Benjamin F Voight

List of Publications by Year
in descending order

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Version: 2024-02-01

114 papers	25,719 citations	61984 43 h-index	39675 94 g-index
145 all docs	145 docs citations	145 times ranked	33356 citing authors

#	Article	IF	Citations
1	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
2	A Map of Recent Positive Selection in the Human Genome. PLoS Biology, 2006, 4, e72.	5.6	2,329
3	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	21.4	1,982
4	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. Lancet, The, 2012, 380, 572-580.	13.7	1,937
5	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
6	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	21.4	1,439
7	Convergent adaptation of human lactase persistence in Africa and Europe. Nature Genetics, 2007, 39, 31-40.	21.4	1,375
8	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	21.4	959
9	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
10	Genome-Wide Association Analysis Identifies Variants Associated with Nonalcoholic Fatty Liver Disease That Have Distinct Effects on Metabolic Traits. PLoS Genetics, 2011, 7, e1001324.	3.5	796
11	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
12	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
13	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	21.4	591
14	Practical aspects of imputation-driven meta-analysis of genome-wide association studies. Human Molecular Genetics, 2008, 17, R122-R128.	2.9	475
15	Discovery of 318 new risk loci for type 2 diabetes and related vascular outcomes among 1.4 million participants in a multi-ancestry meta-analysis. Nature Genetics, 2020, 52, 680-691.	21.4	445
16	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. Nature Genetics, 2014, 46, 357-363.	21.4	428
17	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	3.5	419
18	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. Diabetes, 2010, 59, 3229-3239.	0.6	387

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19	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	21.4	365
20	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
21	Genome-Wide Association Identifies Nine Common Variants Associated With Fasting Proinsulin Levels and Provides New Insights Into the Pathophysiology of Type 2 Diabetes. Diabetes, 2011, 60, 2624-2634.	0.6	335
22	PNPLA3variants specifically confer increased risk for histologic nonalcoholic fatty liver disease but not metabolic disease. Hepatology, 2010, 52, 904-912.	7.3	317
23	Interrogating multiple aspects of variation in a full resequencing data set to infer human population size changes. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 18508-18513.	7.1	244
24	Genome-wide association study implicates novel loci and reveals candidate effector genes for longitudinal pediatric bone accrual. Genome Biology, 2021, 22, 1.	8.8	239
25	Identification of new susceptibility loci for type 2 diabetes and shared etiological pathways with coronary heart disease. Nature Genetics, 2017, 49, 1450-1457.	21.4	218
26	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	2.5	197
27	Confounding from Cryptic Relatedness in Case-Control Association Studies. PLoS Genetics, 2005, 1, e32.	3.5	193
28	The Nephila clavipes genome highlights the diversity of spider silk genes and their complex expression. Nature Genetics, 2017, 49, 895-903.	21.4	190
29	An expanded sequence context model broadly explains variability in polymorphism levels across the human genome. Nature Genetics, 2016, 48, 349-355.	21.4	174
30	A Central Role for GRB10 in Regulation of Islet Function in Man. PLoS Genetics, 2014, 10, e1004235.	3.5	164
31	Causal Assessment of Serum Urate Levels inÂCardiometabolic Diseases Through a Mendelian Randomization Study. Journal of the American College of Cardiology, 2016, 67, 407-416.	2.8	138
32	Detecting Long-Term Balancing Selection Using Allele Frequency Correlation. Molecular Biology and Evolution, 2017, 34, 2996-3005.	8.9	117
33	Genetic Variation Determines PPARÎ³ Function and Anti-diabetic Drug Response InÂVivo. Cell, 2015, 162, 33-44.	28.9	107
34	A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. PLoS Genetics, 2020, 16, e1008629.	3.5	101
35	Power in the phenotypic extremes: a simulation study of power in discovery and replication of rare variants. Genetic Epidemiology, 2011, 35, 236-246.	1.3	97
36	Projected Prevalence of Actionable Pharmacogenetic Variants and Level A Drugs Prescribed Among US Veterans Health Administration Pharmacy Users. JAMA Network Open, 2019, 2, e195345.	5.9	95

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37	Mapping the genetic architecture of human traits to cell types in the kidney identifies mechanisms of disease and potential treatments. Nature Genetics, 2021, 53, 1322-1333.	21.4	87
38	Large-Scale trans -eQTLs Affect Hundreds of Transcripts and Mediate Patterns of Transcriptional Co-regulation. American Journal of Human Genetics, 2017, 100, 581-591.	6.2	86
39	Epigenomic and transcriptomic analyses define core cell types, genes and targetable mechanisms for kidney disease. Nature Genetics, 2022, 54, 950-962.	21.4	71
40	A multiancestry genome-wide association study of unexplained chronic ALT elevation as a proxy for nonalcoholic fatty liver disease with histological and radiological validation. Nature Genetics, 2022, 54, 761-771.	21.4	68
41	Relative contribution of type 1 and type 2 diabetes loci to the genetic etiology of adult-onset, non-insulin-requiring autoimmune diabetes. BMC Medicine, 2017, 15, 88.	5.5	67
42	Patterns of shared signatures of recent positive selection across human populations. Nature Ecology and Evolution, 2018, 2, 713-720.	7.8	63
43	The relationship between circulating lipids and breast cancer risk: A Mendelian randomization study. PLoS Medicine, 2020, 17, e1003302.	8.4	63
44	Genetics of height and risk of atrial fibrillation: A Mendelian randomization study. PLoS Medicine, 2020, 17, e1003288.	8.4	51
45	Genetic analysis in European ancestry individuals identifies 517 loci associated with liver enzymes. Nature Communications, 2021, 12, 2579.	12.8	51
46	Multiethnic Genetic Association Studies Improve Power for Locus Discovery. PLoS ONE, 2010, 5, e12600.	2.5	50
47	BetaScan2: Standardized Statistics to Detect Balancing Selection Utilizing Substitution Data. Genome Biology and Evolution, 2020, 12, 3873-3877.	2.5	49
48	Prioritizing the Role of Major Lipoproteins and Subfractions as Risk Factors for Peripheral Artery Disease. Circulation, 2021, 144, 353-364.	1.6	47
49	Systolic Blood Pressure and Risk of Type 2 Diabetes: A Mendelian Randomization Study. Diabetes, 2017, 66, 543-550.	0.6	45
50	A single genetic locus controls both expression of DPEP1/CHMP1A and kidney disease development via ferroptosis. Nature Communications, 2021, 12, 5078.	12.8	45
51	Genetics of Smoking and Risk of Atherosclerotic Cardiovascular Diseases. JAMA Network Open, 2021, 4, e2034461.	5.9	42
52	Natural human genetic variation determines basal and inducible expression of PM20D1 , an obesity-associated gene. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23232-23242.	7.1	35
53	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. International Journal of Epidemiology, 2020, 49, 1022-1031.	1.9	34
54	Pathway and network-based strategies to translate genetic discoveries into effective therapies. Human Molecular Genetics, 2016, 25, R94-R98.	2.9	33

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55	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
56	Genetically Determined Later Puberty Impacts Lowered Bone Mineral Density in Childhood and Adulthood. Journal of Bone and Mineral Research, 2018, 33, 430-436.	2.8	31
57	Signals of Variation in Human Mutation Rate at Multiple Levels of Sequence Context. Molecular Biology and Evolution, 2019, 36, 955-965.	8.9	28
58	Genetic variants primarily associated with type 2 diabetes are related to coronary artery disease risk. Atherosclerosis, 2015, 241, 419-426.	0.8	26
59	Serum calcium and risk of migraine: a Mendelian randomization study. Human Molecular Genetics, 2017, 26, ddw416.	2.9	26
60	Bivariate Genome-Wide Association Scan Identifies 6 Novel Loci Associated With Lipid Levels and Coronary Artery Disease. Circulation Genomic and Precision Medicine, 2018, 11, e002239.	3.6	26
61	Association Between Genetic Variation in Blood Pressure and Increased Lifetime Risk of Peripheral Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 2027-2034.	2.4	24
62	Genetic Discrimination Between LADA and Childhood-Onset Type 1 Diabetes Within the MHC. Diabetes Care, 2020, 43, 418-425.	8.6	23
63	Type 1 diabetes in Africa: an immunogenetic study in the Amhara of North-West Ethiopia. Diabetologia, 2020, 63, 2158-2168.	6.3	17
64	A unified framework identifies new links between plasma lipids and diseases from electronic medical records across large-scale cohorts. Nature Genetics, 2021, 53, 972-981.	21.4	17
65	Polygenic Risk Scores in Alzheimerâ€™s Disease Genetics: Methodology, Applications, Inclusion, and Diversity. Journal of Alzheimer's Disease, 2022, 89, 1-12.	2.6	17
66	Validating a non-invasive, ALT-based non-alcoholic fatty liver phenotype in the million veteran program. PLoS ONE, 2020, 15, e0237430.	2.5	15
67	Multi-trait association studies discover pleiotropic loci between Alzheimerâ€™s disease and cardiometabolic traits. Alzheimer's Research and Therapy, 2021, 13, 34.	6.2	15
68	Genetically Determined Birthweight Associates With Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2020, 13, e002553.	3.6	13
69	Genetic Evidence for Repurposing of GLP1R (Glucagonâ€Like Peptideâ€1 Receptor) Agonists to Prevent Heart Failure. Journal of the American Heart Association, 2021, 10, e020331.	3.7	13
70	Assessing the general population frequency of rare coding variants in the EXT1 and EXT2 genes previously implicated in hereditary multiple exostoses. Bone, 2016, 92, 196-200.	2.9	12
71	Multiâ€phenotype analyses of hemostatic traits with cardiovascular events reveal novel genetic associations. Journal of Thrombosis and Haemostasis, 2022, 20, 1331-1349.	3.8	12
72	A multi-population phenome-wide association study of genetically-predicted height in the Million Veteran Program. PLoS Genetics, 2022, 18, e1010193.	3.5	12

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73	A Missense Variant in the IL-6 Receptor and Protection From Peripheral Artery Disease. Circulation Research, 2021, 129, 968-970.	4.5	11
74	Golden orb-weaving spider (Trichonephila clavipes) silk genes with sex-biased expression and atypical architectures. G3: Genes, Genomes, Genetics, 2021, 11, 1-10.	1.8	11
75	Cis-regulatory architecture of human ESC-derived hypothalamic neuron differentiation aids in variant-to-gene mapping of relevant complex traits. Nature Communications, 2021, 12, 6749.	12.8	11
76	Genetic colocalization atlas points to common regulatory sites and genes for hematopoietic traits and hematopoietic contributions to disease phenotypes. BMC Medical Genomics, 2020, 13, 89.	1.5	10
77	Separating the direct effects of traits on atherosclerotic cardiovascular disease from those mediated by type 2 diabetes. Diabetologia, 2022, 65, 790-799.	6.3	9
78	Characterization of the genome and silk-gland transcriptomes of Darwinâ€™s bark spider (Caerostris) Tj ETQq0 0 0 rgBT /Overlock 10 T	2.5	8
79	MR_predictor: a simulation engine for Mendelian Randomization studies. Bioinformatics, 2014, 30, 3432-3434.	4.1	7
80	MeRP: a high-throughput pipeline for Mendelian randomization analysis. Bioinformatics, 2015, 31, 957-959.	4.1	7
81	Human genetics shines a light on ischaemic stroke. Lancet Neurology, The, 2016, 15, 130-131.	10.2	6
82	De novo mutational profile in RB1 clarified using a mutation rate modeling algorithm. BMC Genomics, 2017, 18, 155.	2.8	6
83	Genetic determinants of increased body mass index mediate the effect of smoking on increased risk for type 2 diabetes but not coronary artery disease. Human Molecular Genetics, 2020, 29, 3327-3337.	2.9	6
84	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. Circulation Genomic and Precision Medicine, 2020, 13, e002769.	3.6	5
85	Gene Set Enrichment Analyses: lessons learned from the heart failure phenotype. BioData Mining, 2017, 10, 18.	4.0	4
86	Postmenopausal osteoporotic fracture-associated COLIA1 variant impacts bone accretion in girls. Bone, 2019, 121, 221-226.	2.9	4
87	Keen on the tenure track job, are you? Know these things, you should. Genome Biology, 2019, 20, 6.	8.8	4
88	Body mass index and adipose distribution have opposing genetic impacts on human blood traits. ELife, 2022, 11, .	6.0	4
89	Disentangling the Causal Association of Plasma Lipid Traits and Type 2 Diabetes Using Human Genetics. JAMA Cardiology, 2016, 1, 631.	6.1	3
90	Multi-Trait Genome-Wide Association Study of Atherosclerosis Detects Novel Pleiotropic Loci. Frontiers in Genetics, 2021, 12, 787545.	2.3	3

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91	Dissecting an adiposity locus with an arsenal of genomics. Genome Biology, 2018, 19, 74.	8.8	1
92	Tropomyosin 1 Genetically Constrains in Vitro Megakaryopoiesis. Blood, 2019, 134, 3612-3612.	1.4	1
93	Type 2 Diabetes Genes Gleaned by Making a Î²-Cell Screen Routine. Diabetes, 2016, 65, 3541-3543.	0.6	0
94	RA- cing Toward Drugs from a Genetics Starting Line. Science Translational Medicine, 2013, 5, .	12.4	0
95	Ironing Out Parkinsonâ€™s Disease. Science Translational Medicine, 2013, 5, .	12.4	0
96	The Virtue of Intolerance. Science Translational Medicine, 2013, 5, .	12.4	0
97	Thinking Before We Act. Science Translational Medicine, 2013, 5, .	12.4	0
98	Right Place, Right Time. Science Translational Medicine, 2013, 5, .	12.4	0
99	A Metabolic Relic. Science Translational Medicine, 2014, 6, .	12.4	0
100	SORT ing Out That Pesky Cholesterol. Science Translational Medicine, 2014, 6, .	12.4	0
101	Genetically Determined Obesity and Adipose Distribution Impact Human Blood Trait Variation across Cell Lineages. Blood, 2021, 138, 1876-1876.	1.4	0
102	Manipulation of Tropomysin 1 in iPSCs to Enhance in Vitro Blood Cell Production. Blood, 2020, 136, 34-35.	1.4	0
103	Genetics of height and risk of atrial fibrillation: A Mendelian randomization study. , 2020, 17, e1003288.		0
104	Genetics of height and risk of atrial fibrillation: A Mendelian randomization study. , 2020, 17, e1003288.		0
105	Genetics of height and risk of atrial fibrillation: A Mendelian randomization study. , 2020, 17, e1003288.		0
106	Genetics of height and risk of atrial fibrillation: A Mendelian randomization study. , 2020, 17, e1003288.		0
107	Genetics of height and risk of atrial fibrillation: A Mendelian randomization study. , 2020, 17, e1003288.		0
108	The relationship between circulating lipids and breast cancer risk: A Mendelian randomization study. , 2020, 17, e1003302.		0

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109	The relationship between circulating lipids and breast cancer risk: A Mendelian randomization study. , 2020, 17, e1003302.		0
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112	The relationship between circulating lipids and breast cancer risk: A Mendelian randomization study. , 2020, 17, e1003302.		0
113	The relationship between circulating lipids and breast cancer risk: A Mendelian randomization study. , 2020, 17, e1003302.		0
114	The relationship between circulating lipids and breast cancer risk: A Mendelian randomization study. , 2020, 17, e1003302.		0