USA), Oct 12-14 2022 – Poster presentation.
14. **Sarnowski C**, Shade LMP, Fornage M, Meigs JB, Seshadri S, Morrison AC, on behalf of the TOPMed Diabetes and Neurocognitive working groups. Leveraging multi-ancestry and whole genome sequence data to improve our understanding of the genetic architecture of neurological traits – applications from the NHLBI Trans-Omics for Precision Medicine (TOPMed) program. [International Stroke Genetics Consortium \(ISGC\)](#), Bordeaux (France), Sept 21-23 2022 – Oral presentation.
15. **Sarnowski C**, Hivert MF, Liu C, Lin H, Beiser A, DeCarli C, Dupuis J, DeJager P, Morrison AC, Seshadri S. Epigenetic signatures of insulin resistance associated with Alzheimer's Disease and related traits. [International Genetic Epidemiology Society \(IGES\)](#), Paris (France), Sept 07-09 2022 – Poster presentation.
16. **Sarnowski C**, Hivert MF, Liu C, Satizabal CL, Lin H, Beiser A, DeCarli C, DeStefano AL, Dupuis J, Morrison AC, Seshadri S. Epigenetic signatures of insulin resistance associated with Alzheimer's Disease and related traits. [Alzheimer's Association International Conference \(AAIC\)](#), San Diego (USA), July 31-Aug 04 2022 – Poster presentation.
17. Lee S, Shi B, Peloso GM, Wang Y, Heard-Costa N, Lin H, Pitsillides AN, **Sarnowski C**, Boerwinkle E, De Jager PL, Dupuis J, Seshadri S, Wijsman E, Destefano AL, Fornage M.

Functional Annotations-Informed Whole Genome Sequence Analysis Identifies Novel Rare Variants for AD in the Alzheimer's Disease Sequencing Project. [Alzheimer's Association International Conference \(AAIC\)](#), San Diego (USA), July 31-Aug 04 2022 – Oral presentation.

18. Shade LMP, Satizabal CL, Glahn D, Mosley T, Heckbert S, Launer L, Yanek LR, Bis JC, Smith JA, DeCarli CS, Arnett DK, Psaty BM, Nyquist PA, Mathias RA, Rotter JI, Rich SS, Blangero J, DeStefano AL, Fardo DW, Fornage M, Seshadri S, **Sarnowski C**, on behalf of the TOPMed Neurocognitive working group. Whole Genome Sequence Association Analysis of Brain MRI Measures. [Alzheimer's Association International Conference \(AAIC\)](#), San Diego (USA), July 31-Aug 04 2022 – Oral presentation.
19. Shade LMP, Fardo DW, Fornage M, Seshadri S, **Sarnowski C**. Whole Genome Sequence Association Analysis of Brain MRI Measures. [Cohorts for Heart and Aging Research in Genomic Epidemiology \(CHARGE\) meeting](#), Philadelphia (USA), April 27-29 2022 – Poster presentation.
20. Bouzid H, Belk J, Jan M, Qi Y, **Sarnowski C**, [...], Keene CD, Seshadri S, Satpathy AT, Montine T, and Jaiswal S. Clonal Hematopoiesis is Associated with Reduced Risk of Alzheimer's Disease. [American Society of Hematology](#), Atlanta (USA), Dec 11-14, 2021 – Oral presentation.
21. Smith JA, Kho M, Bressler J, **Sarnowski C**, Zhao W, Chaar D, Wang YZ, Ammous F, Bis JC, Nyquist P, Heckbert SR, Satizabal C, Yang Q, Snively B, Rodrigue A, Litkowski E, Glahn D, Hayden KM, Fitzpatrick A, Psaty B, Kardia SLR, Fornage M, Seshadri S, on behalf of the TOPMed Neurocognitive Working Group. [American Society of Human Genetics \(ASHG\)](#), virtual, 18-22 Oct 2021 - Poster presentation.
22. Zhang Y, Meigs JB, Liu CT, Dupuis J, **Sarnowski C**. Leveraging family history in genetic association analyses of binary traits. [International Genetic Epidemiology Society](#), virtual, 13-16 October 2021 – Poster presentation.
23. **Sarnowski C**, Ghanbari M, Bis JC, Logue M, Fornage M, Mishra A, the Alzheimer's Disease Neuroimaging Initiative, DeBette S, Dufouil C, Launer LJ, Kremen WS, Longstreth WT, Ikram MA, Seshadri S. [Cohorts for Heart and Aging Research in Genomic Epidemiology \(CHARGE\) meeting](#), virtual, 06-08 October 2021 – Blitz presentation.
24. **Sarnowski C**, Cousminer DL, Franceschini N, Raffield LM, Jia G, Demerath EW, Fernández-Rhodes L, Bradfield JP, Palmer JR, Murabito JM, Lunetta KL, on behalf of the ReproGen working group. Large trans-ethnic meta-analysis identifies AKR1C4 as a novel gene associated with age at menarche. [Cohorts for Heart and Aging Research in Genomic Epidemiology \(CHARGE\) meeting](#), virtual, 06-07 May 2021 – Blitz presentation.
25. Naj AC, Rajabli F, Hamilton-Nelson KL, Kunkle B, Jian X, Wang Y, Peloso GM, Lin H, **Sarnowski C**, Pitsillides A, Satizabal C, Bush WS, Thornton TA, Wijsman E, Seshadri S, Haines JL, Dupuis J, Byrd GS, Mayeux R, DeStefano AL, Martin ER, Pericak-Vance MA, Fornage M, for the ADSP. Comparative Trans-Ethnic Meta-Analysis of Whole Exome Sequencing Variation for Alzheimer's Disease (AD) in 18,402 individuals of the

Alzheimer's Disease Sequencing Project (ADSP). [Alzheimer's Association International Conference \(AAIC\)](#), virtual, 26-30 July 2020 - Poster presentation.

26. Peloso GM, Wang Y, Lin H, **Sarnowski C**, Pitsillides A, Lim E, Fornage M, Ramos J, Martin ER, Naj AC, Pericak-Vance MA, Beecham GW, Hamilton-Nelson KL, Thornton TA, Wijsman E, Seshadri S, Haines JL, Dupuis J, DeStefano AL, Kunkle BW, on behalf of the Alzheimer Disease Sequencing Project. Assessing whole genome sequencing variation for Alzheimer's disease in 4732 individuals from the Alzheimer's disease Sequencing Project (ADSP). [Alzheimer's Association International Conference \(AAIC\)](#), virtual, 26-30 July 2020 – Poster presentation.
27. Scalici A, Peloso GM, Wang Y, Lin H, **Sarnowski C**, Pitsillides AN, Dupuis J, Seshadri S, Destefano AL. Frequency of familial Alzheimer's disease gene mutations within the Alzheimer Disease Sequencing Project (ADSP): Genetics/genetic factors of Alzheimer's disease. [Alzheimer's Association International Conference \(AAIC\)](#), virtual, 26-30 July 2020 – Poster presentation.
28. **Sarnowski C**, Satizabal CL Yanek LR, Bis JC, Smith JA, DeCarli CS, Arnett DK, Psaty BM, Nyquist PA, Mathias RA, DeStefano AL, Seshadri S on behalf of the TOPMed Neurocognitive working group. Whole Genome Sequence Association Analyses of Brain Volumes in the TOPMed Program. [Alzheimer's Association International Conference \(AAIC\)](#), virtual, 26-30 July 2020 - Oral presentation.
29. **Sarnowski C** for the TOPMed Longevity and Healthy Aging Working Group. Leveraging multi-ethnic populations along with multiple handgrip measurements in association analyses with sequence data: the Trans-Omics for Precision Medicine (TOPMed) Program. [Cohorts for Heart and Aging Research in Genomic Epidemiology \(CHARGE\) meeting](#), Houston (USA), 30-31 January 2020 - Oral presentation.
30. **Sarnowski C**, Chen H, Biggs ML, Wassertheil-Smoller S, Bressler J, Irvin M, O'Connell JR, Ryan KA, Fardo DW, Karasik D, Kiel DP, Murabito J, Lunetta KL for the TOPMed Longevity and Healthy Aging Working Group. Association analysis of handgrip strength in targeted loci from GWAS using longitudinal measures and whole-genome sequence data from the Trans-Omics for Precision Medicine (TOPMed) Program. [American Society of Human Genetics \(ASHG\)](#), Houston (USA), 15-19 Oct 2019 - Poster presentation.
31. **Sarnowski C**, Chen H, Biggs ML, Wassertheil-Smoller S, Bressler J, Irvin M, O'Connell JR, Ryan KA, Murabito J, Lunetta KL for the TOPMed Longevity and Healthy Aging Working Group. Association analyses of handgrip strength in multi-ethnic population using sequence data from the Trans-Omics for Precision Medicine (TOPMed) Program. [International Genetic Epidemiology Society \(IGES\)](#), Houston (USA), 13-15 Oct 2019 - Poster presentation.
32. **Sarnowski C**, Satizabal CL, Chouraki V, Pase MP, DeCarli C, Cupples LA, Vasan RS, Beiser AS, DeStefano AL, Seshadri S. Genome-wide association of plasma tau levels in the Framingham Study. [Alzheimer's Association International Conference \(AAIC\)](#), Los Angeles (USA), 14-18 July 2019 - Oral presentation.

33. **Sarnowski C**, Satizabal CL, Chouraki V, Pase MP, DeCarli C, Cupples LA, Vasan RS, Beiser AS, DeStefano AL, Seshadri S. Genome-wide association of plasma tau levels in the Framingham Study. [Cohorts for Heart and Aging Research in Genomic Epidemiology \(CHARGE\) meeting](#), Saint Louis (USA), 27-28 June 2019 - Poster presentation.
34. **Sarnowski C**, Leong A, DiCorpo D, Raffield L, Guo X, de Vries P for the TOPMed Diabetes Working Group. Chromosome X association analysis of Hemoglobin A1c (A1C) in African Americans using sequence data from the Trans-Omics for Precision Medicine (TOPMed) Program. [Trans-Omics for Precision Medicine \(TOPMed\) meeting](#), Tysons (USA), 05-07 Dec 2018 – Oral presentation.
35. **Sarnowski C**, Leong A, DiCorpo D, Raffield L, Guo X, de Vries P for the TOPMed Diabetes Working Group. Chromosome X association analysis of Hemoglobin A1c (A1C) in African Americans using sequence data from the Trans-Omics for Precision Medicine (TOPMed) Program. [GSI Symposium](#), Boston (USA), 15 Nov 2018 – Poster presentation.
36. **Sarnowski C**, Leong A, DiCorpo D, Raffield L, Guo X, de Vries PS for the TOPMed Diabetes Working Group. Chromosome X association analysis of Hemoglobin A1c (HbA1c) in African Americans using TOPMed whole genome sequence (WGS) data. [Cohorts for Heart and Aging Research in Genomic Epidemiology \(CHARGE\) meeting](#), Baltimore (USA), 11-12 Oct 2018 - Poster presentation.
37. **Sarnowski C**, Satizabal CL, Chouraki V, Pase MP, DeCarli C, Cupples LA, Vasan RS, Beiser AS, DeStefano AL, Seshadri S. Genome-wide association of plasma tau levels in the Framingham Study. [American Society of Human Genetics \(ASHG\)](#), San Diego (USA), 16-20 Oct. 2018 - Poster presentation.
38. **Sarnowski C**, Leong A, DiCorpo D, Raffield L, Guo X, de Vries PS for the TOPMed Diabetes Working Group. Chromosome X association analysis of Hemoglobin A1c (HbA1c) in African Americans using TOPMed whole genome sequence (WGS) data. [International Genetic Epidemiology Society \(IGES\)](#), San Diego (USA), 14-16 Oct 2018 - Poster presentation.
39. **Sarnowski C**, Leong A, Raffield L for the TOPMed Diabetes working group. Ancestral differences in Hemoglobin A1c (A1C) associations of erythrocyte genes using NHLBI Trans-Omics for Precision Medicine (TOPMed) Whole Genome Sequence (WGS) data. [American Diabetes Association \(ADA\) meeting](#), Orlando (USA), 22-26 June 2018 - Poster presentation.
40. **Sarnowski C**, Leong A, Raffield L for the TOPMed Diabetes working group. NHLBI Trans-Omics for Precision Medicine (TOPMed) trans-ethnic association analysis of Hemoglobin A1c (A1C) in erythrocyte genes using Whole Genome Sequence (WGS) data. [Cohorts for Heart and Aging Research in Genomic Epidemiology \(CHARGE\) meeting](#), Rotterdam (Netherlands), 18-19 April 2018 - Poster presentation.
41. **Sarnowski C**, Leong A, Raffield L for the TOPMed Diabetes working group. TOPMed trans-ethnic fine-mapping of HbA1c erythrocytic GWAS loci using WGS data. [Trans-Omics for Precision Medicine \(TOPMed\) meeting](#), Tysons (USA), 29 Nov-01 Dec 2017 - Oral presentation.

42. Aron E, Dupuis J, Liu CT, and **Sarnowski C**. Identification of Potential Causal Variants on Type II Diabetes Associated Loci through Fine-Mapping. [Annual Biomedical Research Conference for Minority Students \(ABRCMS\)](#), Phoenix (USA), 1-4 Nov 2017. Poster presentation.
43. Wu Peitao, **Sarnowski C**, for the TOPMed Diabetes working group. Whole Genome Sequence Association Analysis of Fasting Glucose in the Trans-Omics for Precision Medicine (TOPMed) program. [Cohorts for Heart and Aging Research in Genomic Epidemiology \(CHARGE\) meeting](#), Boston (USA), 27-28 Sept 2017. Poster presentation.
44. **Sarnowski C**, Huan T, Liu C, Yao C, Joehanes R, Levy D, Dupuis J. JEM: A joint test to estimate the effect of multiple genetic variants on DNA methylation. [International Genetic Epidemiology Society \(IGES\)](#), Cambridge (UK), 09-11 Sept 2017. Oral presentation.
45. Sugier PE*, **Sarnowski C***, Granell R, Jarvis D, Ege MJ, Laprise C, von Mutius E, Dizier MH, Henderson AJ, Kogevinas M, Demenais F, Bouzigon E. Interaction between genetic variants and secondhand smoke exposure in early life on asthma-onset. [International Genetic Epidemiology Society \(IGES\)](#), Cambridge (UK), 09-11 Sept 2017. Poster presentation.
46. Margaritte-Jeannin P, Babron MC, Laprise C, **Sarnowski C**, Brossard M, Moffatt M, Cookson WO, Bouzigon E, Demenais F, Dizier MH. The COL5A3 and MMP9 Genes Interact in Eczema Susceptibility. [International Genetic Epidemiology Society \(IGES\)](#), Cambridge (UK), 09-11 Sept 2017. Poster presentation.
47. **Sarnowski C**, Satizabal CL, DeCarli CS, Pitsillides AN, Beiser AS, Destefano AL, Dupuis J, Seshadri S. TOPMed Whole Genome Sequence (WGS) Associations with Brain MRI Measures in the Framingham Study. [Alzheimer's Association International Conference \(AAIC\)](#), 16-20 July 2017, London (UK). Oral presentation.
48. **Sarnowski C**, Leong A, Raffield L for the TOPMed Diabetes working group. TOPMed Whole Genome Sequence (WGS) Associations with Hemoglobin A1c (A1C) in White and Black Populations. [American Diabetes Association \(ADA\) meeting](#), San Diego (USA), 9-13 June 2017. Poster presentation.
49. Manning AK, Cade B, Hidalgo B, Lin X, Liu Q, Raffield L, Ryan K, **Sarnowski C**, Wessel J, Xu H, on behalf of the Trans-Omics for Precision Medicine (TOPMed) Program Diabetes Working Group. Whole genome association sequence analysis of fasting glucose and fasting insulin from 7,121 non-diabetic individuals in Trans-Omics for Precision Medicine (TOPMed). [American Diabetes Association \(ADA\) meeting](#), San Diego (USA), 9-13 June 2017. Oral presentation.
50. Sargurupremraj M, **Sarnowski C**, Jian X, Adams H, Chauhan G et al on behalf of neuroCHARGE working group. Genome-wide interaction analysis with hypertension in association with white matter hyperintensity burden: The Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. [European Stroke Organization Conference \(ESOC\)](#), Prague (Czech Republic), 16-18 May, 2017. Oral presentation.

51. **Sarnowski C**, Leong A, Raffield L for the TOPMed Diabetes working group. Trans-ethnic association analysis of Hemoglobin A1c (A1C) using TOPMed Whole Genome Sequence (WGS) data. [Cohorts for Heart and Aging Research in Genomic Epidemiology \(CHARGE\) meeting](#), New-York (USA), 23-24 March 2017 - Oral presentation.
52. Lent S, Xu H, Wang L, Wang Z, **Sarnowski C**, Hivert M-F, Dupuis J. Comparison of novel and existing methods for detecting differentially methylated regions. [Genetic Analysis Workshop 20 \(GAW20\)](#), 04-08 March 2017 San Diego (USA). Group presentation.
53. Fisher V, Wang L, Deng X, **Sarnowski C**, Cupples AL, Liu C-T. Do Changes in DNA Methylation Mediate or Interact with SNP Variation? A Pharmacoepigenetic Analysis. [Genetic Analysis Workshop 20 \(GAW20\)](#), 04-08 March 2017 San Diego (USA). Poster and Group presentation.
54. **Sarnowski C**, Lent S, Dupuis J. Investigation of parent-of-origin effects induced by treatment on triglycerides levels. [Genetic Analysis Workshop 20 \(GAW20\)](#), 04-08 March 2017 San Diego (USA). Oral and Group presentation.
55. **Sarnowski C**, Manning A.K, for the TOPMed T2D working group. Rare variant analysis of fasting glucose and fasting insulin using TOPMed-Framingham Heart Study whole genome sequence data. [GSI Symposium](#), Boston (USA), 16 Nov 2016 – Oral presentation.
56. **Sarnowski C**, Satizabal C.L, DeCarli C, Pitsillides A.N, Beiser A, DeStefano A.L, Dupuis J, Seshadri S. Whole genome sequence analysis of brain MRI measures in the Framingham Study. [International Stroke Genetics Consortium \(ISGC\)](#). Milan (Italy), 03-04 Nov 2016 – Oral presentation. Abstract published in ***Neurol Genet***, March 2017 3:S12-S18, http://ng.neurology.org/content/3/1_Supplement_1/S12.extract
57. **Sarnowski C**, Manning A.K, for the TOPMed T2D working group. Rare variant analysis of fasting glucose and fasting insulin using TOPMed-Framingham Heart Study whole genome sequence data. [Cohorts for Heart and Aging Research in Genomic Epidemiology \(CHARGE\) meeting](#), Charlottesville (USA), 28-29 Sept 2016 – Poster presentation.
58. **Sarnowski C**, Satizabal C.L, DeCarli C, Pitsillides A.N, Beiser A, DeStefano A.L, Dupuis J, Seshadri S. Whole genome sequence analysis of brain MRI measures in the Framingham Study. [Cohorts for Heart and Aging Research in Genomic Epidemiology \(CHARGE\) meeting](#), Charlottesville (USA), 28-29 Sept 2016 – Poster presentation.
59. **Sarnowski C**, Lunetta K.L, Murabito J.M. Risk of cardiovascular event in relation to age-at-menopause associated genetic variants in the Framingham Heart Study. [International Genetic Epidemiology Society \(IGES\)](#), Toronto (Canada), 24-26 Oct 2016 – Poster presentation.
60. **Sarnowski C**, Dizier M-H, Granell R, Jarvis D, Ege M, Laprise C, Sugier P-E, Margaritte-Jeannin P, Cookson W.O.C, Moffatt M, Pin I, Lathrop M, Von Mutius E, Siroux V, Henderson AJ, Kogevinas M, Demenais F, Bouzigon E. Taking into account gene-by-early environmental tobacco smoke exposure interactions to detect genetic variants influencing

time-to-asthma onset. [International Genetic Epidemiology Society \(IGES\)](#), Toronto (Canada), 24-26 Oct 2016 – Poster presentation.

61. Dizier MH, Margaritte-Jeannin P, Pain L, **Sarnowski C**, Brossard M, Mohamdi H, Lavielle N, Just J, Lathrop M, Bouzigon E#, Laprise C#, Demenais F*, Nadif R*. Interactive effect between ATPase-related genes and early-life tobacco smoke exposure on bronchial hyper-responsiveness detected in asthma-ascertained families. [International Genetic Epidemiology Society \(IGES\)](#), Toronto (Canada), 24-26 Oct 2016 – Poster presentation.
62. **Sarnowski C**, Satizabal C.L, DeCarli C, Pitsillides A.N, Beiser A, DeStefano A.L, Dupuis J, Seshadri S. Whole genome sequence analysis of brain MRI measures in the Framingham Study. [American Society of Human Genetics \(ASHG\)](#). Vancouver (Canada), 18-22 Oct 2016 – Poster presentation.
63. Dizier MH, Margaritte-Jeannin P, Pain L, **Sarnowski C**, Brossard M, Mohamdi H, Lavielle N, Just J, Lathrop M, Bouzigon E#, Laprise C#, Demenais F*, Nadif R*. Interactive effect between ATPase-related genes and early-life tobacco smoke exposure on bronchial hyper-responsiveness detected in asthma-ascertained families. [American Society of Human Genetics \(ASHG\)](#). Vancouver (Canada), 18-22 Oct 2016 – Poster presentation.
64. **Sarnowski C**, Dizier M-H, Granell R, Jarvis D, Ege M, Laprise C, Sugier P-E, Margaritte-Jeannin P, Cookson W.O.C, Moffatt M, Pin I, Lathrop M, Von Mutius E, Siroux V, Henderson AJ, Kogevinas M, Demenais F, Bouzigon E. Influence of gene-by-early environmental tobacco smoke exposure interactions on time-to-asthma onset. [European Respiratory Society \(ERS\)](#), London (UK), 03-07 Sept 2016. – Oral presentation.
65. **Sarnowski C**, Dizier M-H, Granell R, Jarvis D, Ege M, Laprise C, Sugier P-E, Margaritte-Jeannin P, Cookson W.O.C, Moffatt M, Pin I, Lathrop M, Von Mutius E, Siroux V, Henderson AJ, Kogevinas M, Demenais F, Bouzigon E. Genome-wide interaction study of time-to-asthma onset with early environmental tobacco smoke exposure. [European Society of Human Genetics \(ESHG\)](#), Barcelone (Spain), 21-24 May 2016 – Poster presentation. Abstract 2016-A-424-ESHG.
66. Sugier P-E, Brossard M, Vaysse A, **Sarnowski C**, Dizier M-H, Lathrop M, Laprise C, Demenais F, Bouzigon E. Integration of text mining and epistasis analysis identifies new genes underlying atopy. [American Society of Human Genetics \(ASHG\)](#), Baltimore (USA), 06-10 Oct. 2015 – Poster presentation. Abstract 1410W.
67. Liu Y , Brossard M, **Sarnowski C**, Margaritte-Jeannin P, Llinares F, Vaysse A, Dizier M.H., Bouzigon E, Demenais F and GABRIEL asthma consortium. Integration of genome-wide association data and human protein interaction networks identifies a gene sub-network underlying childhood-onset asthma. [American Society of Human Genetics \(ASHG\)](#), Baltimore (USA), 06-10 Oct. 2015 – Platform presentation.
68. Sugier P-E, Brossard M, Vaysse A, **Sarnowski C**, Dizier M-H, Lathrop M, Laprise C, Demenais F, Bouzigon E. Combining text mining and epistasis analyses identifies new atopy genes. [International Genetic Epidemiology Society \(IGES\)](#), Baltimore (USA), 04-06 Oct. 2015, *Genetic Epidemiology*. 2015; 39(7):529-599 – Poster presentation. Abstract 144.

69. Liu Y , Brossard M, **Sarnowski C**, Margaritte-Jeannin P, Llinares F, Vaysse A, Dizier M.H., Bouzigon E, Demenais F. Network-based analysis of genome-wide association data identifies a gene sub-network underlying childhood-onset asthma. [International Genetic Epidemiology Society \(IGES\)](#), Baltimore (USA), 04-06 Oct. 2015, **Genetic Epidemiology**. 2015; 39(7):529-599 – Poster presentation. Abstract 98.
70. **Sarnowski C**, Laprise C, Moffatt M, Malerba G, Morin A, Vincent Q, Rohde K, Dizier M-H, Esparza-Gordillo J, Margaritte-Jeannin P, Liang L, Lee Y-A, Pignatti P.F, Cookson W.O.C, Pastinen T, Lathrop M, Demenais F, Bouzigon E. Identification of imprinted 4q35 variant associated with the combined asthma-plus-rhinitis phenotype using both genetic and epigenetic data, [American Society of Human Genetics \(ASHG\)](#), San Diego (United-States), 18-22 Oct. 2014 – Poster presentation. Abstract 486T online at <http://www.ashg.org/2014meeting/abstracts/fulltext/f140120363.htm>
71. **Sarnowski C**, Laprise C, Moffatt M, Malerba G, Morin A, Vincent Q, Rohde K, Dizier M-H, Esparza-Gordillo J, Margaritte-Jeannin P, Liang L, Lee Y-A, Pignatti P.F, Cookson W.O.C, Pastinen T, Lathrop M, Demenais F, Bouzigon E. Combining genetic and epigenetic information identified imprinted 4q35 variant associated with the combined asthma-plus-rhinitis phenotype, [International Genetic Epidemiology Society \(IGES\)](#), Vienne (Austria), 28-30 Aug. 2014 – Poster presentation. Abstract P26 online at <http://www.geneticepi.org/wp-content/uploads/2013/11/Abstracts-23rd-IGES-meeting.pdf>
72. Dizier M-H, Nadif R, Margaritte-Jeannin P, Barton S , Madore A-M, **Sarnowski C**, Brossard M, Lavielle N, Just J, Lathrop M, Holloway J, Laprise C, Bouzigon E, Demenais F, Interactive effect between DNAH9 gene and early-life tobacco smoke exposure in bronchial hyper-responsiveness, [International Genetic Epidemiology Society \(IGES\)](#), Vienne (Austria), 28-30 Aug. 2014 – Poster presentation. Abstract P23 online at <http://www.geneticepi.org/wp-content/uploads/2013/11/Abstracts-23rd-IGES-meeting.pdf>
73. Vaillancourt V.T, Bouzigon E, **Sarnowski C**, Monier F, Dizier M-H, Demenais F, Laprise C. Genes involved in interleukin-1 receptor type II (IL1R2) activities are associated with asthma related phenotypes, [European Society of Human Genetics \(ESHG\)](#), Milan (Italy), 31st May–3rd June 2014, **Eur J Hum Genet** 2014; 22(Suppl1): 328 – Poster presentation (P17.40-M)
74. **Sarnowski C**, Dizier M-H, Ahmed I, Margaritte-Jeannin P, Lathrop M, Demenais F, Bouzigon E. Bouzigon. Identification of genetic factors underlying asthma age-of-onset sub-phenotypes, [American Society of Human Genetics \(ASHG\)](#), Boston (United-States), 22-26 Oct. 2013 – Poster presentation. Abstract 902F online at <http://www.ashg.org/2013meeting/pages/abstracts.shtml>
75. **Sarnowski C**, Dizier M-H, Ahmed I, Margaritte-Jeannin P, Lathrop M, Demenais F, Bouzigon E. Use of multinomial regression model to identify loci underlying diseases with variable age of onset, [International Genetic Epidemiology Society \(IGES\)](#), Chicago (United-States), 15-17 Sept. 2013 – Poster presentation (114). ISBN 978—1-940377-00-1. pp. 51. Abstract 114 online at <http://www.geneticepi.org/meeting-abstracts/>

76. Sugier P-E, Vaysse A, Loucoubar C, **Sarnowski C**, Margaritte-Jeannin P, Dizier M-H, Lathrop M, Demenais F, Bouzigon E. Identification of common and specific genetic determinants to skin prick test reactivity using genome-wide association study and gene-based test approaches, [American Society of Human Genetics \(ASHG\)](#), San Francisco (United-States), 6-10 Nov. 2012 – Poster presentation. Abstract 2079W online at <http://www.ashg.org/2012meeting/pages/abstracts.shtml/>
77. **Sarnowski C**, Malerba G, Vincent Q, Laprise C, Rohde K, Moffatt M, Margaritte-Jeannin P, Dizier M-H, Pignatti P-F, Cookson W-O-C, Lathrop M, Demenais F, Bouzigon E, Accounting for parent-of-origin effects detects association between 4q35 genetic variants and combined asthma-plus-rhinitis phenotype, [American Society of Human Genetics \(ASHG\)](#), San Francisco (United-States), 6-10 Nov. 2012 – Poster presentation. Abstract 1361W online at: <http://www.ashg.org/2012meeting/pages/abstracts.shtml/>
78. **Sarnowski C**, Malerba G, Vincent Q, Laprise C, Rohde K, Moffatt M, Margaritte-Jeannin P, Dizier M-H, Pignatti P-F, Cookson W-O-C, Lathrop M, Demenais F, Bouzigon E. Imprinting and maternal genotype effects of 4q35 genetic variants on combined asthma-plus-rhinitis phenotype, [Capita Selecta in Complex Disease Analysis \(CSCDA\)](#), Liège (Belgium), 30 May-1st June. 2012 – Oral presentation.
79. **Sarnowski C**, Malerba G, Vincent Q, Laprise C, Rohde K, Moffatt M, Margaritte-Jeannin P, Dizier M-H, Pignatti P-F, Cookson W-O-C, Lathrop M, Demenais F, Bouzigon E, Imprinting and maternal genotype effects of 4q35 variants on combined asthma-plus-rhinitis phenotype, [American Society of Human Genetics \(ASHG\)](#), Montréal (Canada), 11-15 Oct. 2011 – Poster presentation. Abstract 637T online at <http://www.ichg2011.org/>
80. **Sarnowski C**, Malerba G, Vincent Q, Laprise C, Rohde K, Moffatt M, Margaritte-Jeannin P, Dizier M-H, Pignatti P-F, Cookson W-O-C, Lathrop M, Demenais F, Bouzigon E, Taking into account imprinting and maternal genotype effects facilitates detection of new genes, [International Genetic Epidemiology Society \(IGES\)](#), Heidelberg (Germany), 18-20 Sept. 2011, **Genetic Epidemiology**. 2012; 36(2):122-3 – Oral presentation.
81. **Sarnowski C**, Carbonell P, Elati M, Faulon JL. Prediction of catalytic efficiency to discover new enzymatic activities, Fourth International Workshop on Machine Learning in Systems Biology, Edinburgh (Scotland), 15-16 Oct. 2010, **Proc. of Machine Learning in Systems Biology**. 2010, p153-156 – Poster presentation.

B. Peer Reviewed Publications

1. Wang N, DiCorpo DA, Zhang Y, Kleinbrink E, Arnett DK, Barnard J, Blangero J, Bowden DW, Carson AP, Chen YI, Chung MK, Curran JE, Darbar D, Duggirala R, Ellinor PT, Fatkin D, Fornage M, Heard-Costa N, He J, Hou L, Kardia SLR, Kooperberg C, Loos RJF, McManus DD, Mitchell BD, Minster RL, North KE, Psaty BM, Raffield LM, Redline S, Rich SS, Roden D, Rotter JI, Shoemaker MB, Smith JD, Van Wagoner DR, Aguet F, Ardlie K, Bis JC, Brody JA, Cade BE, Clish CB, de Vries PS, Floyd JS, Freedman BI, Gabriel S, Gerzsten RE, Goodarzi MO, Gu C, Guo X, Gupta N, Heckbert SR, Hsu S, Hung YJ, Kalyani RR, Kelly TN, Kinney GL, Li C, Liu S, Liu Y, Lloyd-Jones DM, Manson JE, Mathias

- RA, Mercader JM, Morrison AC, Naseri T, Onengut S, Palmer ND, Peyser PA, Qi Q, Raghavan S, Reiner AP, Rooney MR, Sevilla-Gonzalez M, **Sarnowski C**, Smith JD, Smith JA, Spartano NL, Tahir U, Taylor KD, Tobias DK, Tracy RP, Viali S, Wang H, Wood AC, Yanek LR, Zhao W, Zheng Y, Dupuis J, Liu CT, Sladek R, Wessel J, Meigs JB, Manning AK; NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium. Colocalization of eQTLs With Type 2 Diabetes and Glycemic Traits Using Whole-Genome Sequences in Diverse Populations From the NHLBI Trans-Omics in Precision Medicine (TOPMed) Program. **Diabetes**. 2026 Aug 1;75:1477-1491.
2. Wyss AB, Brown M, Li X, Spitzer BW, Huang Z, Wang H, Saxena R, Gallo L, Qi Q, Tarraf W, Kaplan R, Lamar M, González HM, DeCarli C, Fornage M, Rotter JI, Rich SS, Taylor KD, Guo X, Wood AC, Liu PY, Heckbert SR, **Sarnowski C**, Bressler J, Morrison AC, Yu B, Lutsey PL, Isasi CR, Redline S, Sofer T. Using Polygenic Risk Scores to Evaluate Definitions of Self-Reported Sleep Phenotypes Across Cohorts. **Sleep**. 2026 Jul 21.
3. Zhang Y, Nguyen NQH, Hanson PA, Sevilla-Gonzalez M, Haessler J, **Sarnowski C**, Yao J, Yu B, Jamshidi A, Boerwinkle E, Brown MR, Chen Z, Ida Chen Y, Clish C, DiCorpo D, Durda P, Gerszten R, Goodarzi MO, Guo X, Heard-Costa NL, Johnson WC, Kooperberg C, Pankow JS, Post WS, Reiner AP, Rich SS, Rotter JI, de Vries PS, Wood AC, Taylor KD, Manning AK, Dupuis J, Meigs JB, Liu CT. Plasma metabolomic profiles associated with cardiovascular disease in type 2 diabetes from the Trans-Omics for Precision Medicine (TOPMed) program. **Atherosclerosis** 2026 Jun:417:120758.
4. **Sarnowski C**, Zhang Y, Ammous F, [...], Fornage M, Seshadri S, Morrison AC. Association of genetic scores related to insulin resistance with neurological outcomes in ancestrally diverse cohorts from the Trans-Omics for Precision Medicine (TOPMed) program. **Commun Biol**. 2025 Sep 24;8(1):1352.
5. Shin J, Bressler J, Grove ML, Brown M, Selvin E, Pankow JS, Fornage M, Morrison AC, **Sarnowski C**. DNA methylation markers of insulin resistance surrogate measures in the Atherosclerosis Risk in Communities (ARIC) Study. **Epigenetics**. 2025 Dec;20:2498857.
6. Wang Y*, **Sarnowski C***, Lin H, Pitsillides AN, Heard-Costa NL, Choi SH, Wang D, Bis JC, Blue EE, Boerwinkle E, De Jager PL, Fornage M, Wijsman EM, Seshadri S, Dupuis J, Peloso GM, DeStefano AL. Key variants via Alzheimer's Disease Sequencing Project whole genome sequence data. **Alzheimers Dement**. 2024 May;20:3290-3304.
7. Suzuki K, Hatzikotoulas K, Southam L, [...], **Sarnowski C**, [...], Voight BF, Morris AP, Zeggini E. Genetic drivers of heterogeneity in type 2 diabetes pathophysiology. **Nature**. 2024 Feb 19.
8. Hasbani NR, Westerman KE, Heon Kwak S, [...], **Sarnowski C**, [...], Meigs JB, Manning AK, de Vries PS. Type 2 Diabetes Modifies the Association of CAD Genomic Risk Variants With Subclinical Atherosclerosis. **Circ Genom Precis Med**. 2023 Nov 28:e004176.
9. **Sarnowski C**, Huan T, Ma Y, Joehanes R, Beiser A, DeCarli CS, Heard-Costa NL, Levy D, Lin H, Liu CT, Liu C, Meigs JB, Satizabal CL, Florez JC, Hivert MF, Dupuis J, De Jager PL, Bennett DA, Seshadri S, Morrison AC. Multi-tissue epigenetic analysis identifies

- distinct associations underlying insulin resistance and Alzheimer's disease at *CPT1A* locus. ***Clin Epigenetics***. 2023 Oct 27;15:173.
10. Bouzid H, Belk JA, Jan M, [...], **Sarnowski C**, Satpathy AT, Montine TJ, Jaiswal S. Clonal hematopoiesis is associated with protection from Alzheimer's disease. ***Nat Med***. 2023 Jul;29:1662-1670.
 11. Williamson A, Norris DM, Yin X, [...], **Sarnowski C**, [...], O'Rahilly S, Fazakerley DJ, Langenberg C. Genome-wide association study and functional characterization identifies candidate genes for insulin-stimulated glucose uptake. ***Nat Genet***. 2023 Jun;55:973-983.
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 14. Zhang Y, Meigs JB, Liu CT, Dupuis J, **Sarnowski C**. Leveraging family history in genetic association analyses of binary traits. ***BMC Genomics***. 2022 Oct 1;23:678.
 15. DiCorpo D, Gaynor SM, Russell EM, [...], **Sarnowski C**, [...], Meigs JB, Wessel J, Manning AK. Whole genome sequence association analysis of fasting glucose and fasting insulin levels in diverse cohorts from the NHLBI TOPMed program. ***Commun Biol***. 2022. Jul 28;5:756.
 16. Mahajan A, Spracklen CN, Zhang W, [...], **Sarnowski C**, [...], Rotter JI, McCarthy MI, Morris AP. Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. ***Nat Genet***. 2022 May;54:560-572
 17. **Sarnowski C**^{*}, Ghanbari M^{*}, Bis JC^{*}, Logue M^{*}, Fornage M^{*}, Mishra A^{*}, [...], DeBette S^{**}, Dufouil C^{**}, Launer LJ^{**}, Kremen WS^{**}, Longstreth WT^{**}, Ikram MA^{**}, Seshadri S^{**}. Meta-analysis of genome-wide association studies identifies ancestry-specific associations underlying circulating total tau levels. ***Commun Biol***. 2022 Apr 8;5:336
 18. Bellenguez C, Küçükali F, Jansen IE, [...], **Sarnowski C**, [...], Ruiz A, Ramirez A, Lambert JC. New insights into the genetic etiology of Alzheimer's disease and related dementias. ***Nat Genet***. 2022 Apr;54:412-436
 19. DiCorpo D, LeClair J, Cole JB, **Sarnowski C**, [...], Meigs JB, Dupuis J, Udler MS. Type 2 Diabetes Partitioned Polygenic Scores Associate With Disease Outcomes in 454,193 individuals Across 13 Cohorts. ***Diabetes Care***. 2022 Mar 1;45:674-683.
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 21. Hu Y, Haessler JW, Manansala R, [...], **Sarnowski C**, [...], Auer PL, Reiner AP, Kooperberg C. Whole-Genome Sequencing Association Analyses of Stroke and Its

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 23. Ruth KS, Day FR, Hussain J, [...], **Sarnowski C**, [...], Murray A, Roig I, Perry JRB. Genetic insights into biological mechanisms governing human ovarian ageing. **Nature**. 2021 Aug;596:393-397.
 24. **Sarnowski C**, Chen H, Biggs ML, [...], Kiel DP, Murabito JM, Lunetta KL. Identification of novel and rare variants associated with handgrip strength using whole genome sequence data from the NHLBI Trans-Omics in Precision Medicine (TOPMed) Program. **PLoS One**. 2021 Jul2;16:e0253611.
 25. **Sarnowski C**, Cousminer DL, Franceschini N, [...], Zheng W, Murabito JM, Lunetta KL. Large trans-ethnic meta-analysis identifies AKR1C4 as a novel gene associated with age at menarche. **Hum Reprod**. 2021 Jun 18;36:1999-2010.
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