Youlian Pan

List of Publications by Year
in descending order

51 papers	1,037 citations	471371 17 h-index	434063 31 g-index
55 all docs	55 docs citations	55 times ranked	1340 citing authors

#	ARTICLE	IF	CITATIONS
1	Novel Transcriptional and Translational Biomarkers of Tularemia Vaccine Efficacy in a Mouse Inhalation Model: Proof of Concept. Microorganisms, 2022, 10, 36.	1.6	0
2	Identification of transcriptional subtypes in lung adenocarcinoma and squamous cell carcinoma through integrative analysis of microarray and RNA sequencing data. Scientific Reports, 2021, 11, 8709.	1.6	8
3	Elucidating the biochemical basis of *trans*‑16:1 fatty acid change in leaves during cold acclimation in wheat. Plant-Environment Interactions, 2021, 2, 101-111.	0.7	4
4	Wheat transcriptome profiling reveals abscisic and gibberellic acid treatments regulate early-stage phytohormone defense signaling, cell wall fortification, and metabolic switches following Fusarium graminearum-challenge. BMC Genomics, 2021, 22, 798.	1.2	18
5	Vascular contributions to 16p11.2 deletion autism syndrome modeled in mice. Nature Neuroscience, 2020, 23, 1090-1101.	7.1	70
6	Personalized prediction of genes with tumor-causing somatic mutations based on multi-modal deep Boltzmann machine. Neurocomputing, 2019, 324, 51-62.	3.5	10
7	Multiclass Nonnegative Matrix Factorization for Comprehensive Feature Pattern Discovery. IEEE Transactions on Neural Networks and Learning Systems, 2019, 30, 615-629.	7.2	5
8	The Transcriptional Landscape of Polyploid Wheats and Their Diploid Ancestors during Embryogenesis and Grain Development. Plant Cell, 2019, 31, 2888-2911.	3.1	57
9	Transcriptional and hormonal profiling of Fusarium graminearum-infected wheat reveals an association between auxin and susceptibility. Physiological and Molecular Plant Pathology, 2019, 107, 33-39.	1.3	29
10	Characterization of QTL and eQTL controlling early Fusarium graminearum infection and deoxynivalenol levels in a Wuhan 1 x Nyubai doubled haploid wheat population. BMC Plant Biology, 2019, 19, 536.	1.6	8
11	Subspace Clustering of DNA Microarray Data. , 2019, , 210-264.		0
12	Integrated transcriptome and hormone profiling highlight the role of multiple phytohormone pathways in wheat resistance against fusarium head blight. PLoS ONE, 2018, 13, e0207036.	1.1	63
13	Transcriptome dynamics associated with resistance and susceptibility against fusarium head blight in four wheat genotypes. BMC Genomics, 2018, 19, 642.	1.2	71
14	Bioinformatics identification of new targets for improving low temperature stress tolerance in spring and winter wheat. BMC Bioinformatics, 2017, 18, 174.	1.2	8
15	Computational selection of antibody-drug conjugate targets for breast cancer. Oncotarget, 2016, 7, 2555-2571.	0.8	15
16	Prior knowledge guided eQTL mapping for identifying candidate genes. BMC Bioinformatics, 2016, 17, 531.	1.2	0
17	Integration of 3D gene expression patterns and gene regulatory networks for clinical applications in epithelial ovarian cancer. , 2016, , .		0
18	Enrichment of Triticum aestivum gene annotations using ortholog cliques and gene ontologies in other plants. BMC Genomics, 2015, 16, 299.	1.2	7

#	Article	IF	Citations
19	Digitization of trait representation in microarray data analysis of wheat infected by fusarium graminearum. , 2015, , .		3
20	Semi-supervised consensus clustering for gene expression data analysis. BioData Mining, 2014, 7, 7.	2.2	28
21	Subspace Clustering of DNA Microarray Data. International Journal of Computational Models and Algorithms in Medicine, 2014, 4, 1-52.	0.4	1
22	A generic model of transcriptional regulatory networks: Application to plants under abiotic stress. , 2013, , .		2
23	Mining biological information from 3D short time-series gene expression data: the OPTricluster algorithm. BMC Bioinformatics, 2012, 13, 54.	1.2	34
24	Utilization of gene ontology in semi-supervised clustering. , 2011, , .		2
25	Biclustering of DNA Microarray Data. , 2011, , 148-186.		8
26	GOAL: A software tool for assessing biological significance of genes groups. BMC Bioinformatics, 2010, 11, 229.	1.2	27
27	A MULTI-STRATEGY APPROACH TO INFORMATIVE GENE IDENTIFICATION FROM GENE EXPRESSION DATA. Journal of Bioinformatics and Computational Biology, 2010, 08, 19-38.	0.3	10
28	Towards a temporal modeling of the genetic network controlling Systemic Acquired Resistance in Arabidopsis thaliana. , 2010, , .		1
29	Integrative Data Mining in Functional Genomics of Brassica napus and Arabidopsis thaliana. Lecture Notes in Computer Science, 2010, , 92-101.	1.0	2
30	Data Integration and Knowledge Discovery in Life Sciences. Lecture Notes in Computer Science, 2010, , 102-111.	1.0	3
31	Differences in Promoters of Orthologous Genes. Open Bioinformatics Journal, 2010, 4, 41-49.	1.0	0
32	Probing the endosperm gene expression landscape in Brassica napus. BMC Genomics, 2009, 10, 256.	1.2	22
33	Goal Driven Analysis of cDNA Microarray Data. , 2009, , .		2
34	Towards the reconstruction of Brassica napus seed development FA metabolism dynamic regulatory map. , 2009, , .		0
35	A novel pattern based clustering methodology for time-series microarray data. International Journal of Computer Mathematics, 2007, 84, 585-597.	1.0	15
36	Prediction of Co-Regulated Gene Groups through Gene Ontology. , 2007, , .		0

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37	MicroRNAs preferentially target the genes with high transcriptional regulation complexity. Biochemical and Biophysical Research Communications, 2007, 352, 733-738.	1.0	130
38	Evolution of motif variants and positional bias of the cyclic-AMP response element. BMC Evolutionary Biology, 2007, 7, S15.	3.2	19
39	Advances in the Discovery of cis-Regulatory Elements. Current Bioinformatics, 2006, 1, 321-336.	0.7	10
40	Growth and photosynthetic rates of Chlamydomonas plethora and Nitzschia frustula cultures isolated from Kuwait Bay, Arabian Gulf, and their potential as live algal food for tropical mariculture. Marine Ecology, 2005, 26, 63-71.	0.4	5
41	MODULAR NEURAL NETWORKS AND THEIR APPLICATION IN EXON PREDICTION. , 2005, , .		2
42	DISCOVERY OF FUNCTIONAL GENES FOR SYSTEMIC ACQUIRED RESISTANCE IN ARABIDOPSIS THALIANA THROUGH INTEGRATED DATA MINING. Journal of Bioinformatics and Computational Biology, 2004, 02, 639-655.	0.3	24
43	Production of Domoic Acid by <i>Pseudoâ€nitzschia multiseries</i> H<scp>asle</scp>, Affected by Lithium. Marine Ecology, 1998, 19, 31-36.	0.4	17
44	Environmental stress and domoic acid production byPseudo-nitzschia: a physiological perspective. Natural Toxins, 1998, 6, 127-135.	1.0	103
45	Impacts of domestic sewage effluent on phytoplankton from Bedford Basin, eastern Canada. Marine Pollution Bulletin, 1997, 34, 1001-1005.	2.3	21
46	CHANGES IN DOMOIC ACID PRODUCTION AND CELLULAR CHEMICAL COMPOSITION OF THE TOXIGENIC DIATOM PSEUDO-NITZSCHIA MULTISERIES UNDER PHOSPHATE LIMITATION1. Journal of Phycology, 1996, 32, 371-381.	1.0	109
47	Acclimation to low light intensity in photosynthesis and growth of Pseudo-nitzschia multiseris Hasle, a neurotoxigenic diatom. Journal of Plankton Research, 1996, 18, 1427-1438.	0.8	22
48	Photosynthetic characteristics of Dinophysis norvegica Claparede & Lachmann, a red-tide dinoflagellate. Journal of Plankton Research, 1993, 15, 965-976.	0.8	13
49	Photosynthesis and growth of Nitzschia pungens f. multiseries Hasle, a neurotoxin producing diatom. Journal of Experimental Marine Biology and Ecology, 1991, 154, 77-96.	0.7	20
50	Selection of putative cis-regulatory motifs through regional and global conservation. , 0, , .		0
51	Biclustering of DNA Microarray Data. , 0, , 513-551.		3