# Quan Long

## List of Publications by Citations

**Source:** https://exaly.com/author-pdf/8997906/quan-long-publications-by-citations.pdf
**Version:** 2024-04-28

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

| # | Paper | IF | Citations |
|---|---|---|---|
| 27 | Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans. *Science*, **2015**, 348, 648-60 | 33.3 | 3242 |
| 26 | 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 |
| 25 | A mixed-model approach for genome-wide association studies of correlated traits in structured populations. *Nature Genetics*, **2012**, 44, 1066-71 | 36.3 | 273 |
| 24 | Massive genomic variation and strong selection in Arabidopsis thaliana lines from Sweden. *Nature Genetics*, **2013**, 45, 884-890 | 36.3 | 264 |
| 23 | 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 |
| 22 | PoolHap: inferring haplotype frequencies from pooled samples by next generation sequencing. *PLoS ONE*, **2011**, 6, e15292 | 3.7 | 28 |
| 21 | 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 |
| 20 | Inter-tissue coexpression network analysis reveals DPP4 as an important gene in heart to blood communication. *Genome Medicine*, **2016**, 8, 15 | 14.4 | 20 |
| 19 | Detecting disease-associated genotype patterns. *BMC Bioinformatics*, **2009**, 10 Suppl 1, S75 | 3.6 | 19 |
| 18 | AprioriGWAS, a new pattern mining strategy for detecting genetic variants associated with disease through interaction effects. *PLoS Computational Biology*, **2014**, 10, e1003627 | 5 | 18 |
| 17 | HI: haplotype improver using paired-end short reads. *Bioinformatics*, **2009**, 25, 2436-7 | 7.2 | 12 |
| 16 | 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 |
| 15 | Nucleocytoplasmic transport of the RNA-binding protein CELF2 regulates neural stem cell fates. *Cell Reports*, **2021**, 35, 109226 | 10.6 | 6 |
| 14 | Evaluation of A Phylogenetic Pipeline to Examine Transmission Networks in A Canadian HIV Cohort. *Microorganisms*, **2020**, 8, | 4.9 | 5 |
| 13 | kTWAS: integrating kernel machine with transcriptome-wide association studies improves statistical power and reveals novel genes. *Briefings in Bioinformatics*, **2021**, 22, | 13.4 | 5 |
| 12 | Power analysis of transcriptome-wide association study: Implications for practical protocol choice. *PLoS Genetics*, **2021**, 17, e1009405 | 6 | 5 |
| 11 | Reconstruction of Microbial Haplotypes by Integration of Statistical and Physical Linkage in Scaffolding. *Molecular Biology and Evolution*, **2021**, 38, 2660-2672 | 8.3 | 4 |

# List of Publications

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|---|---|---|---|
| 10 | Computational Haplotype Inference from Pooled Samples. *Methods in Molecular Biology*, **2017**, 1551, 309-319 | 1.4 | 3 |
| 9 | PRESM: personalized reference editor for somatic mutation discovery in cancer genomics. *Bioinformatics*, **2019**, 35, 1445-1452 | 7.2 | 3 |
| 8 | An extended TajimaXs D neutrality test incorporating SNP calling and imputation uncertainties. *Statistics and Its Interface*, **2015**, 8, 447-456 | 0.4 | 2 |
| 7 | OCMA: Fast, Memory-Efficient Factorization of Prohibitively Large Relationship Matrices. *G3: Genes, Genomes, Genetics*, **2019**, 9, 13-19 | 3.2 | 1 |
| 6 | Reconstruction of microbial haplotypes by integration of statistical and physical linkage in scaffolding | | 1 |
| 5 | WgLink: reconstructing whole-genome viral haplotypes using □L0+L1-regularization. *Bioinformatics*, **2021**, | 7.2 | 1 |
| 4 | Genetic variations of DNA bindings of FOXA1 and co-factors in breast cancer susceptibility. *Nature Communications*, **2021**, 12, 5318 | 17.4 | 1 |
| 3 | Reconstructing SARS-CoV-2 infection dynamics through the phylogenetic inference of unsampled sources of infection.. *PLoS ONE*, **2021**, 16, e0261422 | 3.7 | 1 |
| 2 | An Individualized Approach for Somatic Variant Discovery. *Methods in Molecular Biology*, **2020**, 2120, 11-36 | 1.4 | |
| 1 | SimPEL: Simulation-based power estimation for sequencing studies of low-prevalence conditions. *Genetic Epidemiology*, **2018**, 42, 480-487 | 2.6 | |