Yaqun Wang

List of Publications by Year
in descending order

23 papers	286 citations	1163117 8 h-index	940533 16 g-index
25 all docs	25 docs citations	25 times ranked	413 citing authors

#	Article	IF	Citations
1	Identification of a GrgA-Euo-HrcA Transcriptional Regulatory Network in Chlamydia. MSystems, 2021, 6, e0073821.	3.8	9
2	Comparing the Incidence of Buccal Mucosa Cancer in South Asian, White, and Black Populations Residing in the United States: A Cross-Sectional Analysis. Asian Pacific Journal of Cancer Prevention, 2021, 22, 195-199.	1.2	1
3	A Phase 2 Randomized Pilot Study Comparing High-Dose-Rate Brachytherapy and Low-Dose-Rate Brachytherapy as Monotherapy in Localized Prostate Cancer. Advances in Radiation Oncology, 2019, 4, 631-640.	1.2	21
4	An omnidirectional visualization model of personalized gene regulatory networks. Npj Systems Biology and Applications, 2019, 5, 38.	3.0	20
5	Functional mapping of N deficiency–induced response in wheat yield–component traits by implementing high–throughput phenotyping. Plant Journal, 2019, 97, 1105-1119.	5.7	18
6	Inference of Gene Regulatory Network Through Adaptive Dynamic Bayesian Network Modeling. ICSA Book Series in Statistics, 2019, , 91-113.	0.2	1
7	Hyperacute Monocyte Gene Response Patterns Are Associated With Lower Extremity Vein Bypass Graft Failure. Circulation Genomic and Precision Medicine, 2018, 11, e001970.	3.6	4
8	Applications and extensions of epigenetic game theory. Physics of Life Reviews, 2017, 20, 153-154.	2.8	1
9	A multi-Poisson dynamic mixture model to cluster developmental patterns of gene expression by RNA-seq. Briefings in Bioinformatics, 2015, 16, 205-215.	6.5	6
10	Towards a comprehensive picture of the genetic landscape of complex traits. Briefings in Bioinformatics, 2014, 15, 30-42.	6.5	9
11	A Model Framework for Identifying Genes that Guide the Evolution of Heterochrony. Molecular Biology and Evolution, 2014, 31, 2238-2247.	8.9	17
12	Systems mapping of genes controlling chemotherapeutic drug efficiency for cancer stem cells. Drug Discovery Today, 2014, 19, 1125-1130.	6.4	4
13	A bi-Poisson model for clustering gene expression profiles by RNA-seq. Briefings in Bioinformatics, 2014, 15, 534-541.	6.5	6
14	A Computational Algorithm for Functional Clustering of Proteome Dynamics During Development. Current Genomics, 2014, 15, 237-243.	1.6	1
15	Modeling Expression Plasticity of Genes that Differentiate Drug-sensitive from Drug-resistant Cells to Chemotherapeutic Treatment. Current Genomics, 2014, 15, 349-356.	1.6	1
16	Delivering systems pharmacogenomics towards precision medicine through mathematics. Advanced Drug Delivery Reviews, 2013, 65, 905-911.	13.7	8
17	A quantitative model of transcriptional differentiation driving host-pathogen interactions. Briefings in Bioinformatics, 2013, 14, 713-723.	6.5	6
18	Reconstructing regulatory networks from the dynamic plasticity of gene expression by mutual information. Nucleic Acids Research, 2013, 41, e97-e97.	14.5	37

#	Article	IF	Citations
19	How to cluster gene expression dynamics in response to environmental signals. Briefings in Bioinformatics, 2012, 13, 162-174.	6.5	50
20	Systems mapping of HIV-1 infection. BMC Genetics, 2012, 13, 91.	2.7	1
21	Differential Gene Expression in Tamoxifen-Resistant Breast Cancer Cells Revealed by a New Analytical Model of RNA-Seq Data. PLoS ONE, 2012, 7, e41333.	2.5	53
22	Dynamic Modeling of Genes Controlling Cancer Stem Cell Proliferation. Frontiers in Genetics, 2012, 3, 84.	2.3	6
23	How to compute which genes control drug resistance dynamics. Drug Discovery Today, 2011, 16, 339-344.	6.4	6