

# Youlian Pan

## List of Publications by Year in descending order

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Version: 2024-02-01

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	MicroRNAs preferentially target the genes with high transcriptional regulation complexity. <i>Biochemical and Biophysical Research Communications</i> , 2007, 352, 733-738.	1.0	130
2	CHANGES IN DOMOIC ACID PRODUCTION AND CELLULAR CHEMICAL COMPOSITION OF THE TOXIGENIC DIATOM PSEUDO-NITZSCHIA MULTISERIES UNDER PHOSPHATE LIMITATION1. <i>Journal of Phycology</i> , 1996, 32, 371-381.	1.0	109
3	Environmental stress and domoic acid production by Pseudo-nitzschia: a physiological perspective. <i>Natural Toxins</i> , 1998, 6, 127-135.	1.0	103
4	Transcriptome dynamics associated with resistance and susceptibility against fusarium head blight in four wheat genotypes. <i>BMC Genomics</i> , 2018, 19, 642.	1.2	71
5	Vascular contributions to 16p11.2 deletion autism syndrome modeled in mice. <i>Nature Neuroscience</i> , 2020, 23, 1090-1101.	7.1	70
6	Integrated transcriptome and hormone profiling highlight the role of multiple phytohormone pathways in wheat resistance against fusarium head blight. <i>PLoS ONE</i> , 2018, 13, e0207036.	1.1	63
7	The Transcriptional Landscape of Polyploid Wheats and Their Diploid Ancestors during Embryogenesis and Grain Development. <i>Plant Cell</i> , 2019, 31, 2888-2911.	3.1	57
8	Mining biological information from 3D short time-series gene expression data: the OPTricluster algorithm. <i>BMC Bioinformatics</i> , 2012, 13, 54.	1.2	34
9	Transcriptional and hormonal profiling of Fusarium graminearum-infected wheat reveals an association between auxin and susceptibility. <i>Physiological and Molecular Plant Pathology</i> , 2019, 107, 33-39.	1.3	29
10	Semi-supervised consensus clustering for gene expression data analysis. <i>BioData Mining</i> , 2014, 7, 7.	2.2	28
11	GOAL: A software tool for assessing biological significance of genes groups. <i>BMC Bioinformatics</i> , 2010, 11, 229.	1.2	27
12	DISCOVERY OF FUNCTIONAL GENES FOR SYSTEMIC ACQUIRED RESISTANCE IN ARABIDOPSIS THALIANA THROUGH INTEGRATED DATA MINING. <i>Journal of Bioinformatics and Computational Biology</i> , 2004, 02, 639-655.	0.3	24
13	Acclimation to low light intensity in photosynthesis and growth of Pseudo-nitzschia multiseris Hasle, a neurotoxic diatom. <i>Journal of Plankton Research</i> , 1996, 18, 1427-1438.	0.8	22
14	Probing the endosperm gene expression landscape in Brassica napus. <i>BMC Genomics</i> , 2009, 10, 256.	1.2	22
15	Impacts of domestic sewage effluent on phytoplankton from Bedford Basin, eastern Canada. <i>Marine Pollution Bulletin</i> , 1997, 34, 1001-1005.	2.3	21
16	Photosynthesis and growth of Nitzschia pungens f. multiseris Hasle, a neurotoxin producing diatom. <i>Journal of Experimental Marine Biology and Ecology</i> , 1991, 154, 77-96.	0.7	20
17	Evolution of motif variants and positional bias of the cyclic-AMP response element. <i>BMC Evolutionary Biology</i> , 2007, 7, S15.	3.2	19
18	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. <i>BMC Genomics</i> , 2021, 22, 798.	1.2	18

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19	Production of Domoic Acid by <i>Pseudo-nitzschia multiseries</i> , Affected by Lithium. <i>Marine Ecology</i> , 1998, 19, 31-36.	0.4	17
20	A novel pattern based clustering methodology for time-series microarray data. <i>International Journal of Computer Mathematics</i> , 2007, 84, 585-597.	1.0	15
21	Computational selection of antibody-drug conjugate targets for breast cancer. <i>Oncotarget</i> , 2016, 7, 2555-2571.	0.8	15
22	Photosynthetic characteristics of <i>Dinophysis norvegica</i> Claparede & Lachmann, a red-tide dinoflagellate. <i>Journal of Plankton Research</i> , 1993, 15, 965-976.	0.8	13
23	Advances in the Discovery of cis-Regulatory Elements. <i>Current Bioinformatics</i> , 2006, 1, 321-336.	0.7	10
24	A MULTI-STRATEGY APPROACH TO INFORMATIVE GENE IDENTIFICATION FROM GENE EXPRESSION DATA. <i>Journal of Bioinformatics and Computational Biology</i> , 2010, 08, 19-38.	0.3	10
25	Personalized prediction of genes with tumor-causing somatic mutations based on multi-modal deep Boltzmann machine. <i>Neurocomputing</i> , 2019, 324, 51-62.	3.5	10
26	Bioinformatics identification of new targets for improving low temperature stress tolerance in spring and winter wheat. <i>BMC Bioinformatics</i> , 2017, 18, 174.	1.2	8
27	Characterization of QTL and eQTL controlling early <i>Fusarium graminearum</i> infection and deoxynivalenol levels in a Wuhan 1 x Nyubai doubled haploid wheat population. <i>BMC Plant Biology</i> , 2019, 19, 536.	1.6	8
28	Identification of transcriptional subtypes in lung adenocarcinoma and squamous cell carcinoma through integrative analysis of microarray and RNA sequencing data. <i>Scientific Reports</i> , 2021, 11, 8709.	1.6	8
29	Biclustering of DNA Microarray Data. , 2011, , 148-186.		8
30	Enrichment of <i>Triticum aestivum</i> gene annotations using ortholog cliques and gene ontologies in other plants. <i>BMC Genomics</i> , 2015, 16, 299.	1.2	7
31	Growth and photosynthetic rates of <i>Chlamydomonas plethora</i> and <i>Nitzschia frustula</i> cultures isolated from Kuwait Bay, Arabian Gulf, and their potential as live algal food for tropical mariculture. <i>Marine Ecology</i> , 2005, 26, 63-71.	0.4	5
32	Multiclass Nonnegative Matrix Factorization for Comprehensive Feature Pattern Discovery. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2019, 30, 615-629.	7.2	5
33	Elucidating the biochemical basis of <i>trans</i> -16:1 fatty acid change in leaves during cold acclimation in wheat. <i>Plant-Environment Interactions</i> , 2021, 2, 101-111.	0.7	4
34	Digitization of trait representation in microarray data analysis of wheat infected by <i>Fusarium graminearum</i> . , 2015, , .		3
35	Data Integration and Knowledge Discovery in Life Sciences. <i>Lecture Notes in Computer Science</i> , 2010, , 102-111.	1.0	3
36	Biclustering of DNA Microarray Data. , 0, , 513-551.		3

#	ARTICLE	IF	CITATIONS
37	Goal Driven Analysis of cDNA Microarray Data. , 2009, , .		2
38	Utilization of gene ontology in semi-supervised clustering. , 2011, , .		2
39	A generic model of transcriptional regulatory networks: Application to plants under abiotic stress. , 2013, , .		2
40	Integrative Data Mining in Functional Genomics of Brassica napus and Arabidopsis thaliana. Lecture Notes in Computer Science, 2010, , 92-101.	1.0	2
41	MODULAR NEURAL NETWORKS AND THEIR APPLICATION IN EXON PREDICTION. , 2005, , .		2
42	Towards a temporal modeling of the genetic network controlling Systemic Acquired Resistance in Arabidopsis thaliana. , 2010, , .		1
43	Subspace Clustering of DNA Microarray Data. International Journal of Computational Models and Algorithms in Medicine, 2014, 4, 1-52.	0.4	1
44	Selection of putative cis-regulatory motifs through regional and global conservation. , 0, , .		0
45	Prediction of Co-Regulated Gene Groups through Gene Ontology. , 2007, , .		0
46	Towards the reconstruction of Brassica napus seed development FA metabolism dynamic regulatory map. , 2009, , .		0
47	Prior knowledge guided eQTL mapping for identifying candidate genes. BMC Bioinformatics, 2016, 17, 531.	1.2	0
48	Integration of 3D gene expression patterns and gene regulatory networks for clinical applications in epithelial ovarian cancer. , 2016, , .		0
49	Differences in Promoters of Orthologous Genes. Open Bioinformatics Journal, 2010, 4, 41-49.	1.0	0
50	Subspace Clustering of DNA Microarray Data. , 2019, , 210-264.		0
51	Novel Transcriptional and Translational Biomarkers of Tularemia Vaccine Efficacy in a Mouse Inhalation Model: Proof of Concept. Microorganisms, 2022, 10, 36.	1.6	0