Toby Johnson

List of Publications by Year
in descending order

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93 papers	39,437 citations	13087 68 h-index	37183 96 g-index
101 all docs	101 docs citations	101 times ranked	41143 citing authors

#	Article	IF	Citations
1	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	5.8	87
2	Disentangling the genetics of lean mass. American Journal of Clinical Nutrition, 2019, 109, 276-287.	2.2	38
3	Identification of new therapeutic targets for osteoarthritis through genome-wide analyses of UK Biobank data. Nature Genetics, 2019, 51, 230-236.	9.4	331
4	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.	0.4	7
5	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	5.8	147
6	Phenome-wide association study using research participantsâ€™ self-reported data provides insight into the Th17 and IL-17 pathway. PLoS ONE, 2017, 12, e0186405.	1.1	16
7	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.	1.0	1
8	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.	1.2	23
9	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. American Journal of Human Genetics, 2016, 98, 857-868.	2.6	21
10	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	9.4	362
11	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.	0.9	36
12	HLA-B*57:01 Confers Susceptibility to Pazopanib-Associated Liver Injury in Patients with Cancer. Clinical Cancer Research, 2016, 22, 1371-1377.	3.2	80
13	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	6.0	438
14	BRCA1/2 mutations associated with progression-free survival in ovarian cancer patients in the AGO-OVAR 16 study. Gynecologic Oncology, 2016, 140, 443-449.	0.6	47
15	The genetics of drug efficacy: opportunities and challenges. Nature Reviews Genetics, 2016, 17, 197-206.	7.7	93
16	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
17	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	1.1	64
18	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.	2.6	158

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19	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.	1.4	28
20	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.	2.6	109
21	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.	2.6	73
22	The shared allelic architecture of adiponectin levels and coronary artery disease. Atherosclerosis, 2013, 229, 145-148.	0.4	30
23	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. American Journal of Human Genetics, 2013, 93, 236-248.	2.6	60
24	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	9.4	2,641
25	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	9.4	754
26	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	1.4	141
27	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
28	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
29	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	1.5	371
30	The Metabochip, a Custom Genotyping Array for Genetic Studies of Metabolic, Cardiovascular, and Anthropometric Traits. PLoS Genetics, 2012, 8, e1002793.	1.5	448
31	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.	1.5	419
32	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.	1.3	144
33	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.	2.0	97
34	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	9.4	746
35	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. Lancet, The, 2012, 380, 572-580.	6.3	1,937
36	Impact of Common Variation in Bone-Related Genes on Type 2 Diabetes and Related Traits. Diabetes, 2012, 61, 2176-2186.	0.3	31

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37	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.	1.2	101
38	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838.	2.6	227
39	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
40	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.	9.4	762
41	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. American Journal of Human Genetics, 2012, 90, 410-425.	2.6	239
42	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. American Journal of Human Genetics, 2012, 90, 753.	2.6	4
43	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2012, 90, 1116-1117.	2.6	0
44	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	9.4	501
45	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	2.6	122
46	Blood Pressure Loci Identified with a Gene-Centric Array. American Journal of Human Genetics, 2011, 89, 688-700.	2.6	159
47	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.	2.5	128
48	Methods for testing association between uncertain genotypes and quantitative traits. Biostatistics, 2011, 12, 1-17.	0.9	35
49	Association of Hypertension Drug Target Genes With Blood Pressure and Hypertension in 86 588 Individuals. Hypertension, 2011, 57, 903-910.	1.3	181
50	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.	1.4	168
51	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	9.4	403
52	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. Nature Genetics, 2011, 43, 1082-1090.	9.4	367
53	Four Genetic Loci Influencing Electrocardiographic Indices of Left Ventricular Hypertrophy. Circulation: Cardiovascular Genetics, 2011, 4, 626-635.	5.1	28
54	A Comprehensive Evaluation of Potential Lung Function Associated Genes in the SpiroMeta General Population Sample. PLoS ONE, 2011, 6, e19382.	1.1	56

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55	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. Nature, 2010, 464, 713-720.	13.7	737
56	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
57	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
58	Genome-wide association study identifies five loci associated with lung function. Nature Genetics, 2010, 42, 36-44.	9.4	518
59	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	9.4	591
60	Genetic loci influencing kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 373-375.	9.4	246
61	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.	9.4	836
62	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
63	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	9.4	308
64	Common Variants in the ATP2B1 Gene Are Associated With Susceptibility to Hypertension. Hypertension, 2010, 56, 973-980.	1.3	96
65	Genetic Variants Influencing Circulating Lipid Levels and Risk of Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 2264-2276.	1.1	369
66	Genome-Wide Meta-Analysis for Serum Calcium Identifies Significantly Associated SNPs near the Calcium-Sensing Receptor (CASR) Gene. PLoS Genetics, 2010, 6, e1001035.	1.5	84
67	Genome-Wide Association Study of Blood Pressure Extremes Identifies Variant near UMOD Associated with Hypertension. PLoS Genetics, 2010, 6, e1001177.	1.5	312
68	Replication of the five novel loci for uric acid concentrations and potential mediating mechanisms. Human Molecular Genetics, 2010, 19, 387-395.	1.4	89
69	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	9.4	1,982
70	Meta-Analysis of 28,141 Individuals Identifies Common Variants within Five New Loci That Influence Uric Acid Concentrations. PLoS Genetics, 2009, 5, e1000504.	1.5	572
71	The genetic architecture of blood pressure variation. Current Cardiovascular Risk Reports, 2009, 3, 418-425.	0.8	12
72	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	9.4	1,572

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73	Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81.	9.4	662
74	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	9.4	1,104
75	Gene-centric Association Signals for Lipids and Apolipoproteins Identified via the HumanCVD BeadChip. American Journal of Human Genetics, 2009, 85, 628-642.	2.6	183
76	Population-Based Genome-wide Association Studies Reveal Six Loci Influencing Plasma Levels of Liver Enzymes. American Journal of Human Genetics, 2008, 83, 520-528.	2.6	402
77	Genes mirror geography within Europe. Nature, 2008, 456, 98-101.	13.7	1,287
78	Genome-wide association analysis identifies 20 loci that influence adult height. Nature Genetics, 2008, 40, 575-583.	9.4	742
79	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	9.4	1,179
80	LDL-cholesterol concentrations: a genome-wide association study. Lancet, The, 2008, 371, 483-491.	6.3	329
81	Bayesian method for gene detection and mapping, using a case and control design and DNA pooling. Biostatistics, 2007, 8, 546-565.	0.9	20
82	MCALIGN2: faster, accurate global pairwise alignment of non-coding DNA sequences based on explicit models of indel evolution. BMC Bioinformatics, 2006, 7, 292.	1.2	28
83	Performance of Marker-Based Relatedness Estimators in Natural Populations of Outbred Vertebrates. Genetics, 2006, 173, 2091-2101.	1.2	250
84	Theoretical models of selection and mutation on quantitative traits. Philosophical Transactions of the Royal Society B: Biological Sciences, 2005, 360, 1411-1425.	1.8	304
85	MCALIGN: Stochastic Alignment of Noncoding DNA Sequences Based on an Evolutionary Model of Sequence Evolution. Genome Research, 2004, 14, 442-450.	2.4	52
86	The fixation probability of a beneficial allele in a population dividing by binary fission. Genetica, 2002, 115, 283-287.	0.5	19
87	General Models of Multilocus Evolution. Genetics, 2002, 161, 1727-1750.	1.2	198
88	The Effect of Deleterious Alleles on Adaptation in Asexual Populations. Genetics, 2002, 162, 395-411.	1.2	131
89	The evolution of mutation rates: separating causes from consequences. BioEssays, 2000, 22, 1057-1066.	1.2	403
90	Quantitative genetics: Resolving wing shape genes. Current Biology, 2000, 10, R113-R115.	1.8	3

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91	The evolution of mutation rates: separating causes from consequences. , 2000, 22, 1057.		4
92	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.	1.2	96
93	Beneficial Mutations, Hitchhiking and the Evolution of Mutation Rates in Sexual Populations. Genetics, 1999, 151, 1621-1631.	1.2	104