

Toby Johnson

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

94
papers

32,304
citations

67
h-index

101
g-index

101
ext. papers

36,755
ext. citations

17.3
avg, IF

5.11
L-index

#	Paper	IF	Citations
94	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021 , 12, 24	17.4	30
93	Identification of new therapeutic targets for osteoarthritis through genome-wide analyses of UK Biobank data. <i>Nature Genetics</i> , 2019 , 51, 230-236	36.3	143
92	Disentangling the genetics of lean mass. <i>American Journal of Clinical Nutrition</i> , 2019 , 109, 276-287	7	24
91	Genetic variants in PPARGC1B and CNTN4 are associated with thromboxane A formation and with cardiovascular event free survival in the Anglo-Scandinavian Cardiac Outcomes Trial (ASCOT). <i>Atherosclerosis</i> , 2018 , 269, 42-49	3.1	2
90	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 2017 , 8, 80	17.4	88
89	Phenome-wide association study using research participants self-reported data provides insight into the Th17 and IL-17 pathway. <i>PLoS ONE</i> , 2017 , 12, e0186405	3.7	14
88	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016 , 48, 1171-1184	36.3	251
87	A phenome-wide association study of a lipoprotein-associated phospholipase A2 loss-of-function variant in 90 000 Chinese adults. <i>International Journal of Epidemiology</i> , 2016 , 45, 1588-1599	7.8	24
86	HLA-B*57:01 Confers Susceptibility to Pazopanib-Associated Liver Injury in Patients with Cancer. <i>Clinical Cancer Research</i> , 2016 , 22, 1371-7	12.9	71
85	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. <i>Science</i> , 2016 , 351, 1166-71	33.3	325
84	BRCA1/2 mutations associated with progression-free survival in ovarian cancer patients in the AGO-OVAR 16 study. <i>Gynecologic Oncology</i> , 2016 , 140, 443-9	4.9	41
83	The genetics of drug efficacy: opportunities and challenges. <i>Nature Reviews Genetics</i> , 2016 , 17, 197-206	30.1	72
82	Communicating BRCA research results to patients enrolled in international clinical trials: lessons learnt from the AGO-OVAR 16 study. <i>BMC Medical Ethics</i> , 2016 , 17, 63	2.9	1
81	Lipoprotein-Associated Phospholipase A2 Loss-of-Function Variant and Risk of Vascular Diseases in 90,000 Chinese Adults. <i>Journal of the American College of Cardiology</i> , 2016 , 67, 230-231	15.1	17
80	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. <i>American Journal of Human Genetics</i> , 2016 , 98, 857-868	11	14
79	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015 , 518, 187-196	50.4	920
78	Modulation of genetic associations with serum urate levels by body-mass-index in humans. <i>PLoS ONE</i> , 2015 , 10, e0119752	3.7	31

77	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. <i>Human Molecular Genetics</i> , 2014 , 23, 2498-510	5.6	22
76	Gene-age interactions in blood pressure regulation: a large-scale investigation with the CHARGE, Global BPgen, and ICBP Consortia. <i>American Journal of Human Genetics</i> , 2014 , 95, 24-38	11	80
75	Effects of long-term averaging of quantitative blood pressure traits on the detection of genetic associations. <i>American Journal of Human Genetics</i> , 2014 , 95, 49-65	11	52
74	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. <i>American Journal of Human Genetics</i> , 2014 , 94, 349-60	11	131
73	The shared allelic architecture of adiponectin levels and coronary artery disease. <i>Atherosclerosis</i> , 2013 , 229, 145-8	3.1	25
72	Meta-analysis of gene-level associations for rare variants based on single-variant statistics. <i>American Journal of Human Genetics</i> , 2013 , 93, 236-48	11	49
71	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013 , 45, 1274-1283	36.3	1904
70	Common variants associated with plasma triglycerides and risk for coronary artery disease. <i>Nature Genetics</i> , 2013 , 45, 1345-52	36.3	597
69	Loci influencing blood pressure identified using a cardiovascular gene-centric array. <i>Human Molecular Genetics</i> , 2013 , 22, 1663-78	5.6	119
68	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013 , 45, 501-12	36.3	437
67	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013 , 45, 621-31	36.3	219
66	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. <i>PLoS Genetics</i> , 2013 , 9, e1003500	6	277
65	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. <i>Lancet, The</i> , 2012 , 380, 572-80	40	1523
64	Impact of common variation in bone-related genes on type 2 diabetes and related traits. <i>Diabetes</i> , 2012 , 61, 2176-86	0.9	25
63	Common variation in the NOS1AP gene is associated with drug-induced QT prolongation and ventricular arrhythmia. <i>Journal of the American College of Cardiology</i> , 2012 , 60, 841-50	15.1	87
62	Large-scale gene-centric meta-analysis across 32 studies identifies multiple lipid loci. <i>American Journal of Human Genetics</i> , 2012 , 91, 823-38	11	189
61	A genome-wide association search for type 2 diabetes genes in African Americans. <i>PLoS ONE</i> , 2012 , 7, e29202	3.7	138
60	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycaemic traits and insulin resistance. <i>Nature Genetics</i> , 2012 , 44, 659-69	36.3	615

59	Large-scale gene-centric meta-analysis across 39 studies identifies type 2 diabetes loci. <i>American Journal of Human Genetics</i> , 2012 , 90, 410-25	11	214
58	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. <i>American Journal of Human Genetics</i> , 2012 , 90, 753	11	4
57	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. <i>American Journal of Human Genetics</i> , 2012 , 90, 1116-1117	11	78
56	The metabochip, a custom genotyping array for genetic studies of metabolic, cardiovascular, and anthropometric traits. <i>PLoS Genetics</i> , 2012 , 8, e1002793	6	395
55	Novel loci for adiponectin levels and their influence on type 2 diabetes and metabolic traits: a multi-ethnic meta-analysis of 45,891 individuals. <i>PLoS Genetics</i> , 2012 , 8, e1002607	6	326
54	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. <i>Hypertension</i> , 2012 , 59, 248-55	8.5	124
53	Genome-wide association study of genetic determinants of LDL-c response to atorvastatin therapy: importance of Lp(a). <i>Journal of Lipid Research</i> , 2012 , 53, 1000-1011	6.3	79
52	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , 2012 , 44, 991-1005	36.3	621
51	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. <i>Nature Genetics</i> , 2011 , 43, 1131-8	36.3	415
50	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. <i>American Journal of Human Genetics</i> , 2011 , 88, 6-18	11	103
49	Blood pressure loci identified with a gene-centric array. <i>American Journal of Human Genetics</i> , 2011 , 89, 688-700	11	137
48	Effect of five genetic variants associated with lung function on the risk of chronic obstructive lung disease, and their joint effects on lung function. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2011 , 184, 786-95	10.2	112
47	Methods for testing association between uncertain genotypes and quantitative traits. <i>Biostatistics</i> , 2011 , 12, 1-17	3.7	34
46	Association of hypertension drug target genes with blood pressure and hypertension in 86,588 individuals. <i>Hypertension</i> , 2011 , 57, 903-10	8.5	154
45	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. <i>Human Molecular Genetics</i> , 2011 , 20, 2273-84	5.6	146
44	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011 , 43, 1005-11	36.3	338
43	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. <i>Nature Genetics</i> , 2011 , 43, 1082-90	36.3	313
42	Four genetic loci influencing electrocardiographic indices of left ventricular hypertrophy. <i>Circulation: Cardiovascular Genetics</i> , 2011 , 4, 626-35		22

41	A comprehensive evaluation of potential lung function associated genes in the SpiroMeta general population sample. <i>PLoS ONE</i> , 2011 , 6, e19382	3.7	41
40	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. <i>Nature</i> , 2010 , 464, 713-20	50.4	639
39	Biological, clinical and population relevance of 95 loci for blood lipids. <i>Nature</i> , 2010 , 466, 707-13	50.4	2742
38	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010 , 467, 832-8	50.4	1514
37	Genome-wide association study identifies five loci associated with lung function. <i>Nature Genetics</i> , 2010 , 42, 36-44	36.3	430
36	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. <i>Nature Genetics</i> , 2010 , 42, 142-8	36.3	527
35	Genetic loci influencing kidney function and chronic kidney disease. <i>Nature Genetics</i> , 2010 , 42, 373-5	36.3	205
34	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010 , 42, 949-60	36.3	724
33	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010 , 42, 937-48	36.3	2267
32	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. <i>Nature Genetics</i> , 2010 , 42, 1068-76	36.3	249
31	Common variants in the ATP2B1 gene are associated with susceptibility to hypertension: the Japanese Millennium Genome Project. <i>Hypertension</i> , 2010 , 56, 973-80	8.5	83
30	Genetic variants influencing circulating lipid levels and risk of coronary artery disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2010 , 30, 2264-76	9.4	318
29	Genome-wide meta-analysis for serum calcium identifies significantly associated SNPs near the calcium-sensing receptor (CASR) gene. <i>PLoS Genetics</i> , 2010 , 6, e1001035	6	74
28	Genome-wide association study of blood pressure extremes identifies variant near UMOD associated with hypertension. <i>PLoS Genetics</i> , 2010 , 6, e1001177	6	255
27	Replication of the five novel loci for uric acid concentrations and potential mediating mechanisms. <i>Human Molecular Genetics</i> , 2010 , 19, 387-95	5.6	79
26	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010 , 42, 105-16	36.3	1673
25	Meta-analysis of 28,141 individuals identifies common variants within five new loci that influence uric acid concentrations. <i>PLoS Genetics</i> , 2009 , 5, e1000504	6	495
24	The genetic architecture of blood pressure variation. <i>Current Cardiovascular Risk Reports</i> , 2009 , 3, 418-425	11	11

23	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. <i>Nature Genetics</i> , 2009 , 41, 25-34	36.3	1368
22	Variants in MTNR1B influence fasting glucose levels. <i>Nature Genetics</i> , 2009 , 41, 77-81	36.3	584
21	Genome-wide association study identifies eight loci associated with blood pressure. <i>Nature Genetics</i> , 2009 , 41, 666-76	36.3	970
20	Gene-centric association signals for lipids and apolipoproteins identified via the HumanCVD BeadChip. <i>American Journal of Human Genetics</i> , 2009 , 85, 628-42	11	163
19	Genes mirror geography within Europe. <i>Nature</i> , 2008 , 456, 98-101	50.4	1014
18	Genome-wide association analysis identifies 20 loci that influence adult height. <i>Nature Genetics</i> , 2008 , 40, 575-83	36.3	654
17	Common variants near MC4R are associated with fat mass, weight and risk of obesity. <i>Nature Genetics</i> , 2008 , 40, 768-75	36.3	1048
16	LDL-cholesterol concentrations: a genome-wide association study. <i>Lancet, The</i> , 2008 , 371, 483-91	40	292
15	Population-based genome-wide association studies reveal six loci influencing plasma levels of liver enzymes. <i>American Journal of Human Genetics</i> , 2008 , 83, 520-8	11	336
14	Bayesian method for gene detection and mapping, using a case and control design and DNA pooling. <i>Biostatistics</i> , 2007 , 8, 546-65	3.7	14
13	MCALIGN2: faster, accurate global pairwise alignment of non-coding DNA sequences based on explicit models of indel evolution. <i>BMC Bioinformatics</i> , 2006 , 7, 292	3.6	21
12	Performance of marker-based relatedness estimators in natural populations of outbred vertebrates. <i>Genetics</i> , 2006 , 173, 2091-101	4	205
11	Theoretical models of selection and mutation on quantitative traits. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2005 , 360, 1411-25	5.8	251
10	MCALIGN: stochastic alignment of noncoding DNA sequences based on an evolutionary model of sequence evolution. <i>Genome Research</i> , 2004 , 14, 442-50	9.7	44
9	The fixation probability of a beneficial allele in a population dividing by binary fission. <i>Genetica</i> , 2002 , 115, 283-7	1.5	16
8	General models of multilocus evolution. <i>Genetics</i> , 2002 , 161, 1727-50	4	165
7	The effect of deleterious alleles on adaptation in asexual populations. <i>Genetics</i> , 2002 , 162, 395-411	4	104
6	The evolution of mutation rates: separating causes from consequences. <i>BioEssays</i> , 2000 , 22, 1057-66	4.1	335

5	Quantitative genetics: Resolving wing shape genes. <i>Current Biology</i> , 2000 , 10, R113-5	6.3	2
4	The evolution of mutation rates: separating causes from consequences 2000 , 22, 1057		4
3	The approach to mutation-selection balance in an infinite asexual population, and the evolution of mutation rates. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1999 , 266, 2389-97	4.4	77
2	Beneficial mutations, hitchhiking and the evolution of mutation rates in sexual populations. <i>Genetics</i> , 1999 , 151, 1621-31	4	81
1	Identification of new therapeutic targets for osteoarthritis through genome-wide analyses of UK Biobank		2