Quan Long

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.

27 papers	5,499 citations	11 h-index	29 g-index
29 ext. papers	7,045 ext. citations	9.3 avg, IF	4.65 L-index

#	Paper	IF	Citations
27	kTWAS: integrating kernel machine with transcriptome-wide association studies improves statistical power and reveals novel genes. *Briefings in Bioinformatics*, **2021**, 22,	13.4	5
26	Nucleocytoplasmic transport of the RNA-binding protein CELF2 regulates neural stem cell fates. *Cell Reports*, **2021**, 35, 109226	10.6	6
25	Reconstruction of Microbial Haplotypes by Integration of Statistical and Physical Linkage in Scaffolding. *Molecular Biology and Evolution*, **2021**, 38, 2660-2672	8.3	4
24	WgLink: reconstructing whole-genome viral haplotypes using L0+L1-regularization. *Bioinformatics*, **2021**,	7.2	1
23	Power analysis of transcriptome-wide association study: Implications for practical protocol choice. *PLoS Genetics*, **2021**, 17, e1009405	6	5
22	Genetic variations of DNA bindings of FOXA1 and co-factors in breast cancer susceptibility. *Nature Communications*, **2021**, 12, 5318	17.4	1
21	Reconstructing SARS-CoV-2 infection dynamics through the phylogenetic inference of unsampled sources of infection.. *PLoS ONE*, **2021**, 16, e0261422	3.7	1
20	Evaluation of A Phylogenetic Pipeline to Examine Transmission Networks in A Canadian HIV Cohort. *Microorganisms*, **2020**, 8,	4.9	5
19	An Individualized Approach for Somatic Variant Discovery. *Methods in Molecular Biology*, **2020**, 2120, 11-36	1.4	
18	OCMA: Fast, Memory-Efficient Factorization of Prohibitively Large Relationship Matrices. *G3: Genes, Genomes, Genetics*, **2019**, 9, 13-19	3.2	1
17	PRESM: personalized reference editor for somatic mutation discovery in cancer genomics. *Bioinformatics*, **2019**, 35, 1445-1452	7.2	3
16	SimPEL: Simulation-based power estimation for sequencing studies of low-prevalence conditions. *Genetic Epidemiology*, **2018**, 42, 480-487	2.6	
15	Computational Haplotype Inference from Pooled Samples. *Methods in Molecular Biology*, **2017**, 1551, 309-319	1.4	3
14	Patterns of Polymorphism at the Self-Incompatibility Locus in 1,083 Arabidopsis thaliana Genomes. *Molecular Biology and Evolution*, **2017**, 34, 1878-1889	8.3	25
13	Inter-tissue coexpression network analysis reveals DPP4 as an important gene in heart to blood communication. *Genome Medicine*, **2016**, 8, 15	14.4	20
12	Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans. *Science*, **2015**, 348, 648-60	33.3	3242
11	Synchronized age-related gene expression changes across multiple tissues in human and the link to complex diseases. *Scientific Reports*, **2015**, 5, 15145	4.9	128

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10	An extended Tajima's D neutrality test incorporating SNP calling and imputation uncertainties. *Statistics and Its Interface*, **2015**, 8, 447-456	0.4	2
9	AprioriGWAS, a new pattern mining strategy for detecting genetic variants associated with disease through interaction effects. *PLoS Computational Biology*, **2014**, 10, e1003627	5	18
8	JAWAMix5: an out-of-core HDF5-based java implementation of whole-genome association studies using mixed models. *Bioinformatics*, **2013**, 29, 1220-2	7.2	8
7	Massive genomic variation and strong selection in Arabidopsis thaliana lines from Sweden. *Nature Genetics*, **2013**, 45, 884-890	36.3	264
6	A mixed-model approach for genome-wide association studies of correlated traits in structured populations. *Nature Genetics*, **2012**, 44, 1066-71	36.3	273
5	PoolHap: inferring haplotype frequencies from pooled samples by next generation sequencing. *PLoS ONE*, **2011**, 6, e15292	3.7	28
4	Pindel: a pattern growth approach to detect break points of large deletions and medium sized insertions from paired-end short reads. *Bioinformatics*, **2009**, 25, 2865-71	7.2	1423
3	HI: haplotype improver using paired-end short reads. *Bioinformatics*, **2009**, 25, 2436-7	7.2	12
2	Detecting disease-associated genotype patterns. *BMC Bioinformatics*, **2009**, 10 Suppl 1, S75	3.6	19
1	Reconstruction of microbial haplotypes by integration of statistical and physical linkage in scaffolding		1