BENJAMIN F. VOIGHT
CURRICULUM VITAE

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CV last updated: October, 2019

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:

2019–2021	Linda Pechenik Montague Investigator Award
2014–2020	NIH R01 DK101478: *"Algorithms to identify non-coding mutational burden and disease-relevant pathways"*
2018–2019	NIH R01 DK101478 S1, Supplemental support to applying developed methods to Alzheimer's disease and related traits

Additional:

2017–2021	X01, responding to TOPMED resequencing PAR-16-021, *"Leveraging a highly consanguineous cohort to discover risk factors for MI,"* Role: Co-I (PIs: D. Rader, D. Saleheen).
2018-2020	Dept. of VA IPA, "*Phenotypic and Genomic Architecture of Cardiovascular Disease Subtypes*" Role: Co-I (PIs: S. Damrauer)
2019-2023	NIH R01 HG010067: "*Network-based algorithms for target identification and drug repositioning from genetic associations,"* Role: Co-I (PI: C. Greene)

COMPLETED SUPPORT

As PI:

2016–2019	ITMAT Maturational Human Biology Pilot Grant: *"Characterizing the genetic determinants of pubertal timing and body weight regulation"*
2012–2016	AHA 13SDG14330006: "*Human genetics of high-density lipoprotein to elucidate the etiology of heart disease*"
2013–2014	W.W. Smith Charitable Trust H1201: "*Identifying the etiological basis for heightened risk of cardiovascular disease in the context of glycemic disorder*"
2012–2014	Alfred P. Sloan Foundation Fellowship

Additional:

2015–2016	March of Dimes Preterm Birth Research Center Grant. (Role: Co-Investigator).

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	My Ph.D. Dissertation was awarded 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	Chairman, Genomics and Computational Biology Graduate Group, University of Pennsylvania
2018–Present	Associate Editor, *bioverlay.org*
2018–Present	Statistical Reviewer, *JAMA Network Open*
2018–Present	Director (Bioinformatics Concentration) of the Masters 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, etc.).
2002–Present	External referee for numerous journals (*Nature*, *Nature Genetics, Cell, Lancet, JAMA, PLoS Medicine, Science Translational Medicine*, *Bioinformatics, ATVB, JACC, AJHG,* many others.)
2001–Present	Member: American Society of Human Genetics
2015–2018	Vice Chairman, 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)

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

2019–Present	Guest Lecture, *Statistics for Genomics and Biomedical Informatics* (GCB533)
2013–Present	Director, *Introduction to Bioinformatics* (CIS/MTR/GCB535) Undergrad/grad/post-doc/MD/MD+PhD, 50+ students Includes lectures and administrative responsibilities. 100+ hours total, 50+ direct contact
2015–Present	Guest Lecture, CTSA Summer Internship Seminar
2014	Guest Lecture, *Biology of Human Disease* (BIOL015)
2013	Guest Lecture, *Advanced Computational Biology* (GCB537)
2012	Guest Lecture, *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 STUDENTS

2018–Present	Chris Adams (PhD Student, GCB)
2018–Present	Will Bone (PhD Student, GCB, joint with Marylyn Ritchie)
2018–Present	Sanjana Adurty (Undergraduate, SAS)
2016–Present	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)*
2015–Present	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 Finalist (2019)*
2015–Present	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)*

2014–Present Kelsey Johnson (PhD Student, GE)
- *Selected for Genetics T32 (2014-2016)*

PREVIOUS TRAINEES

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: Post-doc, Price Lab (Harvard School of Public Health)*

2018 Kaushik Visvanathan (Master's student, CS)

2016–2018 Onur Yörük (Grad Student, GCB)
- *Master's Degree, GCB*

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

2015–2017 Rachael ("Rocky") Aikens (Swarthmore Undergrad)
- *Penn Summer Undergrad Internship Program (2016)*
- *Penn CTSA Summer Internship (2015)*
- *Now: PhD Program in Biomedical Informatics at Stanford*

2012–2017 Paul Babb (Post-doc)
- *Post-doc Symposium Poster Award (2014)*

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

2015–2016 David Nicholson (Post-Bac)
- *Selected for the Penn Summer Undergrad Intership Program (2014)*
- *Selected for the PennPrep Program (2015)*
- *Now: PhD Program – University of Pennsylvania – C. Greene Lab*

2013–2015 Peter Yin (Undergrad, now Technical Staff at Transcriptic, Menlo Park)
- *Undergraduate Research and Fellowship Recipient (2015)*
- *Now: Automation Engineer, Zymogen, Emeryville CA*

PUBLICATIONS (FROM >100 PAPERS, H-INDEX=72, CITATIONS=52,946)

LINK TO FULL PUBLICATION LIST:

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

PREPRINTS

[1] Siewert KM and **Voight BF**. BetaScan2: Standardized statistics to detect balancing selection utilizing substitution data. *BioRxiv,* ***doi:*** https://doi.org/10.1101/497255

[2] Thom CS, Jobaliya CD, Lorenz K , Maguire JA, Gagne A, Gadue P, French DL, **Voight BF**. Machine learning-based identification and cellular validation of *Tropomyosin 1* as a genetic inhibitor of hematopoiesis. *BioRxiv,* ***doi:*** https://doi.org/10.1101/631895

[3] Gawronski KAB, Bone W, Park Y, Pashos E, Wang X, Yang W, Rader D, Musunuru K, **Voight BF**, Brown C. Evaluating the contribution of cell-type specific alternative splicing to variation in lipid levels. *BioRxiv,* ***doi:*** https://doi.org/10.1101/659326

[4] Thom CS and **Voight BF**. Genetic colocalization atlas points to common regulatory sites and genes for hematopoietic traits and hematopoietic contributions to disease phenotypes. *BioRxiv,* ***doi:*** https://doi.org/10.1101/787333v1

SELECTED PUBLICATIONS

*: 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.

[15] Bumgarner SL, Neuert G, **Voight BF**, Symbor-Nagrabska A, Grisafi P, van Oudenaarden A, Fink GR. (2012) Single-Cell Analysis Reveals that Noncoding RNAs Contribute to Clonal Heterogeneity by Modulating Transcription Factor Recruitment. *Mol. Cell* Feb 24; 45(4):470-82.

[16] Stahl EA, Wegmann D, Trynka G, Gutierrez-Achury J, Do R, **Voight BF**, Kraft P, Chen R, Kallberg HJ, Kurreeman FA; Diabetes Genetics Replication and Meta-analysis Consortium; Myocardial Infarction Genetics Consortium, Kathiresan S, Wijmenga C, Gregersen PK, Alfredsson L, Siminovitch KA, Worthington J, de Bakker PI, Raychaudhuri S, Plenge RM. (2012). Bayesian inference analyses of the polygenic architecture of rheumatoid arthritis. *Nat Genet*. Mar 25;44(5):483-9.

[17] Neale BM, Kou Y, Liu L, Ma'ayan A, Samocha KE, Sabo A, Lin CF, Stevens C, Wang LS, Makarov V, Polak P, Yoon S, Maguire J, Crawford EL, Campbell NG, Geller ET, Valladares O, Schafer C, Liu H, Zhao T, Cai G, Lihm J, Dannenfelser R, Jabado O, Peralta Z, Nagaswamy U, Muzny D, Reid JG, Newsham I, Wu Y, Lewis L, Han Y, **Voight BF**, …, Gibbs RA, Roeder K, Schellenberg GD, Sutcliffe JS, Daly MJ. (2012) Patterns and rates of exonic de novo mutations in autism spectrum disorders. *Nature* Apr 4;485(7397):242-5.

[18] **Voight BF***, Peloso GM*, Orho-Melander M, Frikke-Schmidt R, Barbalic M, Jensen MK, …, O'Donnell CJ, Salomaa V, Rader DJ, Peltonen L, Schwartz SM, Altshuler D, Kathiresan S. Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. *Lancet* Aug 11;380(9841):572-802.

[19] **Voight BF***, Kang HM*, Ding J, Palmer CD, Sidore C, Chines PS, Burtt NP, Fuchsberger C, Li Y, Erdmann J, et al. (2012). The metabochip, a custom genotyping

array for genetic studies of metabolic, cardiovascular, and anthropometric traits. *PLoS Genet*. Aug;8(8):e1002793.

[20] Perry JR, **Voight BF**, Yengo L, Amin N, Dupuis J, …, Frayling TM, Cauchi S. (2012). Stratifying type 2 diabetes cases by BMI identifies genetic risk variants in LAMA1 and enrichment for risk variants in lean compared to obese cases. *PLoS Genet*. May;8(5):e1002741.

[21] Morris AP*, **Voight BF***, Teslovich TM*, Ferreira T*, Segrè AV*, Steinthorsdottir V, Strawbridge RJ, Khan H, Grallert H, Mahajan A, et al. (2012). Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. *Nat. Genet*. Aug 12;44(9):981-990.

[22] **Voight BF**, Cotsapas C (2012). Human genetics offers an emerging picture of common pathways and mechanisms in autoimmunity. *Curr Opin Immunol*. Oct;24(5):552-7.

[23] Georgi B, **Voight BF**, Bućan M (2013). From mouse to human: evolutionary genomics analysis of human orthologs of essential genes. *PLoS Genet*. May;9(5):e1003484.

[24] Flannick J, Thorleifsson G, Beer NL, Jacobs SB, Grarup N, Burtt NP, Mahajan A, Fuchsberger C, Atzmon G, Benediktsson R, …, **Voight BF**, Wilson JG, Boehnke M, McCarthy MI, Njølstad PR, Pedersen O, Groop L, Cox DR, Stefansson K, Altshuler D. (2014). Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. *Nature Genet.* Apr 4;46(4):357-363.

[25] Prokopenko I, Poon W, Mägi R, Prasad B R, Salehi SA, Almgren P, Osmark P, Bouatia-Naji N, Wierup N, Fall T, …, **Voight BF**, et al. (2014). A central role for GRB10 in regulation of islet function in man. *PLoS Genet* Apr 3;10(4):e1004235.

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[27] **Voight, BF** (2014). MR_predictor: a simulation engine for Mendelian Randomization studies. *Bioinformatics.* Dec 1; 30(23):3432-4.

[28] Yin, P and **Voight, BF** (2015). MeRP: a high-throughput pipeline for Mendelian Randomization Analysis. *Bioinformatics.* Mar 15;31(6):957-9.

[29] Jansen H, Loley C, Lieb W, Pencina MJ, Nelson CP, Kathiresan S, Peloso GM, **Voight BF**, Reilly MP, Assimes TL, Boerwinkle E, Hengstenberg C, Laaksonen R, McPherson R, Roberts R, Thorsteinsdottir U, Peters A, Gieger C, Rawal R, Thompson JR, König IR; CARDIoGRAM consortium, Vasan RS, Erdmann J, Samani NJ, Schunkert H. (2015) Genetic variants primarily associated with type 2 diabetes are related to coronary artery disease risk. *Atherosclerosis* Jun 3;241(2):419-426.

[30] Soccio RE, Chen ER, Rajapurkar SR, Safabakhsh P, Marinis JM, Dispirito JR, Emmett MJ, Briggs ER, Fang B, Everett LJ, Lim HW, Won KJ, Steger DJ, Wu Y, Civelek M, **Voight BF**, Lazar MA. (2015) Genetic Variation Determines PPARγ Function and Anti-diabetic Drug Response in Vivo. *Cell* Jul 2;162(1):33-44.

[31] Gaulton KJ, Ferreira T, Lee Y, Raimondo A, Mägi R, …, **Voight BF**, et al. (2015) Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. *Nat Genet.* 2015 Dec;47(12):1415-25.

[32] Keenan T, Zhao W, Rasheed A, Ho WK, Malik R, …, Rader DJ, **Voight BF***, Saleheen D*. Causal Assessment of Serum Urate Levels in Cardiometabolic Diseases Through a Mendelian Randomization Study. J Am Coll Cardiol. 2016 Feb 2;67(4):407-16.

[33] Aggarwala V, and **Voight BF**. An expanded sequence context model broadly explains variability in polymorphism levels across the human genome. *Nat Genet*. 2016 Apr;48(4):349-55.

[34] Cousminer DL, Arkader A, **Voight BF**, Pacifici M, Grant SF. Assessing the general population frequency of rare coding variants in the EXT1 and EXT2 genes previously implicated in hereditary multiple exostoses. Bone. 2016 Sep 9;92:196-200.

[35] Fuchsberger C, Flannick J, Teslovich TM, Mahajan A, Agarwala V, Gaulton KJ, …, **Voight BF** et al. The genetic architecture of type 2 diabetes. *Nature*. 2016 Aug 4;536(7614):41-7.

[36] Cousminer DL, Arkader A, **Voight BF**, Pacifici M, Grant SF. Assessing the general population frequency of rare coding variants in the EXT1 and EXT2 genes previously implicated in hereditary multiple exostoses. Bone. 2016 Nov;92:196-200.

[37] Aikens RC, Zhao W, Saleheen D, Reilly MP, Epstein SE, Tikkanen E, Salomaa V, **Voight BF**. Systolic Blood Pressure and Risk of Type 2 Diabetes: a Mendelian Randomization Study. Diabetes. 2017 Feb;66(2):543-550.

[38] Yin P, Anttila V, Siewert KM, Palotie A, Smith GD, **Voight BF**. Serum calcium and risk of migraine: a Mendelian randomization study. Hum Mol Genet. 2016 [Epub ahead of print]

[39] Aggarawala V, Ganguly A, **Voight BF**. *De novo* mutational profile in RB1 clarified using a mutation rate modeling algorithm. *BMC Genomics.* 2017 Feb 14;18(1):155.

[40] Brynedal B, Choi J, Raj T, Bjornson R, Stranger BE, Neale BM, **Voight BF**, Cotsapas C. Large-Scale trans-eQTLs Affect Hundreds of Transcripts and Mediate Patterns of Transcriptional Co-regulation. *AJHG*. 2017 100(4):481-591.

[41] Mishra R, Chesi A, Cousminer DL, Hawa MI, Bradfield JP, Hodge KM, Guy VC, Hakonarson H, Bone Mineral Density in Childhood Study, Mauricio D, Schloot NC, Yderstræde KB, **Voight BF**, Schwartz S, Boehm BO, Leslie RD, Grant SFA. Relative contribution of type 1 and type 2 diabetes loci to the genetic etiology of adult-onset, non-insulin-requiring autoimmune diabetes. BMC Med. 2017 Apr 25;15(1):88.

[42] Babb PL, Lahens NF, Correa-Garhwal SM, Nicholson DN, Kim EJ, Hogenesch JB, Kuntner M, Higgins L, Hayashi CY, Agnarsson I, **Voight BF**. The *Nephila clavipes* genome highlights the diversity of spider silk genes and their complex expression. *Nature Genetics.* 2017 Jun;49(6):895-903.

[43] Scott RA, Scott LJ, Mägi R, Marullo L, Gaulton KJ, …, **Voight BF**, Morris AP, Boehnke M, McCarthy MI, Prokopenko I. An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. *Diabetes*. 2017 Nov;66(11):2888-2902

[44] Zhao W, Rasheed A, Tikkanen E, Lee JJ, …, **Voight BF***, Saleheen D*. Identification of new susceptibility loci for type 2 diabetes and shared etiological pathways with coronary heart disease. *Nature Genetics*. 2017 Oct;49(10):1450-1457.

[45] Siewert KM and **Voight BF**. Detecting Long-term Balancing Selection Using Allele Frequency Correlation. *Mol. Biol. Evol*. 2017 Nov;1;34(11):2996-3005.

[46] Tragante V, Gho JMIH, Felix JF, Vasan RS, Smith NL, **Voight BF**; CHARGE Heart Failure Working Group, Palmer C, van der Harst P, Moore JH, Asselbergs FW. Gene Set Enrichment Analyses: lessons learned from the heart failure phenotype. BioData Min. 2017 May 26;10:18.

[47] Cousminer DL, Mitchell JA, Chesi A, Roy SM, Kalkwarf HJ, Lappe JM, Gilsanz V, Oberfield SE, Shepherd JA, Kelly A, McCormack SE, **Voight BF**, Zemel BS, Grant SF. Genetically Determined Later Puberty Impacts Lowered Bone Mineral Density in Childhood and Adulthood. *J Bone Miner Res*. 2018 Mar;33(3):430-436.

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