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	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
2	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
3	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
4	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
5	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
6	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
7	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
8	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
9	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
10	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
11	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
12	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
13	Genome-Wide Association Study for Coronary Artery Calcification With Follow-Up in Myocardial Infarction. Circulation, 2011, 124, 2855-2864.	1.6	269
14	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
15	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
16	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
17	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
18	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158

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19	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
20	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. Nature Genetics, 2022, 54, 581-592.	21.4	142
21	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
22	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
23	Heritability of Coronary Artery Calcium Quantity Measured by Electron Beam Computed Tomography in Asymptomatic Adults. Circulation, 2002, 106, 304-308.	1.6	121
24	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. Nature Communications, 2017, 8, 910.	12.8	118
25	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
26	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
27	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
28	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
29	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
30	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
31	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
32	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
33	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
34	A Statistical Approach for Testing Cross-Phenotype Effects of Rare Variants. American Journal of Human Genetics, 2016, 98, 525-540.	6.2	75
35	Genetics of coronary artery calcification among African Americans, a meta-analysis. BMC Medical Genetics, 2013, 14, 75.	2.1	73
36	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	2.9	73

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37	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
38	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
39	Genome-wide association study of serum liver enzymes implicates diverse metabolic and liver pathology. Nature Communications, 2021, 12, 816.	12.8	64
40	Burden of higher lead exposure in African-Americans starts in utero and persists into childhood. Environment International, 2017, 108, 221-227.	10.0	62
41	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
42	Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. Circulation: Cardiovascular Genetics, 2016, 9, 511-520.	5.1	54
43	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
44	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
45	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	12.8	39
46	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
47	Age-dependent associations between blood pressure and coronary artery calcification in asymptomatic adults. Journal of Hypertension, 2004, 22, 719-725.	0.5	32
48	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
49	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
50	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
51	Genomic loci with pleiotropic effects on coronary artery calcification. Atherosclerosis, 2006, 185, 340-346.	0.8	26
52	Association of mitochondrial DNA copy number with cardiometabolic diseases. Cell Genomics, 2021, 1, 100006.	6.5	26
53	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
54	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

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55	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
56	Genetic discovery and risk characterization in type 2 diabetes across diverse populations. Human Genetics and Genomics Advances, 2021, 2, 100029.	1.7	23
57	A Statistical Approach for Rare-Variant Association Testing in Affected Sibships. American Journal of Human Genetics, 2015, 96, 543-554.	6.2	21
58	Fetal and early postnatal lead exposure measured in teeth associates with infant gut microbiota. Environment International, 2020, 144, 106062.	10.0	21
59	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
60	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
61	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
62	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
63	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
64	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	12.8	17
65	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
66	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
67	Genetic Research and Womenâ€™s Heart Disease: a Primer. Current Atherosclerosis Reports, 2016, 18, 67.	4.8	11
68	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
69	Epigenomic Indicators of Age in African Americans. Hereditary Genetics: Current Research, 2014, 03, .	0.1	10
70	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
71	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. PLoS ONE, 2020, 15, e0230815.	2.5	10
72	Breast Arterial Calcification Is Associated with Reproductive Factors in Asymptomatic Postmenopausal Women. Journal of Women's Health, 2010, 19, 1721-1726.	3.3	9

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73	Electron-beam computed tomography screening for asymptomatic coronary artery disease. Seminars in Roentgenology, 2003, 38, 39-53.	0.6	8
74	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
75	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
76	Epigenome-wide association study of mitochondrial genome copy number. Human Molecular Genetics, 2021, 31, 309-319.	2.9	6
77	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
78	Testing crossâ€phenotype effects of rare variants in longitudinal studies of complex traits. Genetic Epidemiology, 2018, 42, 320-332.	1.3	5
79	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
80	Genetics of Subclinical Coronary Atherosclerosis. Current Genetic Medicine Reports, 2018, 6, 116-123.	1.9	5
81	Neighborhood-Level Poverty at Menarche and Prepregnancy Obesity in African-American Women. Journal of Pregnancy, 2016, 2016, 1-7.	2.4	4
82	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
83	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
84	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	2.8	2
85	Epidemiologic and Genetic Associations of Erythropoietin With Blood Pressure, Hypertension, and Coronary Artery Disease. Hypertension, 2021, 78, 1555-1566.	2.7	1
86	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
87	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
88	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
89	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
90	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0

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91	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0