BENJAMIN F. VOIGHT
CURRICULUM VITAE

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CV last updated: February 2024

EMPLOYMENT HISTORY

2017–Present	Associate Professor (with tenure), Department of Systems Pharmacology and Translational Therapeutics Department of Genetics University of Philadelphia - Perelman School of Medicine Philadelphia, PA
2012–2017	Assistant Professor, Department of Genetics University of Philadelphia - Perelman School of Medicine
2011–2017	Assistant Professor, Department of Systems Pharmacology and Translational Therapeutics, University of Pennsylvania
2006–2011	Postdoctoral Research Fellow (2006-2009) Research Scientist (2009-2011) Advised by Drs. Mark Daly and David Altshuler Massachusetts General Hospital and The Broad Institute of Harvard and MIT, Cambridge, MA

EDUCATION

2006	Ph.D., Advised by Drs. Jonathan Pritchard and Nancy Cox Human Genetics, University of Chicago
2001	B.S. in Biology and B.A. Mathematics University of Washington, Seattle [Transferred from Gonzaga University, Spokane, WA, in 1999]

CURRENT RESEARCH SUPPORT

As PI:

2024-2029 U24 DK138512: *"An interactive resource to generate and provide integrated knowledge of the human pancreas"* (MPIs: K. Gaulton, **B. Voight**, J. Flannick, N. Burtt, A. Gloyn)
Objective: The proposed project will create 'PanKBase': a database for the pancreas of high-value summary data, an analytical library of tools to extract knowledge from data, resources using statistical modeling and machine learning, an open science platform enabling all users to perform analyses and access data, and a robust engagement and outreach program.

2020–2025 UM1 DK126194: *"Functional interrogation of T2D-associated genes in human stem-cell derived models and mice*" (MPIs: P. Seale, **B. Voight**, D. Rader, S. Grant, K. Kaestner, W. Yang)
Objective: Using human genetics data and computational prioritization tools, identify and functionally validate candidate genes underlying susceptibility to type 2 diabetes.

Additional:

2022–2027 VA BX006159: "*Leveraging the genetics of carotid stenosis for identifying novel risk factors and therapeutic opportunities"* (PI: S. Damrauer). Role: Co-I.
Objective: Use human genetics data to identify and characterize causal risk factors underlying carotid stenosis.

2020–2024 U01 DK123594: "*The human pancreas analysis program for type 2 diabetes.*" (PIs: K. Kaestner, A. Naji). Role: Co-I.
Objective: Obtain primary pancreatic islet specimens from deceased donors, perform multi-omics profiling and in-vivo functional characterization of islet function, and release all data to the research community.

2020–2024 R01 DK087635: *"Epigenetic Landscape of Chronic Kidney Disease.*" (PI: K. Susztak). Role: Co-I
Objective: Perform large-scale association studies for measures of kidney function (eGFR) and perform multi-omics profiling to identify variants and genes underlying susceptibility to chronic kidney disease.

2016–2026 UL1 TR001878: Institutional Clinical and Translational Science Award. Role: Key personnel.
Objective: This provides modest support for my training role as Associate Director for the Bioinformatics concentration in the Masters in Translational Research program. In this role, I serve as a bioinformatics mentor for clinicians who aim to develop bioinformatics training towards developing independence as translational researchers.

2021–2024 R01 AI146026: "*Promoter interactome-aided mapping of unexplored CVID genetic landscapes*." (PI: N. Romberg). Role: Co-I
Objective: To identify causal genets underlying CVID, our contribution is to create maps of variation associated with change in gene expression (eQTLs) in primary pediatric immune tissues (obtained from tonsils).

2023–2024 I21 HX003714: "*Precision Pharmacogenomic Perioperative Prediction"* (PI: T. Barrett). Role: Co-I
Objective: The goal of this pilot study is to improve the VA Surgical Quality Improvement Program by incorporating pharmacogenetic information into prediction.

COMPLETED SUPPORT

As PI:

2022–2023 Institute of Translational Medicine and Therapeutics Pilot Grant. *"Interplay of obesity and volumetric breast density with respect to breast cancer risk"* (PIs: A.M. McCarthy, D. Kontos, **B. Voight**)
Objective: Perform genome-wide association for volumetric breast density and use human genetics to perform causal inference between volumetric breast density and risk to cancer.

2020–2022 Penn Chronobiology and Sleep Institute Pilot Project. "*Discovery and analysis of human genetic variation associated with circadian gene expression levels*" (PIs: **B. Voight**, C. Brown, no award number)
Objective: A pilot project to develop computational tools to identify variation associated with gene expression over circadian (24 hour) time.

2014–2021 NIH R01/R56 DK101478: *"Algorithms to identify non-coding mutational burden and disease-relevant pathways"*
Objective: The goal of this proposal was to develop computational approaches to understand the role of non-coding mutational burden in type 2 diabetes.

2019–2020 T2D Accelerating Medicine Partnerships (PIs: K. Susztak, B. Voight, M. Lazar, C. Brown), *"Prioritizing causal genes and variants for diabetic kidney disease"*
Objective: The goal of this proposal was to identify genetic variation associated with change in gene expression in primary kidneys of patients with diabetic kidney disease.

2019–2020 Linda Pechenik Montague Investigator Award (no award number)

Objective: This (non-project) award supported human genetics and causal inference studies across hematopoietic and anthropometric traits.

2018–2019 NIH R01 DK101478 S1, Supplemental support to applying developed methods to Alzheimer's disease and related traits
Objective: The purpose of this supplement was to perform multi-trait association studies between Alzheimer's disease and neurocognitive traits and cardiometabolic traits.

2016–2019 ITMAT Maturational Human Biology Pilot Grant: *"Characterizing the genetic determinants of pubertal timing and body weight regulation"*
Objective: The goal of this pilot study was to perform association studies for puberty and obesity during pediatric development.

2012–2016 AHA 13SDG14330006: "*Human genetics of high-density lipoprotein to elucidate the etiology of heart disease*"
Objective: The goal of this study was to further explore the role of variants linked to lipid levels and heart disease risk, and develop new tools for polygenic risk score prediction.

2013–2014 H1201 W.W. Smith Charitable Trust: "*Identifying the etiological basis for heightened risk of cardiovascular disease in the context of glycemic disorder*"
Objective: The goal of this study was to perform multi-trait association and causal inference studies between type 2 diabetes and heart disease.

2012–2014 Alfred P. Sloan Foundation Fellowship (No award number)
Objective: This fellowship supported computational methods to identify balancing selection and characterize the frequency of polymorphism levels in human populations

Additional:

2021–2023 T01 BX003362: "*Genetics of Cardiometabolic Diseases in the VA Population*." (PI: P. Tsao, K-M. Chang). Role: Co-I
Objective: Using human genetics data from the Million Veteran Program to identify and characterize risk factors for complex metabolic disease, including type 2 diabetes, cardiovascular disease, and liver disease.

2021–2022 MVP-DOE2: "*Phenotypic and Genomic Architecture of Cardiovascular Disease Sub*types." (PI: S. Damrauer). Role: Co-I
Objective: Use human genetics data to characterize the basis of peripheral artery disease and perform causal inference studies.

2019-2020 NIH R01 HG010067: "*Network-based algorithms for target identification and drug repositioning from genetic associations,"* Role: Co-I (PI: C. Greene)
Objective: Apply tools from network-based approaches with human genetics to identify leads for drug repurposing.

2018–2021 MVP-DOE2, "*Phenotypic and Genomic Architecture of Cardiovascular Disease Subtypes*" Role: Co-I (PIs: S. Damrauer)
Objective: Use human genetics data to characterize the basis of peripheral artery disease and perform causal inference studies.

2015–2016 March of Dimes Preterm Birth Research Center Grant. (Role: Co-Investigator).
Objective: To characterize the genetics of pre-term birth and causal genes.

PENDING SUPPORT

As PI:

2024-2029 R01 HG013499. *"Methods for inference of mutation rate and functional constraint with applications in human health".* (MPIs: Z. Gao, I. Mathieson, **B. Voight (contact)**)
Objective: Using a novel computational method we recently developed this proposal will create best-in-class models that capture variability in mutation rates across species, quantifying functional constraint in across the human genome, applying that knowledge to prioritize variants at non-coding complex disease associated signals likely to be causal. *(15th percentile)*

2024-2029 R01 DK140340. *"Mapping the gene regulatory architecture of pancreatic islet-specific cell types to diabetes".* (MPIs: K. Gaulton, **B. Voight (contact)**)
Objective: Use single-cell genomics data generated from pancreatic islets to map variation associated with expression and chromatin accessibility and to characterize cis-regulatory elements across all islet-specific cell types.

2024–2029 R01 NIDDK # pending. *"Target validation for metabolic dysfunction-associated steatotic liver disease using computational approaches and in vivo deep phenotyping*" (MPIs: M. den Hoed, **B. Voight (contact)**)
Objective: To characterize causal variants and genes for non-alcoholic fatty liver disease and perform medium-throughput functionally validation of candidates using the zebrafish model system using high dimension imaging analysis.

AWARDS AND HONORS

2019 Recipient of the Linda Pechenik Montague Investigator Award (see also Grants)

2017	Penn Medicine Award of Excellence Recipient: The Michael S. Brown New Investigator Research Award
2017	Recipient of the 2014 Presidential Early Career Award for Scientist and Engineers (PECASE), Department of Health and Human Services
2012	Selected Alfred P. Sloan Research Fellow (see also Grants)
2009	Semi-finalist, Trainee Research Award, 59th Meeting of the American Society of Human Genetics
2007	Team Award for Outstanding Research, Clinical Research Day, Massachusetts General Hospital
2006	PhD Dissertation Award, Best in the Biological Sciences Division, University of Chicago
2006	New York Times Front Page News article, “Still evolving, human genes tell new story” (Voight et al, see Ref #3)
2000-2006	Numerous travel awards and scholarships (MSRI/PMMB, Keystone Symposium, NHGRI, etc.)
1998-1999	McDonald’s Fellowship for Biological Studies, Gonzaga University
1997-1999	Academic Merit Scholarship and Academic Debate Scholarship, Gonzaga University

PROFESSIONAL ACTIVITIES

2018–Present	Chair, Genomics and Computational Biology Graduate Group, University of Pennsylvania
2018–Present	Statistical Reviewer, *JAMA Network Open*
2018–Present	Associate Director (Bioinformatics Concentration) of the Master of Science in Translational Research program, University of Pennsylvania
2017–Present	Associate Editor, *Circulation: Genomic and Precision Medicine*
2012–Present	Member: The American Diabetes Association Member: The American Heart Association
2011–Present	Member of numerous Penn internal committees (e.g. Curriculum Committee for GCB and GGR, task force for graduate biostatistics, CTSA KL2/ITMAT fellowship reviewer, IBI Faculty Search, Genetics Faculty Search, PennOmics Governance, ITMAT Junior Investigator Symposium, 2024 Penn Genetics Symposium, etc.).
2002–Present	External referee for numerous journals (*Nature*, *Nature Genetics, Cell, Lancet, JAMA, PLoS Medicine, Science Advances*, *Bioinformatics, ATVB, JACC, AJHG,* many others.)
2001–Present	Member: American Society of Human Genetics
2022	Reviewer, VA 2023/01 ZRD1 GAST-L (01) 1, BL/CS Merit Review
2022	Reviewer, NIH 2022/10 GHD
2022	Reviewer, NIH ZRG1 2022/05 ZRG1 GGG-S(55) R (PAR-20-117)
2020	Reviewer, NIH ZRG1 PSE-C(90) Special Emphasis Panel,
2020	Reviewer, NIH RFA-DK19-014, “Catalyst Award in Diabetes, Endocrinology and Metabolic Diseases”
2018–2020	Associate Editor, *bioverlay.org*
2015–2018	Vice Chair, Genomics and Computational Biology Graduate Group, University of Pennsylvania
2012–2018	Co-organizer of the Penn Bioinformatics Forum (with Yoseph Barash)
2012–2018	Editorial Review Board, *Frontiers* (Pop Gen, Stat Gen)

2015–2017	Editorial Board Member, *Circulation: Cardiovascular Genetics*
2016–2017	Member, American Heart Association's Institute for Precision Cardiovascular Medicine Data Science and Technology Committee
2016	Reviewer, NIH Special Emphasis Panel for RFA-DK-15-025, NIH/NIDDK
2016-17, 2019	Program Committee, RECOMB Satellite Meeting on Computational Methods in Genetics
2013-14, 2017	Reviewer for American Heart Association GTOE Study Section
2013–2014	Associate Scientific Advisor, *Science Translational Medicine*
2013	Ad hoc reviewer, NIH Special Emphasis Panel for K23/K99 Career Awards, NIH/NIEHS

INVITED LECTURES (OUTSIDE PHILADELPHIA, SINCE 2017 PROMOTION TO ASSOCIATE)

2024	Thé Svedberg Seminar Series, hosted by the Science for Life Laboratory, Sweden (Uppsala).
2023	SugarScience Webinar Series, Virtual Seminar
2023	Festival of Genomics and Biodata, Boston, MA
2023	Accelerating Medicines Partnerships Common Metabolic Disease Parliament Meeting, Boston, MA
2022	Invited Seminar, Rutgers Institute for Translational Medicine and Science (RITMS), Rutgers University, New Brunswick, NJ
2020	70th Annual Meeting of the American Society of Human Genetics (held virtually)
2020	European Society of Human Genetics, Berlin Germany (held virtually)
2019	Invited Seminar, Regeneron Pharmaceuticals, Tarrytown, NY
2019	Big Data Institute Seminar Series, University of Oxford, Oxford, UK
2019	Special Seminar, University of Exeter, Exeter UK
2019	4th International Conference on Mendelian Randomization, University of Bristol, Bristol, UK
2019	Special Seminar, Glaxo-Smith-Kline, Cambridge UK
2019	MRC Epidemiology Unit Special Seminar, University of Cambridge, Cambridge UK
2019	Department of Human Genetics Seminar Series Alumni Speaker, University of Chicago, IL
2019	Research Seminar Series, Brigham Young University, Provo, UT
2018	Research Seminar Series, HudsonAlpha Institute for Biotechnology, Huntsville, AL
2018	Integrated Biosciences Seminar Series, University of Akron, Akron, OH
2018	Million Veteran's Program Science Conference, Nashville, TN
2017	Center for Computational Medicine and Bioinformatics Seminar Series, University of Michigan, Ann Arbor, MI
2017	5 Points Seminar Series, New York Genome Center, New York, NY
2017	Bioinformatics Seminar Series, GlaxoSmithKline, King of Prussia, PA
2017	67th Annual Meeting of the American Society of Human Genetics (Invited Session Organizer), Orlando, FL
2017	Five Points Lecture Series, New York Genome Center, New York, NY
2017	Genetics and Bioinformatics Seminar Series, Glaxo-Smith-Kline, King of Prussia, PA

INVITED LECTURES (OUTSIDE PHILADELPHIA, 2011-2017)

2017	American Diabetes Association's 77th Annual Meeting, San Diego, CA
2017	Genome Sciences Seminar Series, Center for Public Health Genomics, University of Virginia, Charlottesville, VA
2016	Program in Quantitative Genomics Seminar Series, Harvard School of Public Health, Boston, MA
2016	Frontiers in Bioinformatics and Systems Biology Seminar Series, University of California, San Diego, CA
2016	Genetics Institute Seminar Series, Vanderbilt University, TN
2016	Institute for Personalized Medicine seminar Series, Icahn School of Medicine, Mount Sinai, NY
2016	Seminar Series, University of California at Los Angeles, CA
2016	CIHR – Strategic Training for Advanced Genetic Epidemiology International Speaker Seminar Series, University of Toronto, Canada
2016	New York Area Population Genomics Workshop, Princeton University
2015	Department of Genetics Seminar Series, Yale University, NH
2013	Bioscience Conference on Genomics in Medicine, Copenhagen, Denmark
2013	Keynote Lecture, American Heart Association Epi|NPAM Council's Spring Conference, New Orleans, LA
2013	73rd Meeting of the American Diabetes Association, Chicago, IL
2012	62nd Annual Meeting of the American Society of Human Genetics (Invited Session Organizer), San Francisco, CA
2012	Medical Population Genetics Seminar Series, The Broad Institute of Harvard and MIT, Cambridge, MA
2012	Department of Biology Seminar Series, University of Vermont, Burlington, VT
2012	Session Co-Chair, 25th Annual Cold Spring Harbor Meeting, Biology of Genomes, Cold Spring Harbor, NY
2011	1st Annual Illumina America's Scientific Summit, Clearwater Beach, FL
2011	Botnia 20th Anniversary Symposium, Lund University, Vaasa, Finland
2011	The 2011 European Human Genetics Conference, Amsterdam RAI, The Netherlands
2011	National Institute of Genomic Medicine in Mexico, Ciudad de México, Mexico

TEACHING ACTIVITIES

2013–2019, 2021-Present	Co-Director, *Introduction to Bioinformatics* (CIS/MTR/GCB5350) Undergrad/grad/post-doc/MD/MD+PhD, ~90 students Includes lectures and administrative responsibilities. 100+ hours total, 50+ direct contact
2019–Present	Guest Lecturer, *Statistics for Genomics and Biomedical Informatics* (GCB533)
2019–Present	Guest Lecturer, *Professional Development Series,* MSTR Program
2015–Present	Guest Lecturer, CTSA Summer Internship Seminar
2022	Director, *Introduction to Bioinformatics* - Independent Study (GCB999)

2014 Guest Lecturer, *Biology of Human Disease* (BIOL015)
2013 Guest Lecturer, *Advanced Computational Biology* (GCB537)
2012 Guest Lecturer, *Introduction to Genome Sciences* (GCB534)
2012-2013 Lecturer, Medical School Module One, *Genetic Foundations of Disease*
2006–2011 Organizer of several workshops in statistical genetic analysis

STUDENT AND POSTDOCTORAL MENTORSHIP

CURRENT MENTEES

2023–Present Brandon Wenz (PhD Student, GE)
2021–Present Da (Mia) Lee (PhD Student, PGG)
- Selected for Genomics T32 (2023)

2021–Present Mitch Conery (PhD Student, GCB, joint with Struan Grant)
- Selected for Genomics T32 (2022)
- Reviewer's Choice Abstract, ASHG (2023)

2021–Present Mary Ann Hazuga (PhD Student, GCB, joint with Struan Grant)

PREVIOUS MENTEES

POST-DOCTORAL FELLOWS

2020–2022 Louise Wang (Post-doc, MD Gastroenterology Fellow)
- *VA CDA Award (2022)*
- *Now: Assistant Professor of Medicine, Yale School of Medicine, Section of Digestive Diseases*

2015–2021 Chris Thom (Post-doc, MD/PhD Neonatology Resident)
- *CHOP Senior Resident Research Award (2017)*
- *Selected for Pediatrics T32 (2017)*
- *Foerderer Research Award (2018)*
- *Marshall Klaus Neonatal-Perinatal Research Award (2019)*
- *Philadelphia Perinatal Society Thomas Boggs Research Award (2019)*
- *61st American Society of Hematology Annual Meeting Abstract Achievement Award (2019)*
- *CHOP K-readiness Award (2019)*
- *Eastern Society of Pediatric Research Trainee Young Investigator Award Finalist (2020)*
- *CHOP Distinguished Research Trainee Award (2020)*
- *SPR Fellows' Basic Science Award (2020)*
- *K99 Award Recipient (2021)*
- *Now: Assistant Professor of Pediatrics, Children's Hospital of Philadelphia*

2015–2020 Diana Cousminer (Post-doc, joint with Struan Grant)
- *Young Investigator Travel award, ASBMR Bone-omics Symp. (2016)*
- *ADA Postdoc Fellowship Award Recipient (2016-2018)*

- *ASBMR Young Investigator Award (2018)*
- *CHOP Distinguished Research Trainee Award (2019)*
- *K99 Award recipient (2019-2021)*
- *ASHG Charles J. Epstein Post-doc Award Recipient (2019)*
- *Now: Scientific Leader, GSK*

2012–2017 Paul Babb (Post-doc)
- *Post-doc Symposium Poster Award (2014)*
- *Now, Research Scientist, Karius Inc.*

2015–2017 Kim Lorenz (Post-doc)
- *Selected for a Diabetes/Endocrine Post-doc T32 (2015-2016)*
- *Now: Bioinformatician in my group*

PHD CANDIDATES

2018–2023 Chris Adams (PhD Student, GCB)
- *Now: Quantitative Analyst, Philadelphia Phillies*

2018–2023 Will Bone (PhD Student, GCB, joint with Marylyn Ritchie)
- *AHA Predoctoral Fellowship (2020-2022)*
- *2020 ASHG Abstract Reviewer's Choice Award*
- *Travel Award, 2021 CHARGE Consortium Meeting (Virtual)*
- *2023 Recipient - Saul Winegrad Award for Best Dissertation (GCB)*
- *Now: Computational Biologist, Recursion, Inc.*

2016–2021 Katerina Gawronski (PhD Student, GE, joint with Casey Brown)
- *Selected for Genetics T32 (2016-2018)*
- *American Polish Cultural Society Scholarship (2016-2019)*
- *SAGES Poster Award (2018)*
- *AHA Predoctoral Fellowship (2019-2021)*
- *ASHG Charles J. Epstein Pre-doc Award Semi-Finalist (2019)*
- *Now: Senior Consultant, ClearView (Newton, MA)*

2014–2019 Kelsey Johnson (PhD Student, GE)
- *Selected for Genetics T32 (2014-2016)*
- *Now: Post-doc, Blehkman and Albert Labs (U. of Minnesota)*

2014–2018 Katie Siewert (PhD Student, GCB)
- *Selected for Genomics and Computational Biology T32 (2015-2017)*
- *2019 Recipient - Saul Winegrad Award for Best Dissertation (GCB)*
- *Now: Senior Research Scientist in Computational Genomics, Vertex*

2012–2016 Varun Aggarwala (PhD Student, GCB)
- *Semi-finalist for the ASHG Charles J. Epstein Trainee Award (2015)*
- *Penn Genetics Retreat Poster Award (2015)*
- *Post-doc, Faith Lab, Mt. Sinai*
- *Now: Asst. Professor, JIO Institute, Navi Mumbai, India*

MASTER'S CANDIDATES

2018–2021	Zhuoran Ding (Masters in Biostatistics, GGEB)
	- Now: PhD Student, GGEB, Univ. of Pennsylvania
2018	Kaushik Visvanathan (Master's student, CS)
2016–2018	Onur Yörük (Masters in Genomics and Computational Biology, GCB)

UNDERGRADUATE / POST-BACS

2022	Sanjana Akula (Undergraduate, SAS)
2020–2022	Brian Chen (Undergraduate, SAS)
2018–2020	Sanjana Adurty (Undergraduate, SAS)
	- Now: Medical School, Univ. of Pittsburgh
2015–2017	Rachael ("Rocky") Aikens (Swarthmore Undergrad)
	- Penn Summer Undergrad Internship Program (2016)
	- Penn CTSA Summer Internship (2015)
	- Now: Statistician, Mathematica (Policy Research)
2015–2016	David Nicholson (Post-Bac)
	- Selected for the Penn Summer Undergrad Intership Program (2014)
	- Selected for the PennPrep Program (2015)
	- Now: Data Scientist at Digital Science and Research Solutions Ltd.
2013–2015	Peter Yin (Undergrad)
	- Undergraduate Research and Fellowship Recipient (2015)
	- Now: Automation Engineer, Zymogen, Emeryville CA

PUBLICATIONS (FROM 163 PAPERS, H-INDEX=85, CITATIONS=77,421)

LINK TO FULL PUBLICATION LIST:

https://www.ncbi.nlm.nih.gov/myncbi/benjamin.voight.1/bibliography/public/

PREPRINTS

[1] Tsao NL, Judy R, Levin MG, Shakt G; Regeneron Genetics Center; Penn Medicine BioBank; **Voight BF**, Chen J, Damrauer SM. Evaluation of the Performance of the RECODe Equation with the Addition of Polygenic Risk Scores for Adverse Cardiovascular Outcomes in Individuals with Type II Diabetes. medRxiv. 2023 May 5:2023.05.03.23289457. doi: 10.1101/2023.05.03.23289457.

[2] Lee DSM, DePaolo JS, Aragam KG, Biddinger K, Conery M, Dilitikas O, Hoffman-Andrews L, Judy RL, Khan A, Kulo I, Puckelwartz MJ, Reza N, Satterfield BA, Singhal P; Regeneron Genetics Center; Arany ZP, Cappola TP, Carruth E, Day SM, Do R, Haggarty CM, Joseph J, McNally E, Nadkarni G, Owens AT, Rader DJ, Ritchie MD, Sun Y, **Voight BF**, Levin MG, Damrauer SM. Common- and rare-variant genetic architecture of heart failure across the allele frequency spectrum. medRxiv. 2023 Jul 19:2023.07.16.23292724. doi: 10.1101/2023.07.16.23292724.

[3] Yuan S, Li Y, Wang L, Xu F, Chen J, Levin MG, Xiong Y, Voight BF, Damrauer SM, Gill D, Burgess S, Åkesson A, Michaëlsson K, Li X, Shen X, Larsson SC. Deciphering the

genetic architecture of atrial fibrillation offers insights into disease prediction, pathophysiology and downstream sequelae. medRxiv. 2023 Jul 25:2023.07.20.23292938. doi: 10.1101/2023.07.20.23292938.

***SELECTED KEY PUBLICATIONS* [FROM >150 PAPERS]**

*, **: DENOTES EQUAL CONTRIBUTION

[1] **Voight BF**, Pritchard JK. (2005). Confounding from cryptic relatedness in case-control association studies. *PLoS Genet.* 1(3): e32.

[2] **Voight BF***, Adams AA*, Frisse L, Quan Y, Hudson RR, Di Rienzo A. (2005). Interrogating multiple aspects of variation in a full resequencing data set to infer human population size changes. *Proc Natl Acad Sci USA* 102(51):18508-18513.

[3] **Voight BF***, Kudaravalli S*, Wen X, Pritchard JK. (2006). A map of recent positive selection in the human genome. *PLoS Biol.* 4(3): e72. PMCID: PMC1382018

[4] Tishkoff SA, Reed FA, Ranciaro A, **Voight BF**, Babbitt CC, Silverman JS, Powell K, Mortensen HM, Hirbo JB, Osman M, Ibrahim M, Omar SA, Lema G, Nyambo TB, Ghori J, Bumpstead S, Pritchard JK, Wray GA, Deloukas P. (2007) Convergent adaptation of human lactase persistence in Africa and Europe. *Nat. Genet.* 39(1): 31-40.

[5] Saxena R, **Voight BF**, Lyssenko V, Burtt NP, …, Ricke D, Purcell S. (2007) Genome-wide association analysis identifies loci for type 2 diabetes and triglyceride levels. *Science* 316(5829): 1331-1336.

[6] de Bakker PIW, Ferreira MA, Jia X, Neale BM, Raychaudhuri S, **Voight BF**. (2008). Practical aspects of imputation-driven meta-analysis of genome-wide association studies. *Hum Mol Genet*. 17(R2): R122-R128.

[7] Zeggini E*, Scott LJ*, Saxena R*, **Voight BF*** on behalf of the DIAGRAM Consortium. (2008). Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. Nat. Genet. 40(5): 638-645.

[8] Kathiresan S, Melander O, Guiducci C, Surti A, Burtt NP, Rieder MJ, Cooper GM, Roos C, **Voight BF**, Havulinna AS, Wahlstrand B, Hedner T, Corella D, Tai ES, Ordovas JM, Berglund G, Vartiainen E, Jousilahti P, Hedblad B, Taskinen MR, Newton-Cheh C, Salomaa V, Peltonen L, Groop L, Altshuler DM, Orho-Melander M. (2008) Six new loci associated with blood low-density lipoprotein cholesterol, high-density lipoprotein cholesterol or triglycerides in humans. Nat Genet. 2008 Feb;40(2):189-97.

[9] Kathiresan S, **Voight BF**, Purcell S, Musunuru K, …, Salomaa V, Schwartz SM. (2009) Genome-wide association of early-onset myocardial infarction with single nucleotide polymorphisms and copy number variants. *Nat Genet*. 41(3): 334-341.

[10] **Voight BF***, Scott LJ*, Steinthorsdottir V*, Morris AP*, Dina C* on behalf of the DIAbetes Genome-wide Replication and Meta-Analysis (DIAGRAM) Consortium. (2010). Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. *Nat Genet*. 42(7): 579-589.

[11] Pulit SL, **Voight BF**, de Bakker PI. (2010). Multiethnic genetic association studies improve power for locus discovery. *PLoS ONE* 5(9): e12600.

[12] Guey LT, Kravic J, Melander O, Burtt NP, Laramie JM, Lyssenko V, Jonsson A, Lindholm E, Tuomi T, Isomaa B, Nilsson P, Almgren P, Kathiresan S, Groop L, Seymour AB, Altshuler D, **Voight BF**. (2011). Power in the phenotypic extremes: A simulation study of power in discovery and replication of rare variants. *Gen Epidemiol*. 35(4): 236-246.

[13] Neale BM, Rivas MA, **Voight BF**, Altshuler D, Devlin B, Orho-Melander M, Kathiresan S, Purcell SM, Roeder K, Daly MJ. (2011). Testing for an unusual distribution of rare variants. *PLoS Genet*. 7(3): e1001322.

[14] Cotsapas C*, **Voight BF***, Rossin E, Lage K, Neale BM, Wallace C, Abecasis GR, Barrett JC, Behrens T, Cho J, De Jager PL, Elder JT, Graham RR, Gregersen P, Klareskog L, Siminovitch KA, van Heel DA, Wijmenga C, Worthington J, Todd JA, Hafler DA, Rich SS, Daly MJ; on behalf of the FOCiS Network of Consortia. (2011). Pervasive sharing of genetic effects in autoimmune disease. *PLoS Genet*. 7(8): e1002254.

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