SARNOWSKI Chloé, Ph.D.

Work address: Department of Epidemiology, Human Genetic Center, University of Texas Health Sciences Center at Houston, School of Public Health, 1200 Pressler St, Houston, TX 77030, USA
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EDUCATION

2011-2015 **PhD in Statistical Genetics,** Paris-Sud University, France

2010-2011 **2nd year of M.S. in Genomics and Statistical Genetics (GGS)**, with honors, Evry Val d'Essonne University, France

2008-2010 **B.S. and 1st year of M.S. in Biological and Computer Engineering**, with honors, Evry Val d'Essonne University, France

PROFESSIONAL EXPERIENCES

Research Activities

2022- **Assistant Professor**, Department of Epidemiology, University of Texas Health Sciences Center, School of Public Health, Houston, TX

2021-2022 **Faculty Associate**, Department of Epidemiology Human Genetics and Environmental Sciences, University of Texas Health Sciences Center, School of Public Health, Houston, TX

2019-2020 **Instructor in Biostatistics**, Department of Biostatistics, Boston University School of Public Health, Boston, MA

2016-2019 **Postdoctoral associate in Statistical Genetics**, supervised by J. Dupuis, Department of Biostatistics, Boston University School of Public Health, Boston, MA

2011-2015 **PhD in Statistical Genetics** supervised by E. Bouzigon and F. Demenais, UMR-946, Inserm - Paris Diderot University, Paris, France. Association studies taking into account complex mechanisms: application to asthma.

2011 **Research Engineer in Statistics**, UMR-946, Inserm - Paris Diderot University, Paris, France (3 months).

2011 **M.S internship in Statistical Genetics** supervised by E. Bouzigon, UMR-946, Inserm - Paris Diderot University, Paris, France (5 months). Association study taking into account a parental imprinting mechanism: application to asthma and allergic rhinitis comorbidity and to 4q35 polymorphisms.

2010 **M.S internship in Computational Chemistry** supervised by M. Elati and JL. Faulon, Institute of Systems & Synthetic Biology (ISSB), Evry, France (4 months). Prediction of enzymatic activities: application to the screening of *Acinetobacter baylyi* orfeome.

2009 **B.S internship in Biology** supervised by S. Mateos, Watchfrog, Evry, France (3 months). Detection of endocrine disruptors using small model organisms.

Teaching

2024 Co-instructor – Quantitative Analysis for Public Health Research and Practice PH 2858 Spring 2024

2023 Accessing and Analyzing Whole Genome Sequence Data, Neurepiomics Course, 07-09 October 2023, San Antonio, TX

2023 Co-instructor – Quantitative Analysis for Public Health Research and Practice PH 2858 Spring 2023

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

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

2018	A practical Introduction to the analysis of sequence data with EPACTS. Neurepiomics Course, 17-20 September 2018, Bordeaux, France
	Instructor and Research Mentor - Summer Institute for Research Education in Biostatistics
	Dialogue on Dementia: Can new genetic insights help us find better prevention and treatments for dementia? 14 June 2018, San Antonio, TX
	Co-instructor – Introduction to statistical computing SPH BS723 Spring 2018
2017	A practical Introduction to the analysis of sequence data with EPACTS. Genomics workshop, 1st May 2017, Boston, MA
	Teacher Assistant – Introduction to statistical computing SPH BS723 Spring 2017
2016	A practical Introduction to the analysis of sequence data with EPACTS. Neurepiomics Course, 23-26 September 2016, Boston, MA
2012	Course of Medical Genetics at the "Reproduction and infertility" department at Cochin Institute, Paris, France

Advising

2024	Supervisor of a GRA Student (Hari Kishan Indupuru) on genetic association analyses of insulin resistance stratified by APOE4 in the Framingham Heart Study (FHS)
2023-	Supervisor of a Biostatistician (Jeewoen Shin)
2022-2023	Supervisor of a GRA Student (Jiyuan Tang) on derivation of genetic predictors using machine learning techniques in the Trans-Omics for Precision Medicine (TOPMed) Program
2021-	Faculty Academic Advisor at UTH SPH for MPH students in Epidemiology
2020-2022	Supervisor of a PhD student in Biostatistics (Yixin Zhang) at Boston University School of Public Health (BUSPH) on a project comparing family-based methods applied to association analyses of type 2 diabetes in the Framingham Heart Study (manuscript published in BMC Genomics in 2022).
2020-2023	Supervisor of a PhD student in Epidemiology and Biostatistics (Lincoln Shade) at the University of Kentucky College of Medicine on whole genome sequence association analyses of brain volumes in the Trans-Omics for Precision Medicine (TOPMed) Program.

LAB ACTIVITIES

2011-2015	Organization of UMR-946 Journal Club meetings
2018-2020	Organization of FHS-OMICS Conference Series (FOCuS)

MEMBER OF SCIENTIFIC SOCIETIES

- International Genetic Epidemiology Society (Chair of the Young Investigators Committee, 2021-2024; Member of the Board of Directors, 2024-2026)
- American Society of Human Genetics

DISTINCTIONS

- Tiger Award for the contribution to the consortium at the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) conference (St Louis, 27-28 June 2019)
- Best poster and financial price at the Genome Science Institute Research Symposium (Boston, 15 Nov 2018)
- Finalist of the James V. Neel Award at the International Genetic Epidemiology Society (IGES) meeting (Cambridge, 09-11 Sept 2017)
- Oral presentation and financial price at the Genome Science Institute Research Symposium (Boston, 16 Nov 2016)
- Best abstract from a young investigator submitted to Assembly 6 "Occupation and Epidemiology Assembly" at the European Respiratory Society (London, 03-07 Sept 2016)

PUBLICATIONS/COMMUNICATIONS

Publications in peer-reviewed international journals (53)

https://www.ncbi.nlm.nih.gov/myncbi/chloe.sarnowski.1/bibliography/public/

1. 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(5):3290-3304.
2. 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 Mar;627(8003):347-357.
3. 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.
4. **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(1):173.
5. 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(7):1662-1670.
6. 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(6):973-983.
7. **Sarnowski C**, Conomos MP, Vasan RS, Meigs JB, Dupuis J, Liu CT, Leong A. Genetic Effect on Body Mass Index and Cardiovascular Disease Across Generations. ***Circ Genom Precis Med***. 2023 Feb;16(1):e003858..
8. Mishra A, Malik R, Hachiya T, [...], Kamatani Y, Dichgans M, Debette S. Stroke genetics informs drug discovery and risk prediction across ancestries. ***Nature***. 2022 Nov;611(7934):115-123.
9. 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(1):678.
10. 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.
11. 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
12. **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
13. 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
14. 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.
15. Longchamps RJ, Yang SY, Castellani CA, [...], **Sarnowski C**, [...], Boerwinkle E, Pankratz N, Arking DE. Genome-wide analysis of mitochondrial DNA copy number reveals loci implicated in nucleotide metabolism, platelet activation, and megakaryocyte proliferation. ***Hum Genet***. 2022 Jan;141:127-146.

16. Hu Y, Haessler JW, Manansala R, […], **Sarnowski C**, […], Auer PL, Reiner AP, Kooperberg C. Whole-Genome Sequencing Association Analyses of Stroke and Its Subtypes in Ancestrally Diverse Populations From Trans-Omics for Precision Medicine Project. ***Stroke***. 2022 Mar;53:875-885.

17. Merino J*, Dashti HS*, **Sarnowski C***, […], Dupuis J#, Florez JC#, Saxena R#. Genetic analysis of dietary intake identifies new loci and functional links with metabolic traits. ***Nat Hum Behav***. 2022 Jan;6(1):155-163.

18. 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(7872):393-397.

19. **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(7):e0253611.

20. **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(7):1999-2010.

21. **Sarnowski C**, Huan T, Jain D, 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. ***Genet Epidemiol***. 2021 Apr;45(3):280-292.

22. Taliun D, Harris DN, Kessler MD, […], **Sarnowski C**, […], Hernandez RD, O'Connor TD, Abecasis GR. Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. ***Nature***. 2021 Feb;590(7845):290-299.

23. Jones G, Trajanoska K, Santanasto AJ, […], **Sarnowski C**, […], Rivadeneira F, Kiel DP, Pilling LC. Genome-wide meta-analysis of muscle weakness identifies 15 susceptibility loci in older men and women. ***Nat Commun***. 2021 Jan 28;12(1):654.

24. Sargurupremraj M*, Suzuki H*, Jian X*, **Sarnowski C***, Evans TE*, Bis JC*, […], Adams HH, Matthews PM, Fornage M**, Debette S**. Cerebral small vessel disease genomics and its implications across the lifespan. ***Nat Commun***. 2020 Dec 8;11(1):6285.

25. Bis JC, Jian X, Kunkle BW, […], **Sarnowski C**, […], Naj AC, Fornage M, Farrer LA. Whole Exome Sequencing Study Identifies Novel Rare and Common Alzheimer's-Associated Variants Involved in Immune Response and Transcriptional Regulation. ***Mol Psychiatry***. 2020 Aug;25(8):1859-1875.

26. Merino J, Dashti HS, Li SX, **Sarnowski C**, […], Deloukas P, Lyytikäinen LP, Chasman DI, Chu AY, Tanaka T. Genome-wide meta-analysis of macronutrient intake of 91,114 European ancestry participants from the cohorts for heart and aging research in genomic epidemiology consortium.. ***Mol Psychiatry***. 2019 Dec;24(12):1920-1932.

27. **Sarnowski C***, Leong A*, Raffield LM, […], Manning AK, Dupuis J, Meigs J, on behalf of the Trans-Omics for Precision Medicine (TOPMed) Diabetes and TOPMed Hematology and Hemostasis working groups and the NHLBI TOPMed Consortium. Impact of rare and common genetic variants on diabetes diagnosis by hemoglobin A1c in multi-ancestry cohorts: The Trans-Omics for Precision Medicine Program. ***Am J Hum Genet***. 2019. Oct 3;105(4):706-718.

28. Sugier PE, **Sarnowski C**, Granell R, […], Kogevinas M, Demenais F, Bouzigon E. Genome-wide interaction study of early-life smoking exposure on time-to-asthma onset in childhood. ***Clin Exp Allergy***. 2019 Oct;49(10):1342-1351.

29. Deelen J, Evans DS, Arking DE, […], **Sarnowski C**, […], Lunetta KL, Slagboom PE, Murabito JM. A meta-analysis of genome wide association studies identifies multiple longevity genes. ***Nat Commun***. 2019 Aug 14;10(1):3669.

30. Merino J, Guasch-Ferré M, Ellervik C, Dashti HS, Sharp SJ, Wu P, Overvad K, **Sarnowski C**, […], Dupuis J, Smith CE, Kilpeläinen TO, Chasman DI, Florez JC. Quality of dietary fat and genetic risk of type 2 diabetes: individual participant data meta-analysis. ***BMJ***. 2019 Jul 25;366:l4292.

31. Dizier MH, Margaritte-Jeannin P, Pain L, **Sarnowski C**, Brossard M, Mohamdi H, Lavielle N, Babron MC, Just J, Lathrop M, Laprise C, Bouzigon E, 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. ***Thorax***. 2019 Mar;74:254-260.

32. Kunkle BW, Grenier-Boley B, Sims R, […], **Sarnowski C**, […], Schellenberg GD, Lambert JC, Pericak-Vance MA. Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates Aβ, tau, immunity and lipid processing. ***Nat Genet***. 2019 Mar;51:414-430.

33. Mahajan A, Taliun D, Thurner M, Robertson NR, Torres JM, Rayner NW, Payne AJ, Steinthorsdottir V, Scott RA, Grarup N, Cook JP, Schmidt EM, Wuttke M, **Sarnowski C**, […] Gloyn AL, Morris AP, Boehnke M, McCarthy MI. Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. ***Nat Genet***. 2018 Nov;50:1505-1513.

34. Fuady AM*, Lent S*, **Sarnowski C***, Tintle NL. Application of novel and existing methods to identify genes with evidence of epigenetic association: results from GAW20. ***BMC Genet***. 2018 Sep 17;19(Suppl 1):72.

35. Lent S, Xu H, Wang L, Wang Z, **Sarnowski C**, Hivert MF, Dupuis J. Comparison of novel and existing methods for detecting differentially methylated regions. ***BMC Genet***. 2018 Sep 17;19(Suppl 1):84.

36. **Sarnowski C**, Lent S, Dupuis J. Investigation of parent-of-origin effects induced by fenofibrate treatment on triglycerides levels. ***BMC Genet***. 2018 Sep 17;19(Suppl 1):83.

37. Fisher VA, Wang L, Deng X, **Sarnowski C**, Cupples LA, Liu CT. Do changes in DNA methylation mediate or interact with SNP variation? A pharmacoepigenetic analysis. ***BMC Genet***. 2018 Sep 17;19(Suppl 1):70.

38. **Sarnowski C**, Hivert MF. Impact of Genetic Determinants of HbA1c on Type 2 Diabetes Risk and Diagnosis. ***Curr Diab Rep***. 2018 Jun 21;18:52.

39. Sugier PE, Brossard M*, **Sarnowski C***, Vaysse A, Morin A, Pain L, Margaritte-Jeannin P, Dizier MH, Lathrop M, Laprise C‡, Demenais F‡, Bouzigon E‡. *A novel role for ciliary function in atopy: ADGRV1 and DNAH5 interactions.* ***J Allergy Clin Immunol***, 2018 May;141:1659-1667.

40. **Sarnowski C**, Kavousi M, Isaacs S, Demerath EW, Broer L, Muka T, Larson MG, Franco OH, Ikram MA, Uitterlinden A, Franceschini N, Lunetta KL, Murabito JM. Genetic variants associated with earlier age at menopause increase the risk of cardiovascular events in women. ***Menopause***. 2018 Apr;25:451-457.

41. Malik R, Chauhan G, Traylor M, […], **Sarnowski C**, […], Kamatani Y, Debette S, Dichgans M; MEGASTROKE Consortium. Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. ***Nat Genet.*** 2018 Apr;50:524-537

42. Dizier MH, Margaritte-Jeannin P, Babron MC, Laprise C, Lavielle N, **Sarnowski C**, Brossard M, Moffatt M, Gagné-ouellet V, Etcheto A, Lathrop M, Just J, Cookson WOC, Bouzigon E, Demenais F. The *COL5A3* and *MMP9* genes interact in eczema susceptibility. ***Clin Exp Allergy***. 2018 Mar;48:297-305.

43. **Sarnowski C**, Satizabal CL, DeCarli CS, Pitsillides AN, Cupples AL, Vasan SR, Wilson JG, Bis JC, Fornage M, Beiser AS, DeStefano AL, Dupuis J, Seshadri S, on behalf of the TOPMed Neurology working group. Whole genome sequence analyses of brain imaging measures in the Framingham Study. ***Neurology***. 2018 Jan 16;90:e188-e196

    https://www.alzforum.org/news/research-news/new-genetic-variants-associated-brain-imaging-traits

    https://www.alzforum.org/news/conference-coverage/searching-new-ad-risk-variants-move-beyond-gwas

44. Liu Y, Brossard M, Roqueiro D, Margaritte-Jeannin P, **Sarnowski C**, Bouzigon E, Demenais F. SigMod: an exact and efficient method to identify a strongly interconnected disease-associated module in a gene network. ***Bioinformatics***. 2017 May 15; 33:1536-1544.

45. Nieuwenhuis MAE, Vonk JM, Himes BE, **Sarnowski C**, Minelli C, Jarvis D, Bouzigon E, Nickle DC, Laviolette M, Sin D, Weiss ST, van den Berge M, Koppelman GH, Postma DS. *PTTG1IP* and *MAML3*, novel GWAS genes for severity of hyperresponsiveness in adult asthma. ***Allergy.*** 2017 May; 72:792-801.

46. Liu Y, Brossard M, **Sarnowski C**, Vaysse A, Moffatt M, Margaritte-Jeannin P, Llinares F, Dizier M-H, Lathrop M, Cookson W, Bouzigon E, Demenais F. Network-assisted analysis of GWAS data identifies a functionally-relevant gene module for childhood-onset asthma. ***Sci Rep***. 2017 Apr 20; 7:938.

47. **Sarnowski C**, Sugier P-E, Granell R, Jarvis D, Dizier M-H, Ege M, Imboden M, Laprise C, Khusnutdinova E, Freidin M, Cookson W.O.C, Moffatt M, Siroux V, Lathrop M, Ogorodova L, Karunas A, James A, Probst-Hensch N, Von Mutius E, Pin I, Kogevinas M, Henderson AJ, Demenais F, Bouzigon E. Identification of a new locus at 16q12 associated with time-to-asthma onset. ***J Allergy Clin Immunol***. 2016 Oct; 138:1071-1080.

    Koppelman G: **F1000Prime Recommendation** of [Sarnowski C, Sugier PE et al., J Allergy Clin Immunol 2016]. In F1000Prime, 20 Jun 2016; DOI: 10.3410/f.726322993.793519541. F1000Prime.com/726322993#eval793519541

48. **Sarnowski C**, Laprise C, Malerba G, Moffatt M, Dizier M-H, Morin A, Vincent Q, Rohde K, Esparza-Gordillo J, Margaritte-Jeannin P, Liang L, Lee Y-A, Siroux V, Bousquet J, Pignatti P.F, Cookson W.O.C, Pastinen T, Lathrop M,

Demenais F, Bouzigon E. DNA methylation within *MTNR1A* mediates paternally transmitted genetic variant effect on asthma-plus-rhinitis. ***J Allergy and Clin Immunol*** 2016 Sep; 138:748-53.

49. Madore A-M, T. Vaillancourt V, Bouzigon E, **Sarnowski C**, Monier F, Dizier M-H, Demenais F, Laprise C. Genes Involved in Interleukin-1 Receptor Type II Activities are Associated with Asthmatic Phenotypes. ***Allergy Asthma Immunol Res***. 2016 Sep; 8:466-70.
50. Dizier M-H, Nadif R*, Margaritte-Jeannin P*, Barton S.J, **Sarnowski C**, Gagné-Ouellet V, Brossard M, Lavielle N, Just J, Lathrop M, Holloway J, Laprise C**, Bouzigon E**, Demenais F, Interaction between *DNAH9* gene and early smoke exposure in bronchial hyper-responsiveness. ***Eur Respir J***. 2016 Apr; 47:1072-81.
51. Bouzigon E, Nadif R, Le Moual N, Dizier MH, Aschard H, Boudier A, Bousquet J, Chanoine S, Donnay C, Dumas O, Gormand F, Jacquemin B, Just J, Margaritte-Jeannin P, Matran R, Pison C, Rage E, Rava M, **Sarnowski C**, Smit L.A.M, Temam S, Varraso R, Vignoud L, Lathrop M, Pin I, Demenais F, Kauffmann F, Siroux V. Facteurs génétiques et environnementaux de l'asthme et de l'allergie; Etude EGEA : Synthèse des résultats. ***Rev Mal Respir***. 2015 Oct; 32:822-40.
52. Bouzigon E, Nadif R, Thompson EE, Concas MP, Kuldanek S, Du G, Brossard M, Lavielle N, **Sarnowski C**, Vaysse A, Dessen P, van der Valk RJ, Duijts L, Henderson AJ, Jaddoe VW, de Jongste JC; GABRIEL consortium; EArly Genetics & Lifecourse Epidemiology (EAGLE) Consortium, Casula S, Biino G, Dizier MH, Pin I, Matran R, Lathrop M, Pirastu M, Demenais F, Ober C. A Common variant in *RAB27A* gene is associated with fractional exhaled nitric oxide levels in adults. ***Clin Exp Allergy***. 2015 Apr; 45:797-806.
53. Dizier MH, Margaritte-Jeannin P, Madore AM, Moffatt M, Brossard M, Lavielle N, **Sarnowski C**, Just J, Cookson W, Lathrop M, Laprise C, Bouzigon E, Demenais F. The nuclear factor I/A (*NFIA*) gene is associated with the asthma plus rhinitis phenotype. ***J Allergy Clin Immunol***. 2014 Sep; 134:576-582.

Presentations at international meetings (22 talks, 51 posters, 2 blitz)

1. **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.
2. 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.
3. **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.
4. **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.
5. **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.
6. **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.

7. **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.

8. **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.

9. **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.

10. **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.

11. 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.

12. 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.

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Exploring Common Biological Pathways Underlying Insulin Resistance and Alzheimer Disease using Genetics and Omic Tools

This research project aims to better characterize the biological mechanisms involved in insulin resistance and their role in Alzheimer's disease. The proposed research is *relevant to public health* as it is expected to provide new ways to prevent, delay or treat Alzheimer's disease, by targeting insulin sensitivity. Thus, the project is *relevant to the part of the NIH's mission* that pertains to improving fundamental knowledge that will help to reduce the burdens of complex human diseases such as Alzheimer's disease.

Role: Principal Investigator