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CURRICULUM VITAE

Paul L. Auer PhD

Professor
Department of Institute for Health and Equity
Division of Biostatistics

OFFICE ADDRESS:
Medical Education Building
8701 Watertown Plank Rd
Milwaukee, WI 53226

EDUCATION:

09/1997 - 05/2001 Bachelor of Arts in Mathematics, State University of New York at Geneseo, Genesso, NY
09/2002 - 05/2003 Masters of Professional Studies in Applied Statistics, Cornell University, Ithaca, NY
09/2005 - 08/2010 PhD in Statistics, Purdue University, West Lafayette, IN

POSTGRADUATE TRAINING AND FELLOWSHIP APPOINTMENTS:

09/2010 - 07/2013 Staff Scientist, Cancer Prevention Program, Public Health Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA

FACULTY APPOINTMENTS:

08/2013 - 07/2017 Assistant Professor, School of Public Health, University of Wisconsin-Milwaukee, Milwaukee, WI
08/2017 - 07/2021 Associate Professor, School of Public Health, University of Wisconsin-Milwaukee, Milwaukee, WI
08/2021 - Present Professor, Institute for Health & Equity, Biostatistics, Medical College of Wisconsin, Milwaukee, WI

ADMINISTRATIVE APPOINTMENTS:

08/2020 - 07/2021 Faculty Chair, School of Public Health, University of Wisconsin-Milwaukee, Milwaukee, WI
08/2021 - Present Director of Biostatistics Shared Resource, Institute for Health & Equity, Biostatistics, Medical College of Wisconsin, Milwaukee, WI

AWARDS AND HONORS:

08/2005 - 05/2010 Vertical Integration of Research and Education in the Mathematical Sciences (VIGRE) Fellowship, Purdue University
04/2011 I.W. Burr Graduate Student Dissertation Award, Purdue University
01/2016 Cohorts for Heart and Aging Research in Genetic Epidemiology (CHARGE) Early Career Achievement Award, CHARGE Consortium

MEMBERSHIPS IN HONORARY AND PROFESSIONAL SOCIETIES:

08/2008 - Present American Statistical Association (Member)
08/2010 - Present American Society of Human Genetics (Member)

EDITORSHIPS/EDITORIAL BOARDS/JOURNAL REVIEWS:

Journal Review
2016 - Present Nature Genetics
2016 - Present PLoS Genetics
2017 - Present The American Journal of Human Genetics

Ad-Hoc Reviewer
2014 - Present Bioinformatics
2017 - Present Proceedings of the National Academy of Sciences
2018 - Present Genetics
2018 - Present Biostatistics
2018 - Present Journal of the American Statistical Association
2019 - Present Genome Research

NATIONAL ELECTED/APPOINTED LEADERSHIP AND COMMITTEE POSITIONS:
02/2024 ad hoc reviewer, Genetics of Health and Disease (GHD) Study Section, NIH
05/2024 ad hoc reviewer, Neurological, Mental and Behavioral Health (NMBH)Study Section, NIH

RESEARCH GRANTS/AWARDS/CONTRACTS/PROJECTS:

Active

Peer Review

Title:	Innovative Approaches to Elucidate the Genetic Etiology of Age-related Hearing Impairment
Source:	NIH/NIDCD R01
Role:	MPI
PI:	Suzanne Leal, Paul Auer, Andrew Dewan
Dates:	09/2019 - 08/2024
Title:	Polygenic risk scores and health disparities: the role of blood cells, immune response, and evolutionary adaptation
Source:	NIH/NHBRI U-1
Role:	Co-Investigator
PI:	Yun Li
Dates:	06/2021 - 05/2026
Title:	Genetic and Epigenetic Mechanisms of BP Regulation
Source:	NIH/NHLBI
Role:	Co-Investigator
PI:	Mingyu Liang
Dates:	08/01/2021 - 07/31/2025
Title:	Development of a Surgical Oncology Disparities Research Program
Source:	Advancing a Healthier Wisconsin
Role:	Co-Investigator
PI:	Anai Kothari
Dates:	05/01/2022 - 04/30/2026
Title:	RIGERR: Resources for Investigating Genetic and Epigenetic Regulation of Renal Disease
Source:	NIH/NIDDK
Role:	Co-Investigator
PI:	Mingy Liang
Dates:	07/01/2022 - 06/30/2027
Title:	Structural Variation and Hematologic

	Traits
Source:	NIH/NHLBI
Role:	Co-Investigator
PI:	Alex Reiner
Dates:	07/01/2022 - 06/30/2026
Title:	Establishing the dynamics of lymphoid clonal hematopoiesis and its aging-related disease consequences
Source:	NIH/NIA
Role:	Principal Investigator
PI:	Paul Auer
Dates:	09/01/2023 - 06/30/2028
Title:	Puerto Rican Obesity Intervention for Men
Source:	NIH/NIDDK
Role:	Co-Investigator
PI:	Lisa Sanchez-Johnsen
Dates:	09/01/2023 - 08/31/2026
Title:	A Data Resource for Blood and Marrow Transplants and Adoptive Cellular Therapy Research
Source:	NIH/NCI
Role:	Co-Investigator
PI:	Bronwen Shaw
Dates:	03/01/2024 - 02/29/2028
Title:	Molecular Markers for Tumors Associated with Extrachromosomal HPV
Source:	NIH/NCI
Role:	Co-Investigator
PI:	Akin Ojesina
Dates:	05/01/2024 - 04/30/2029

Prior

Peer Review

Title:	The Women's Health Initiative Sequencing Project
Source:	NIH/NHLBI R01
Role:	Co-Investigator
PI:	Rebecca Jackson
Dates:	08/2010 - 03/2013
Title:	Transdisciplinary Cancer Genomics
Source:	NIH/NCI U19
Role:	Key Personel
PI:	Ross Prentice
Dates:	08/2012 - 06/2013
Title:	Detection of Colorectal Cancer Susceptibility Loci Using Genome-Wide Sequencing
Source:	NIH/NCI U01
Role:	Co-Investigator

PI:	Ulrike Peters
Dates:	09/2012 - 08/2015
Title:	Rare Variants Associated with Cardiovascular Disease Risk and Hormone Therapy Interactions
Source:	NIH/NHLBI R21
Role:	Principal Investigator
PI:	Paul L. Auer
Dates:	06/2014 - 06/2016
Title:	Genetic Architecture of Adiposity in Multiple Large Cohorts
Source:	NIH/NIDDK R01
Role:	Co-Investigator
PI:	Michael Province
Dates:	09/2014 - 06/2017
Title:	Young Women's Health History Study
Source:	NIH/NCI R01
Role:	Co-Investigator
PI:	Ellen Velie
Dates:	05/2015 - 08/2016
Title:	Whole genome sequence analysis of ischemic stroke in the Women's Health Initiative
Source:	NIH/NHLBI R01
Role:	Co-Investigator
PI:	Charles Kooperberg
Dates:	04/2017 - 03/2021
Title:	Thrombosis Genetics in African Americans
Source:	NIH/NHLBI R01
Role:	Co-Investigator
PI:	Alex Reiner
Dates:	04/2017 - 03/2021
Title:	Sequence analysis of hematologic and hemostasis traits in African Americans
Source:	NIH/NHLBI R01
Role:	Co-Investigator
PI:	Ethan Lange
Dates:	06/2017 - 05/2021
Title:	Master regulatory transcription factors driving stage specific regeneration of CNS axons
Source:	UW-Milwaukee Research Growth Initiative
Role:	Co-Investigator
PI:	Ava Udvadia
Dates:	09/2017 - 08/2018
Title:	Family-based methods for analysis of sequence data to elucidate AD etiology

Source:	NIH/NIA
Role:	Co-Investigator
PI:	Suzanne Leal
Dates:	04/2018 - 03/2023
Title:	Next Generation Functional Genomics of Hematology Traits
Source:	NIH/NHLBI R01
Role:	Co-Investigator
PI:	Alex Reiner
Dates:	04/2020 - 03/2024

INVITED LECTURES/WORKSHOPS/PRESENTATIONS:

Local

Paul L. Auer, Statistical analysis of rare-variant genetic data, Division of Biostatistics Seminar, Medical College of Wisconsin, 12/2014

Paul L. Auer, The genetics of blood cell traits as discovered in apparently healthy, population-based samples, Physiology Department Seminar, Medical College of Wisconsin, 03/2017

Paul Auer, Characterizing mosaic chromosomal alterations in diverse populations using whole genome sequencing, MCW Cancer Center Grand Rounds, Milwaukee, WI, 04/2023

Regional

Paul L. Auer, Exploring the drivers of gene-expression in the TCGA data, Biostatistics in the Modern Computing Age Conference, Medical College of Wisconsin, 09/2017

National

Paul L. Auer, Enumeration Status of Census 2000 Enumerations Deemed Insufficient Information for Matching and Follow-up, Joint Statistics Meeting, Minneapolis, MN, 08/2005

Paul L. Auer, Statistical Challenges with Genetic Next-Generation Sequence Data, Joint Statistics Meeting, Miami, FL, 07/2011

Paul L. Auer, Search for Rare Coding Variants Associated with Obesity: The NHLBI Exome-Sequencing Project, The Obesity Society Annual Meeting, Orlando, FL, 10/2011

Paul L. Auer, Associating rare-coding variants with Body Mass Index: The NHLBI Exome-Sequencing Project, The Obesity Society Annual Meeting, San Antonio, TX, 09/2012

Paul L. Auer, Testing Rare Variant Associations in the Presence of Missing Data, American Society of Human Genetics, San Francisco, CA, 11/2012

Paul L. Auer, Identification of new rare coding variants associated with hemoglobin levels and platelet counts, American Society of Human Genetics, Boston, MA, 10/2013

Paul L. Auer, Robust statistics for rare genetic variant association studies, Joint Statistics Meeting, Boston, MA, 08/2014

Paul L. Auer, A rare synonymous variant in GFI1B associated with lower platelet count reveals a role alternative GFI1B splice forms in human hematopoiesis, The American Society of Human Genetics, Baltimore, MD, 09/2015

Paul L. Auer, Can Epigenetic Profiles Predict Genetic Risk for Blood Disorders, ENAR Spring Meeting, Austin, TX, 03/2016

Paul L. Auer, Exploring the drivers of gene-expression in the TCGA data, Department of Epidemiology Seminar, MD Anderson Cancer Center, Houston TX, 06/2017

Paul L. Auer, Integrative methods for multi-omic data reveal multi-level gene and pathway regulation, Bioinformatics Seminar, University of California Los Angeles, 05/2019

Paul Auer, Characterizing mosaic chromosomal alterations in diverse populations using whole genome sequencing, Wake Forest University Department of Biostatistics Seminar, Virtual, 04/2023

Paul Auer, Publicly Available Genomics Resources, American Association for Cancer Research Conference on Health Disparities, Philadelphia, PA, 09/2023

International

Paul L. Auer, A rare synonymous variant in GFI1B associated with lower platelet count reveals a role

alternative GFI1B splice forms in human hematopoiesis, Genomics of Common Diseases, Cambridge, UK, 09/2015

Paul L. Auer, Whole genome sequencing in diverse samples reveals large effect, population specific associations, BTRU Seminar Series, Cambridge UK, 06/2019

MEDICAL COLLEGE TEACHING ACTIVITIES:

Graduate Student Education

09/2022 - 12/2022 Instructor for Methods and Models I: Biostatistics

09/2023 - 12/2023 Instructor for Methods and Models I: Biostatistics

EXTRAMURAL TEACHING:

Graduate Student Education

09/2014 - 07/2021 University of Wisconsin-Milwaukee, Instructor for Biostatistics MS, MPH, and PhD programs

BIBLIOGRAPHY

Refereed Journal Publications/Original Papers

1. Auer PL, Doerge RW. Statistical design and analysis of RNA sequencing data. Genetics. 2010 Jun;185(2):405-16. PMCID: PMC2881125
2. Auer PL, Doerge RW. A two-stage Poisson model for testing RNA-seq data Statistical Applications in Genetics and Molecular Biology. 11(1):57-62.
3. Auer PL, Srivastava S, Doerge RW. Differential expression--the next generation and beyond. Brief Funct Genomics. 2012 Jan;11(1):57-62.
4. Reiner AP, Beleza S, Franceschini N, Auer PL, Robinson JG, Kooperberg C, Peters U, Tang H. Genome-wide association and population genetic analysis of C-reactive protein in African American and Hispanic American women. Am J Hum Genet. 2012 Sep 07;91(3):502-12. PMCID: PMC3511984
5. Auer PL, Johnsen JM, Johnson AD, Logsdon BA, Lange LA, Nalls MA, Zhang G, Franceschini N, Fox K, Lange EM, Rich SS, O'Donnell CJ, Jackson RD, Wallace RB, Chen Z, Graubert TA, Wilson JG, Tang H, Lettre G, Reiner AP, Ganesh SK, Li Y. Imputation of exome sequence variants into population-based samples and blood-cell-trait-associated loci in African Americans: NHLBI GO Exome Sequencing Project. Am J Hum Genet. 2012 Nov 02;91(5):794-808. PMCID: PMC3487117
6. Cambronne XA, Shen R, Auer PL, Goodman RH. Capturing microRNA targets using an RNA-induced silencing complex (RISC)-trap approach. Proc Natl Acad Sci U S A. 2012 Dec 11;109(50):20473-8. PMCID: PMC3528561
7. Roulin A, Auer PL, Libault M, Schlueter J, Farmer A, May G, Stacey G, Doerge RW, Jackson SA. The fate of duplicated genes in a polyploid plant genome. Plant J. 2013 Jan;73(1):143-53.
8. Johnsen JM, Auer PL, Morrison AC, Jiao S, Wei P, Haessler J, Fox K, McGee SR, Smith JD, Carlson CS, Smith N, Boerwinkle E, Kooperberg C, Nickerson DA, Rich SS, Green D, Peters U, Cushman M, Reiner AP, NHLBI Exome Sequencing Project. Common and rare von Willebrand factor (VWF) coding variants, VWF levels, and factor VIII levels in African Americans: the NHLBI Exome Sequencing Project. Blood. 2013 Jul 25;122(4):590-7. PMCID: PMC3724194
9. Auer PL, Wang G, Leal SM. Testing for rare variant associations in the presence of missing data. Genet Epidemiol. 2013 Sep;37(6):529-38. PMCID: PMC4459641
10. Duan Q, Liu EY, Auer PL, Zhang G, Lange EM, Jun G, Bizon C, Jiao S, Buyske S, Franceschini N, Carlson CS, Hsu L, Reiner AP, Peters U, Haessler J, Curtis K, Wassel CL, Robinson JG, Martin LW, Haiman CA, Le Marchand L, Matise TC, Hindorff LA, Crawford DC, Assimes TL, Kang HM, Heiss G, Jackson RD, Kooperberg C, Wilson JG, Abecasis GR, North KE, Nickerson DA, Lange LA, Li Y. Imputation of coding variants in African Americans: better performance using data from the exome sequencing project. Bioinformatics. 2013 Nov 01;29(21):2744-9. PMCID: PMC3799474
11. Stitziel NO, Fouchier SW, Sjouke B, Peloso GM, Moscoso AM, Auer PL, Goel A, Gigante B, Barnes TA, Melander O, Orho-Melander M, Duga S, Sivapalaratnam S, Nikpay M, Martinelli N, Girelli D, Jackson RD, Kooperberg C, Lange LA, Ardissino D, McPherson R, Farrall M, Watkins H, Reilly MP, Rader DJ, de Faire U, Schunkert H, Erdmann J, Samani NJ, Charnas L, Altshuler D, Gabriel S,

Kastelein JJ, Defesche JC, Nederveen AJ, Kathiresan S, Hovingh GK, National Heart, Lung, and Blood Institute GO Exome Sequencing Project. Exome sequencing and directed clinical phenotyping diagnose cholesterol ester storage disease presenting as autosomal recessive hypercholesterolemia. Arterioscler Thromb Vasc Biol. 2013 Dec;33(12):2909-14. PMCID: PMC4002172

12. Gordon AS, Tabor HK, Johnson AD, Snively BM, Assimes TL, Auer PL, Ioannidis JP, Peters U, Robinson JG, Sucheston LE, Wang D, Sotoodehnia N, Rotter JI, Psaty BM, Jackson RD, Herrington DM, O'Donnell CJ, Reiner AP, Rich SS, Rieder MJ, Bamshad MJ, Nickerson DA, NHLBI GO Exome Sequencing Project. Quantifying rare, deleterious variation in 12 human cytochrome P450 drug-metabolism genes in a large-scale exome dataset. Hum Mol Genet. 2014 Apr 15;23(8):1957-63. PMCID: PMC3959810
13. Liu DJ, Peloso GM, Zhan X, Holmen OL, Zawistowski M, Feng S, Nikpay M, Auer PL, Goel A, Zhang H, Peters U, Farrall M, Orho-Melander M, Kooperberg C, McPherson R, Watkins H, Willer CJ, Hveem K, Melander O, Kathiresan S, Abecasis GR. Meta-analysis of gene-level tests for rare variant association. Nat Genet. 2014 Feb;46(2):200-4. PMCID: PMC3939031
14. Logsdon BA, Dai JY, Auer PL, Johnsen JM, Ganesh SK, Smith NL, Wilson JG, Tracy RP, Lange LA, Jiao S, Rich SS, Lettre G, Carlson CS, Jackson RD, O'Donnell CJ, Wurfel MM, Nickerson DA, Tang H, Reiner AP, Kooperberg C, NHLBI GO Exome Sequencing Project. A variational Bayes discrete mixture test for rare variant association. Genet Epidemiol. 2014 Jan;38(1):21-30. PMCID: PMC4030763
15. Peloso GM, Auer PL, Bis JC, Voorman A, Morrison AC, Stitziel NO, Brody JA, Khetarpal SA, Crosby JR, Fornage M, Isaacs A, Jakobsdottir J, Feitosa MF, Davies G, Huffman JE, Manichaikul A, Davis B, Lohman K, Joon AY, Smith AV, Grove ML, Zanoni P, Redon V, Demissie S, Lawson K, Peters U, Carlson C, Jackson RD, Ryckman KK, Mackey RH, Robinson JG, Siscovick DS, Schreiner PJ, Mychaleckyj JC, Pankow JS, Hofman A, Uitterlinden AG, Harris TB, Taylor KD, Stafford JM, Reynolds LM, Marioni RE, Dehghan A, Franco OH, Patel AP, Lu Y, Hindy G, Gottesman O, Bottinger EP, Melander O, Orho-Melander M, Loos RJ, Duga S, Merlini PA, Farrall M, Goel A, Asselta R, Girelli D, Martinelli N, Shah SH, Kraus WE, Li M, Rader DJ, Reilly MP, McPherson R, Watkins H, Ardissino D, NHLBI GO Exome Sequencing Project, Zhang Q, Wang J, Tsai MY, Taylor HA, Correa A, Griswold ME, Lange LA, Starr JM, Rudan I, Eiriksdottir G, Launer LJ, Ordovas JM, Levy D, Chen YD, Reiner AP, Hayward C, Polasek O, Deary IJ, Borecki IB, Liu Y, Gudnason V, Wilson JG, van Duijn CM, Kooperberg C, Rich SS, Psaty BM, Rotter JI, O'Donnell CJ, Rice K, Boerwinkle E, Kathiresan S, Cupples LA. Association of low-frequency and rare coding-sequence variants with blood lipids and coronary heart disease in 56,000 whites and blacks. Am J Hum Genet. 2014 Feb 06;94(2):223-32. PMCID: PMC3928662
16. Lange LA, Hu Y, Zhang H, Xue C, Schmidt EM, Tang ZZ, Bizon C, Lange EM, Smith JD, Turner EH, Jun G, Kang HM, Peloso G, Auer P, Li KP, Flannick J, Zhang J, Fuchsberger C, Gaulton K, Lindgren C, Locke A, Manning A, Sim X, Rivas MA, Holmen OL, Gottesman O, Lu Y, Ruderfer D, Stahl EA, Duan Q, Li Y, Durda P, Jiao S, Isaacs A, Hofman A, Bis JC, Correa A, Griswold ME, Jakobsdottir J, Smith AV, Schreiner PJ, Feitosa MF, Zhang Q, Huffman JE, Crosby J, Wassel CL, Do R, Franceschini N, Martin LW, Robinson JG, Assimes TL, Crosslin DR, Rosenthal EA, Tsai M, Rieder MJ, Farlow DN, Folsom AR, Lumley T, Fox ER, Carlson CS, Peters U, Jackson RD, van Duijn CM, Uitterlinden AG, Levy D, Rotter JI, Taylor HA, Gudnason V Jr, Siscovick DS, Fornage M, Borecki IB, Hayward C, Rudan I, Chen YE, Bottinger EP, Loos RJ, Sætrom P, Hveem K, Boehnke M, Groop L, McCarthy M, Meitinger T, Ballantyne CM, Gabriel SB, O'Donnell CJ, Post WS, North KE, Reiner AP, Boerwinkle E, Psaty BM, Altshuler D, Kathiresan S, Lin DY, Jarvik GP, Cupples LA, Kooperberg C, Wilson JG, Nickerson DA, Abecasis GR, Rich SS, Tracy RP, Willer CJ, NHLBI Grand Opportunity Exome Sequencing Project. Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. Am J Hum Genet. 2014 Feb 06;94(2):233-45. PMCID: PMC3928660
17. Kim DS, Crosslin DR, Auer PL, Suzuki SM, Marsillach J, Burt AA, Gordon AS, Meschia JF, Nalls MA, Worrall BB, Longstreth WT Jr, Gottesman RF, Furlong CE, Peters U, Rich SS, Nickerson DA, Jarvik GP, NHLBI Exome Sequencing Project. Rare coding variation in paraoxonase-1 is associated with ischemic stroke in the NHLBI Exome Sequencing Project. J Lipid Res. 2014 Jun;55(6):1173-8. PMCID: PMC4031948
18. Auer PL, Teumer A, Schick U, O'Shaughnessy A, Lo KS, Chami N, Carlson C, de Denus S, Dubé MP, Haessler J, Jackson RD, Kooperberg C, Perreault LP, Nauck M, Peters U, Rioux JD, Schmidt F, Turcot V, Völker U, Völzke H, Greinacher A, Hsu L, Tardif JC, Diaz GA, Reiner AP, Lettre G. Rare and low-frequency coding variants in CXCR2 and other genes are associated with hematological traits. Nat

Genet. 2014 Jun;46(6):629-34. PMCID: PMC4050975
19. Ellis J, Lange EM, Li J, Dupuis J, Baumert J, Walston JD, Keating BJ, Durda P, Fox ER, Palmer CD, Meng YA, Young T, Farlow DN, Schnabel RB, Marzi CS, Larkin E, Martin LW, Bis JC, Auer P, Ramachandran VS, Gabriel SB, Willis MS, Pankow JS, Papanicolaou GJ, Rotter JI, Ballantyne CM, Gross MD, Lettre G, Wilson JG, Peters U, Koenig W, Tracy RP, Redline S, Reiner AP, Benjamin EJ, Lange LA. Large multiethnic Candidate Gene Study for C-reactive protein levels: identification of a novel association at CD36 in African Americans. Hum Genet. 2014 Aug;133(8):985-95. PMCID: PMC4104766
20. Barrdahl M, Canzian F, Joshi AD, Travis RC, Chang-Claude J, Auer PL, Gapstur SM, Gaudet M, Diver WR, Henderson BE, Haiman CA, Schumacher FR, Le Marchand L, Berg CD, Chanock SJ, Hoover RN, Rudolph A, Ziegler RG, Giles GG, Baglietto L, Severi G, Hankinson SE, Lindström S, Willet W, Hunter DJ, Buring JE, Lee IM, Zhang S, Dossus L, Cox DG, Khaw KT, Lund E, Naccarati A, Peeters PH, Quirós JR, Riboli E, Sund M, Trichopoulos D, Prentice RL, Kraft P, Kaaks R, Campa D. Post-GWAS gene-environment interplay in breast cancer: results from the Breast and Prostate Cancer Cohort Consortium and a meta-analysis on 79,000 women. Hum Mol Genet. 2014 Oct 01;23(19):5260-70. PMCID: PMC4159150
21. TG and HDL Working Group of the Exome Sequencing Project, National Heart, Lung, and Blood Institute, Crosby J, Peloso GM, Auer PL, Crosslin DR, Stitziel NO, Lange LA, Lu Y, Tang ZZ, Zhang H, Hindy G, Masca N, Stirrups K, Kanoni S, Do R, Jun G, Hu Y, Kang HM, Xue C, Goel A, Farrall M, Duga S, Merlini PA, Asselta R, Girelli D, Olivieri O, Martinelli N, Yin W, Reilly D, Speliotes E, Fox CS, Hveem K, Holmen OL, Nikpay M, Farlow DN, Assimes TL, Franceschini N, Robinson J, North KE, Martin LW, DePristo M, Gupta N, Escher SA, Jansson JH, Van Zuydam N, Palmer CN, Wareham N, Koch W, Meitinger T, Peters A, Lieb W, Erbel R, Konig IR, Kruppa J, Degenhardt F, Gottesman O, Bottinger EP, O'Donnell CJ, Psaty BM, Ballantyne CM, Abecasis G, Ordovas JM, Melander O, Watkins H, Orho-Melander M, Ardissino D, Loos RJ, McPherson R, Willer CJ, Erdmann J, Hall AS, Samani NJ, Deloukas P, Schunkert H, Wilson JG, Kooperberg C, Rich SS, Tracy RP, Lin DY, Altshuler D, Gabriel S, Nickerson DA, Jarvik GP, Cupples LA, Reiner AP, Boerwinkle E, Kathiresan S. Loss-of-function mutations in APOC3, triglycerides, and coronary disease. N Engl J Med. 2014 Jul 03;371(1):22-31. PMCID: PMC4180269
22. Du M, Auer PL, Jiao S, Haessler J, Altshuler D, Boerwinkle E, Carlson CS, Carty CL, Chen YD, Curtis K, Franceschini N, Hsu L, Jackson R, Lange LA, Lettre G, Monda KL, National Heart, Lung, and Blood Institute (NHLBI) GO Exome Sequencing Project, Nickerson DA, Reiner AP, Rich SS, Rosse SA, Rotter JI, Willer CJ, Wilson JG, North K, Kooperberg C, Heard-Costa N, Peters U. Whole-exome imputation of sequence variants identified two novel alleles associated with adult body height in African Americans. Hum Mol Genet. 2014 Dec 15;23(24):6607-15. PMCID: PMC4240196
23. Tabor HK, Auer PL, Jamal SM, Chong JX, Yu JH, Gordon AS, Graubert TA, O'Donnell CJ, Rich SS, Nickerson DA, NHLBI Exome Sequencing Project, Bamshad MJ. Pathogenic variants for Mendelian and complex traits in exomes of 6,517 European and African Americans: implications for the return of incidental results. Am J Hum Genet. 2014 Aug 07;95(2):183-93. PMCID: PMC4129409
24. Myocardial Infarction Genetics Consortium Investigators, Stitziel NO, Won HH, Morrison AC, Peloso GM, Do R, Lange LA, Fontanillas P, Gupta N, Duga S, Goel A, Farrall M, Saleheen D, Ferrario P, König I, Asselta R, Merlini PA, Marziliano N, Notarangelo MF, Schick U, Auer P, Assimes TL, Reilly M, Wilensky R, Rader DJ, Hovingh GK, Meitinger T, Kessler T, Kastrati A, Laugwitz KL, Siscovick D, Rotter JI, Hazen SL, Tracy R, Cresci S, Spertus J, Jackson R, Schwartz SM, Natarajan P, Crosby J, Muzny D, Ballantyne C, Rich SS, O'Donnell CJ, Abecasis G, Sunaev S, Nickerson DA, Buring JE, Ridker PM, Chasman DI, Austin E, Kullo IJ, Weeke PE, Shaffer CM, Bastarache LA, Denny JC, Roden DM, Palmer C, Deloukas P, Lin DY, Tang ZZ, Erdmann J, Schunkert H, Danesh J, Marrugat J, Elosua R, Ardissino D, McPherson R, Watkins H, Reiner AP, Wilson JG, Altshuler D, Gibbs RA, Lander ES, Boerwinkle E, Gabriel S, Kathiresan S. Inactivating mutations in NPC1L1 and protection from coronary heart disease. N Engl J Med. 2014 Nov 27;371(22):2072-82. PMCID: PMC4335708
25. Rosse SA, Auer PL, Carlson CS. Functional annotation of putative regulatory elements at cancer susceptibility Loci. Cancer Inform. 2014;13(Suppl 2):5-17. PMCID: PMC4179605
26. Jiang H, An L, Baladandayuthapani V, Auer PL. Classification, predictive modelling, and statistical analysis of cancer data (a). Cancer Inform. 2014;13(Suppl 2):1-3. PMCID: PMC4179642
27. Naik RP, Derebail VK, Grams ME, Franceschini N, Auer PL, Peloso GM, Young BA, Lettre G, Peralta CA, Katz R, Hyacinth HI, Quarells RC, Grove ML, Bick AG, Fontanillas P, Rich SS, Smith JD, Boerwinkle E, Rosamond WD, Ito K, Lanzkron S, Coresh J, Correa A, Sarto GE, Key NS, Jacobs DR,

Kathiresan S, Bibbins-Domingo K, Kshirsagar AV, Wilson JG, Reiner AP. Association of sickle cell trait with chronic kidney disease and albuminuria in African Americans. JAMA. 2014 Nov 26;312(20):2115-25. PMCID: PMC4356116

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