# Lawrence F Bielak

List of Publications by Year
in descending order



| 91 | 11,018 | 66343 42 | 45317 90 |
|---|---|---|---|
| papers | citations | h-index | g-index |

| 99 | 99 | 99 | 17425 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Epigenetics of single-site and multi-site atherosclerosis in African Americans from the Genetic Epidemiology Network of Arteriopathy (GENOA). Clinical Epigenetics, 2022, 14, 10. | 4.1 | 6 |
| 2 | Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96. | 6.2 | 24 |
| 3 | Type 2 Diabetes Partitioned Polygenic Scores Associate With Disease Outcomes in 454,193 Individuals Across 13 Cohorts. Diabetes Care, 2022, 45, 674-683. | 8.6 | 29 |
| 4 | Multivariate, regionâ€based genetic analyses of facets of reproductive aging in White and Black women. Molecular Genetics & Genomic Medicine, 2022, 10, e1896. | 1.2 | 1 |
| 5 | Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148. | 2.8 | 2 |
| 6 | Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572. | 21.4 | 250 |
| 7 | Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. Nature Genetics, 2022, 54, 581-592. | 21.4 | 142 |
| 8 | Epigenome-wide association study identifies DNA methylation sites associated with target organ damage in older African Americans. Epigenetics, 2021, 16, 862-875. | 2.7 | 10 |
| 9 | A Noncoding Variant Near PPP1R3B Promotes Liver Glycogen Storage and MetS, but Protects Against Myocardial Infarction. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 372-387. | 3.6 | 12 |
| 10 | Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. Human Genetics and Genomics Advances, 2021, 2, 100013. | 1.7 | 2 |
| 11 | Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24. | 12.8 | 87 |
| 12 | Genome-wide association study of serum liver enzymes implicates diverse metabolic and liver pathology. Nature Communications, 2021, 12, 816. | 12.8 | 64 |
| 13 | Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299. | 27.8 | 1,069 |
| 14 | Epigenetic age acceleration is associated with cardiometabolic risk factors and clinical cardiovascular disease risk scores in African Americans. Clinical Epigenetics, 2021, 13, 55. | 4.1 | 37 |
| 15 | Associations between polygenic risk score for age at menarche and menopause, reproductive timing, and serum hormone levels in multiple race/ethnic groups. Menopause, 2021, 28, 819-828. | 2.0 | 8 |
| 16 | Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. American Journal of Human Genetics, 2021, 108, 564-582. | 6.2 | 18 |
| 17 | Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182. | 12.8 | 17 |
| 18 | Allele-specific variation atAPOEincreases nonalcoholic fatty liver disease and obesity but decreases risk of Alzheimerâ€™s disease and myocardial infarction. Human Molecular Genetics, 2021, 30, 1443-1456. | 2.9 | 20 |

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|---|---|---|---|
| 19 | Genetic discovery and risk characterization in type 2 diabetes across diverse populations. Human Genetics and Genomics Advances, 2021, 2, 100029. | 1.7 | 23 |
| 20 | The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860. | 21.4 | 341 |
| 21 | Epigenome-wide association study of mitochondrial genome copy number. Human Molecular Genetics, 2021, 31, 309-319. | 2.9 | 6 |
| 22 | Multiethnic Genome-Wide Association Study of Subclinical Atherosclerosis in Individuals With Type 2 Diabetes. Circulation Genomic and Precision Medicine, 2021, 14, e003258. | 3.6 | 4 |
| 23 | Epidemiologic and Genetic Associations of Erythropoietin With Blood Pressure, Hypertension, and Coronary Artery Disease. Hypertension, 2021, 78, 1555-1566. | 2.7 | 1 |
| 24 | Association of mitochondrial DNA copy number with cardiometabolic diseases. Cell Genomics, 2021, 1, 100006. | 6.5 | 26 |
| 25 | The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679. | 27.8 | 353 |
| 26 | Western Dietary Pattern Derived by Multiple Statistical Methods Is Prospectively Associated with Subclinical Carotid Atherosclerosis in Midlife Women. Journal of Nutrition, 2020, 150, 579-591. | 2.9 | 24 |
| 27 | Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768. | 27.8 | 376 |
| 28 | Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332. | 21.4 | 91 |
| 29 | Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nature Genetics, 2020, 52, 969-983. | 21.4 | 146 |
| 30 | Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417. | 12.8 | 39 |
| 31 | Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125. | 7.9 | 17 |
| 32 | Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. PLoS ONE, 2020, 15, e0230815. | 2.5 | 10 |
| 33 | Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. Circulation Genomic and Precision Medicine, 2020, 13, e002772. | 3.6 | 11 |
| 34 | Fetal and early postnatal lead exposure measured in teeth associates with infant gut microbiota. Environment International, 2020, 144, 106062. | 10.0 | 21 |
| 35 | Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815. | | 0 |
| 36 | Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815. | | 0 |

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| 37 | Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815. | | 0 |
| 38 | Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815. | | 0 |
| 39 | Prospective associations between beverage intake during the midlife and subclinical carotid atherosclerosis: The Study of Womenâ€™s Health Across the Nation. PLoS ONE, 2019, 14, e0219301. | 2.5 | 8 |
| 40 | Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957. | 12.8 | 84 |
| 41 | Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054. | 3.4 | 85 |
| 42 | Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376. | 12.8 | 64 |
| 43 | A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633. | 2.9 | 31 |
| 44 | Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648. | 21.4 | 112 |
| 45 | In utero metal exposures measured in deciduous teeth and birth outcomes in a racially-diverse urban cohort. Environmental Research, 2019, 171, 444-451. | 7.5 | 17 |
| 46 | Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469. | 21.4 | 89 |
| 47 | Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. American Journal of Human Genetics, 2019, 104, 260-274. | 6.2 | 103 |
| 48 | Testing crossâ€phenotype effects of rare variants in longitudinal studies of complex traits. Genetic Epidemiology, 2018, 42, 320-332. | 1.3 | 5 |
| 49 | Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571. | 21.4 | 356 |
| 50 | A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400. | 6.2 | 123 |
| 51 | Relationships of Clinical and Computed Tomography-Imaged Adiposity with Cognition in Middle-Aged and Older African Americans. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2018, 73, 492-498. | 3.6 | 5 |
| 52 | Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. Nature Genetics, 2018, 50, 1505-1513. | 21.4 | 1,331 |
| 53 | Genetics of Subclinical Coronary Atherosclerosis. Current Genetic Medicine Reports, 2018, 6, 116-123. | 1.9 | 5 |
| 54 | Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166. | 2.5 | 94 |

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|---|---|---|---|
| 55 | Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41. | 21.4 | 286 |
| 56 | Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190. | 27.8 | 544 |
| 57 | Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977. | 12.8 | 169 |
| 58 | Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. Nature Genetics, 2017, 49, 125-130. | 21.4 | 116 |
| 59 | Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. Nature Communications, 2017, 8, 910. | 12.8 | 118 |
| 60 | Burden of higher lead exposure in African-Americans starts in utero and persists into childhood. Environment International, 2017, 108, 221-227. | 10.0 | 62 |
| 61 | Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528. | 3.5 | 158 |
| 62 | Neighborhood-Level Poverty at Menarche and Prepregnancy Obesity in African-American Women. Journal of Pregnancy, 2016, 2016, 1-7. | 2.4 | 4 |
| 63 | An Empirical Comparison of Joint and Stratified Frameworks for Studying G Ã— E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Geneâ€Lifestyle Interactions Working Group. Genetic Epidemiology, 2016, 40, 404-415. | 1.3 | 18 |
| 64 | Mapping adipose and muscle tissue expression quantitative trait loci in African Americans to identify genes for type 2 diabetes and obesity. Human Genetics, 2016, 135, 869-880. | 3.8 | 44 |
| 65 | Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. Circulation: Cardiovascular Genetics, 2016, 9, 511-520. | 5.1 | 54 |
| 66 | Genetic Research and Womenâ€™s Heart Disease: a Primer. Current Atherosclerosis Reports, 2016, 18, 67. | 4.8 | 11 |
| 67 | Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472. | 21.4 | 284 |
| 68 | Trans-ethnic Meta-analysis and Functional Annotation Illuminates theÂGenetic Architecture of Fasting Glucose and Insulin. American Journal of Human Genetics, 2016, 99, 56-75. | 6.2 | 55 |
| 69 | Arsenic exposure is associated with diminished insulin sensitivity in nonâ€diabetic Amish adults. Diabetes/Metabolism Research and Reviews, 2016, 32, 565-571. | 4.0 | 30 |
| 70 | A Statistical Approach for Testing Cross-Phenotype Effects of Rare Variants. American Journal of Human Genetics, 2016, 98, 525-540. | 6.2 | 75 |
| 71 | A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370. | 2.9 | 73 |
| 72 | Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462. | 27.8 | 173 |

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| 73 | A Statistical Approach for Rare-Variant Association Testing in Affected Sibships. American Journal of Human Genetics, 2015, 96, 543-554. | 6.2 | 21 |
| 74 | Epigenomic Indicators of Age in African Americans. Hereditary Genetics: Current Research, 2014, 03, . | 0.1 | 10 |
| 75 | Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. PLoS Genetics, 2014, 10, e1004517. | 3.5 | 191 |
| 76 | Abstract 18767: Association of Protein-Coding Genetic Variants with Coronary Arterial Calcification in 21,000 Individuals of European and African Ancestries. Circulation, 2014, 130, . | 1.6 | 0 |
| 77 | Genetics of coronary artery calcification among African Americans, a meta-analysis. BMC Medical Genetics, 2013, 14, 75. | 2.1 | 73 |
| 78 | Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005. | 21.4 | 746 |
| 79 | A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669. | 21.4 | 762 |
| 80 | Genome-Wide Association Study for Coronary Artery Calcification With Follow-Up in Myocardial Infarction. Circulation, 2011, 124, 2855-2864. | 1.6 | 269 |
| 81 | Breast Arterial Calcification Is Associated with Reproductive Factors in Asymptomatic Postmenopausal Women. Journal of Women's Health, 2010, 19, 1721-1726. | 3.3 | 9 |
| 82 | Circulating CD34+ Cell Count is Associated with Extent of Subclinical Atherosclerosis in Asymptomatic Amish Men, Independent of 10-Year Framingham Risk. Clinical Medicine Cardiology, 2009, 3, CMC.S2111. | 0.1 | 24 |
| 83 | Differences in prevalence and severity of coronary artery calcification between two non-Hispanic white populations with diverse lifestyles. Atherosclerosis, 2008, 196, 888-895. | 0.8 | 14 |
| 84 | Genomic loci with pleiotropic effects on coronary artery calcification. Atherosclerosis, 2006, 185, 340-346. | 0.8 | 26 |
| 85 | Age-dependent associations between blood pressure and coronary artery calcification in asymptomatic adults. Journal of Hypertension, 2004, 22, 719-725. | 0.5 | 32 |
| 86 | Electron-beam computed tomography screening for asymptomatic coronary artery disease. Seminars in Roentgenology, 2003, 38, 39-53. | 0.6 | 8 |
| 87 | Heritability of Coronary Artery Calcium Quantity Measured by Electron Beam Computed Tomography in Asymptomatic Adults. Circulation, 2002, 106, 304-308. | 1.6 | 121 |
| 88 | Gender- and age-dependent relationships between the E-selectin S128R polymorphism and coronary artery calcification. Journal of Molecular Medicine, 2001, 79, 390-398. | 3.9 | 66 |
| 89 | Long-Term Prognostic Value of Coronary Calcification Detected by Electron-Beam Computed Tomography in Patients Undergoing Coronary Angiography. Circulation, 2001, 104, 412-417. | 1.6 | 363 |
| 90 | Association of Fibrinogen With Quantity of Coronary Artery Calcification Measured by Electron Beam Computed Tomography. Arteriosclerosis, Thrombosis, and Vascular Biology, 2000, 20, 2167-2171. | 2.4 | 41 |

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|---|---|---|---|
| 91 | Probabilistic Model for Prediction of Angiographically Defined Obstructive Coronary Artery Disease Using Electron Beam Computed Tomography Calcium Score Strata. Circulation, 2000, 102, 380-385. | 1.6 | 140 |