Toby Johnson

List of Publications by Year
in descending order

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93 papers	39,437 citations	13099 68 h-index	37204 96 g-index
101 all docs	101 docs citations	101 times ranked	41143 citing authors

#	Article	IF	Citations
1	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	27.8	3,249
2	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
3	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	21.4	2,634
4	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
5	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. Lancet, The, 2012, 380, 572-580.	13.7	1,937
6	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
7	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	21.4	1,572
8	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
9	Genes mirror geography within Europe. Nature, 2008, 456, 98-101.	27.8	1,287
10	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	21.4	1,179
11	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	21.4	1,104
12	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	21.4	836
13	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
14	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	21.4	754
15	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
16	Genome-wide association analysis identifies 20 loci that influence adult height. Nature Genetics, 2008, 40, 575-583.	21.4	742
17	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. Nature, 2010, 464, 713-720.	27.8	737
18	Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81.	21.4	662

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19	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	21.4	591
20	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	21.4	578
21	Meta-Analysis of 28,141 Individuals Identifies Common Variants within Five New Loci That Influence Uric Acid Concentrations. PLoS Genetics, 2009, 5, e1000504.	3.5	572
22	Genome-wide association study identifies five loci associated with lung function. Nature Genetics, 2010, 42, 36-44.	21.4	518
23	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	21.4	501
24	The Metabochip, a Custom Genotyping Array for Genetic Studies of Metabolic, Cardiovascular, and Anthropometric Traits. PLoS Genetics, 2012, 8, e1002793.	3.5	448
25	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	12.6	438
26	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
27	The evolution of mutation rates: separating causes from consequences. BioEssays, 2000, 22, 1057-1066.	2.5	403
28	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
29	Population-Based Genome-wide Association Studies Reveal Six Loci Influencing Plasma Levels of Liver Enzymes. American Journal of Human Genetics, 2008, 83, 520-528.	6.2	402
30	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	3.5	371
31	Genetic Variants Influencing Circulating Lipid Levels and Risk of Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 2264-2276.	2.4	369
32	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. Nature Genetics, 2011, 43, 1082-1090.	21.4	367
33	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
34	Identification of new therapeutic targets for osteoarthritis through genome-wide analyses of UK Biobank data. Nature Genetics, 2019, 51, 230-236.	21.4	331
35	LDL-cholesterol concentrations: a genome-wide association study. Lancet, The, 2008, 371, 483-491.	13.7	329
36	Genome-Wide Association Study of Blood Pressure Extremes Identifies Variant near UMOD Associated with Hypertension. PLoS Genetics, 2010, 6, e1001177.	3.5	312

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37	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	21.4	308
38	Theoretical models of selection and mutation on quantitative traits. Philosophical Transactions of the Royal Society B: Biological Sciences, 2005, 360, 1411-1425.	4.0	304
39	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
40	Performance of Marker-Based Relatedness Estimators in Natural Populations of Outbred Vertebrates. Genetics, 2006, 173, 2091-2101.	2.9	250
41	Genetic loci influencing kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 373-375.	21.4	246
42	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. American Journal of Human Genetics, 2012, 90, 410-425.	6.2	239
43	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838.	6.2	227
44	General Models of Multilocus Evolution. Genetics, 2002, 161, 1727-1750.	2.9	198
45	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	2.5	197
46	Gene-centric Association Signals for Lipids and Apolipoproteins Identified via the HumanCVD BeadChip. American Journal of Human Genetics, 2009, 85, 628-642.	6.2	183
47	Association of Hypertension Drug Target Genes With Blood Pressure and Hypertension in 86 588 Individuals. Hypertension, 2011, 57, 903-910.	2.7	181
48	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Human Molecular Genetics, 2011, 20, 2273-2284.	2.9	168
49	Blood Pressure Loci Identified with a Gene-Centric Array. American Journal of Human Genetics, 2011, 89, 688-700.	6.2	159
50	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	6.2	158
51	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	12.8	147
52	Genomewide Association Study Using a High-Density Single Nucleotide Polymorphism Array and Case-Control Design Identifies a Novel Essential Hypertension Susceptibility Locus in the Promoter Region of Endothelial NO Synthase. Hypertension, 2012, 59, 248-255.	2.7	144
53	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	2.9	141
54	The Effect of Deleterious Alleles on Adaptation in Asexual Populations. Genetics, 2002, 162, 395-411.	2.9	131

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55	Effect of Five Genetic Variants Associated with Lung Function on the Risk of Chronic Obstructive Lung Disease, and Their Joint Effects on Lung Function. American Journal of Respiratory and Critical Care Medicine, 2011, 184, 786-795.	5.6	128
56	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	6.2	122
57	Gene-Age Interactions in Blood Pressure Regulation: A Large-Scale Investigation with the CHARGE, Global BPgen, and ICBP Consortia. American Journal of Human Genetics, 2014, 95, 24-38.	6.2	109
58	Beneficial Mutations, Hitchhiking and the Evolution of Mutation Rates in Sexual Populations. Genetics, 1999, 151, 1621-1631.	2.9	104
59	Common Variation in the NOS1AP Gene Is Associated With Drug-Induced QT Prolongation and Ventricular Arrhythmia. Journal of the American College of Cardiology, 2012, 60, 841-850.	2.8	101
60	Genome-wide association study of genetic determinants of LDL-c response to atorvastatin therapy: importance of Lp(a). Journal of Lipid Research, 2012, 53, 1000-1011.	4.2	97
61	The approach to mutationâ€“selection balance in an infinite asexual population, and the evolution of mutation rates. Proceedings of the Royal Society B: Biological Sciences, 1999, 266, 2389-2397.	2.6	96
62	Common Variants in the ATP2B1 Gene Are Associated With Susceptibility to Hypertension. Hypertension, 2010, 56, 973-980.	2.7	96
63	The genetics of drug efficacy: opportunities and challenges. Nature Reviews Genetics, 2016, 17, 197-206.	16.3	93
64	Replication of the five novel loci for uric acid concentrations and potential mediating mechanisms. Human Molecular Genetics, 2010, 19, 387-395.	2.9	89
65	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
66	Genome-Wide Meta-Analysis for Serum Calcium Identifies Significantly Associated SNPs near the Calcium-Sensing Receptor (CASR) Gene. PLoS Genetics, 2010, 6, e1001035.	3.5	84
67	HLA-B*57:01 Confers Susceptibility to Pazopanib-Associated Liver Injury in Patients with Cancer. Clinical Cancer Research, 2016, 22, 1371-1377.	7.0	80
68	Effects of Long-Term Averaging of Quantitative Blood Pressure Traits on the Detection of Genetic Associations. American Journal of Human Genetics, 2014, 95, 49-65.	6.2	73
69	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	2.5	64
70	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. American Journal of Human Genetics, 2013, 93, 236-248.	6.2	60
71	A Comprehensive Evaluation of Potential Lung Function Associated Genes in the SpiroMeta General Population Sample. PLoS ONE, 2011, 6, e19382.	2.5	56
72	MCALIGN: Stochastic Alignment of Noncoding DNA Sequences Based on an Evolutionary Model of Sequence Evolution. Genome Research, 2004, 14, 442-450.	5.5	52

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73	BRCA1/2 mutations associated with progression-free survival in ovarian cancer patients in the AGO-OVAR 16 study. Gynecologic Oncology, 2016, 140, 443-449.	1.4	47
74	Disentangling the genetics of lean mass. American Journal of Clinical Nutrition, 2019, 109, 276-287.	4.7	38
75	A phenome-wide association study of a lipoprotein-associated phospholipase A₂loss-of-function variant in 90 000 Chinese adults. International Journal of Epidemiology, 2016, 45, 1588-1599.	1.9	36
76	Methods for testing association between uncertain genotypes and quantitative traits. Biostatistics, 2011, 12, 1-17.	1.5	35
77	Impact of Common Variation in Bone-Related Genes on Type 2 Diabetes and Related Traits. Diabetes, 2012, 61, 2176-2186.	0.6	31
78	The shared allelic architecture of adiponectin levels and coronary artery disease. Atherosclerosis, 2013, 229, 145-148.	0.8	30
79	MCALIGN2: faster, accurate global pairwise alignment of non-coding DNA sequences based on explicit models of indel evolution. BMC Bioinformatics, 2006, 7, 292.	2.6	28
80	Four Genetic Loci Influencing Electrocardiographic Indices of Left Ventricular Hypertrophy. Circulation: Cardiovascular Genetics, 2011, 4, 626-635.	5.1	28
81	Gene-centric meta-analyses for central adiposity traits in up to 57 412 individuals of European descent confirm known loci and reveal several novel associations. Human Molecular Genetics, 2014, 23, 2498-2510.	2.9	28
82	Lipoprotein-Associated Phospholipase A 2 Loss-of-Function Variant and Risk of Vascular Diseases in 90,000 Chinese Adults. Journal of the American College of Cardiology, 2016, 67, 230-231.	2.8	23
83	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. American Journal of Human Genetics, 2016, 98, 857-868.	6.2	21
84	Bayesian method for gene detection and mapping, using a case and control design and DNA pooling. Biostatistics, 2007, 8, 546-565.	1.5	20
85	The fixation probability of a beneficial allele in a population dividing by binary fission. Genetica, 2002, 115, 283-287.	1.1	19
86	Phenome-wide association study using research participantsâ€™ self-reported data provides insight into the Th17 and IL-17 pathway. PLoS ONE, 2017, 12, e0186405.	2.5	16
87	The genetic architecture of blood pressure variation. Current Cardiovascular Risk Reports, 2009, 3, 418-425.	2.0	12
88	Genetic variants in PPARGC1B and CNTN4 are associated with thromboxane A2 formation and with cardiovascular event free survival in the Anglo-Scandinavian Cardiac Outcomes Trial (ASCOT). Atherosclerosis, 2018, 269, 42-49.	0.8	7
89	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. American Journal of Human Genetics, 2012, 90, 753.	6.2	4
90	The evolution of mutation rates: separating causes from consequences. , 2000, 22, 1057.		4

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91	Quantitative genetics: Resolving wing shape genes. Current Biology, 2000, 10, R113-R115.	3.9	3
92	Communicating BRCA research results to patients enrolled in international clinical trials: lessons learnt from the AGO-OVAR 16 study. BMC Medical Ethics, 2016, 17, 63.	2.4	1
93	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2012, 90, 1116-1117.	6.2	0