Todd A Johnson

List of Publications by Year
in descending order

34 papers	8,243 citations	257450 24 h-index	395702 33 g-index
35 all docs	35 docs citations	35 times ranked	16306 citing authors

#	Article	IF	Citations
1	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	27.8	4,137
2	Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918.	27.8	1,788
3	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	27.8	424
4	Genetic variants in GPR126 are associated with adolescent idiopathic scoliosis. Nature Genetics, 2013, 45, 676-679.	21.4	240
5	A genome-wide association study identifies common variants near LBX1 associated with adolescent idiopathic scoliosis. Nature Genetics, 2011, 43, 1237-1240.	21.4	233
6	Genome-wide association study identifies three novel loci for type 2 diabetes. Human Molecular Genetics, 2014, 23, 239-246.	2.9	158
7	Association analyses of East Asian individuals and trans-ancestry analyses with European individuals reveal new loci associated with cholesterol and triglyceride levels. Human Molecular Genetics, 2017, 26, 1770-1784.	2.9	135
8	A Genome-Wide Association Study Identifies 2 Susceptibility Loci for Crohn's Disease in a Japanese Population. Gastroenterology, 2013, 144, 781-788.	1.3	125
9	Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. Human Molecular Genetics, 2015, 24, 1791-1800.	2.9	105
10	Shortage of Cellular ATP as a Cause of Diseases and Strategies to Enhance ATP. Frontiers in Pharmacology, 2019, 10, 98.	3.5	91
11	Expression of the immunoglobulin VH gene 51p1 is proportional to its germline gene copy number.. Journal of Clinical Investigation, 1996, 97, 2074-2080.	8.2	87
12	A meta-analysis identifies adolescent idiopathic scoliosis association withLBX1locus in multiple ethnic groups. Journal of Medical Genetics, 2014, 51, 401-406.	3.2	79
13	Combined Genetic and Genealogic Studies Uncover a Large BAP1 Cancer Syndrome Kindred Tracing Back Nine Generations to a Common Ancestor from the 1700s. PLoS Genetics, 2015, 11, e1005633.	3.5	76
14	Identification of a Susceptibility Locus for Severe Adolescent Idiopathic Scoliosis on Chromosome 17q24.3. PLoS ONE, 2013, 8, e72802.	2.5	59
15	Genome-wide association study in Japanese females identifies fifteen novel skin-related trait associations. Scientific Reports, 2018, 8, 8974.	3.3	59
16	Genetic Variation in the SLC8A1 Calcium Signaling Pathway Is Associated With Susceptibility to Kawasaki Disease and Coronary Artery Abnormalities. Circulation: Cardiovascular Genetics, 2016, 9, 559-568.	5.1	45
17	A genome-wide association analysis identifies NMNAT2 and HCP5 as susceptibility loci for Kawasaki disease. Journal of Human Genetics, 2017, 62, 1023-1029.	2.3	40
18	Attenuation of T-lymphocyte demargination and adhesion molecule expression in response to moderate exercise in physically fit individuals. Journal of Applied Physiology, 2005, 98, 1057-1063.	2.5	39

#	Article	IF	Citations
19	Enhanced efficacy of regulatory T cell transfer against increasing resistance, by elevated Foxp3 expression induced in arthritic murine hosts. Arthritis and Rheumatism, 2007, 56, 2947-2956.	6.7	34
20	Genome-wide meta-analysis and replication studies in multiple ethnicities identify novel adolescent idiopathic scoliosis susceptibility loci. Human Molecular Genetics, 2018, 27, 3986-3998.	2.9	34
21	The Construction of Risk Prediction Models Using GWAS Data and Its Application to a Type 2 Diabetes Prospective Cohort. PLoS ONE, 2014, 9, e92549.	2.5	31
22	Genome-wide association study of warfarin maintenance dose in a Brazilian sample. Pharmacogenomics, 2015, 16, 1253-1263.	1.3	29
23	Genome-wide association study of self-reported food reactions in Japanese identifies shrimp and peach specific loci in the HLA-DR/DQ gene region. Scientific Reports, 2018, 8, 1069.	3.3	29
24	Immunoglobulin V Gene Expression in CD5 B-Cell Malignanciesa. Annals of the New York Academy of Sciences, 1992, 651, 373-383.	3.8	27
25	Association of an IGHV3-66 gene variant with Kawasaki disease. Journal of Human Genetics, 2021, 66, 475-489.	2.3	27
26	Anti-B cell autoantibodies encoded by VH 4â€“21 genes in human fetal spleen do not requirein vivo somatic selection. European Journal of Immunology, 1994, 24, 2941-2949.	2.9	25
27	Improved Parkinsons disease motor score in a single-arm open-label trial of febuxostat and inosine. Medicine (United States), 2020, 99, e21576.	1.0	16
28	Xanthine Oxidase Inhibitor Withdrawal Syndrome? Comment on the Article by Choi et al. Arthritis and Rheumatology, 2019, 71, 1966-1967.	5.6	15
29	Japanese GWAS identifies variants for bust-size, dysmenorrhea, and menstrual fever that are eQTLs for relevant protein-coding or long non-coding RNAs. Scientific Reports, 2018, 8, 8502.	3.3	11
30	Linkage disequilibrium of evolutionarily conserved regions in the human genome. BMC Genomics, 2006, 7, 326.	2.8	9
31	Genome-wide association study identifies pharmacogenomic loci linked with specific antihypertensive drug treatment and new-onset diabetes. Pharmacogenomics Journal, 2018, 18, 106-112.	2.0	7
32	Expression of an Ig VHGene, 51p1, Is Proportional to Its Germline Gene Copy Number. Annals of the New York Academy of Sciences, 1997, 815, 478-480.	3.8	4
33	hzAnalyzer: detection, quantification, and visualization of contiguous homozygosity in high-density genotyping datasets. Genome Biology, 2011, 12, R21.	9.6	3
34	Abstract 33: A Meta-analysis Of Three Genome-wide Association Studies Identifies A Novel Susceptibility Locus For Kawasaki Disease.. Circulation, 2015, 131, .	1.6	0