

# Ming Chen

## List of Publications by Year in descending order

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209  
papers

10,586  
citations

44069

48  
h-index

42399

92  
g-index

223  
all docs

223  
docs citations

223  
times ranked

16169  
citing authors

#	ARTICLE	IF	CITATIONS
1	LIN28 coordinately promotes nucleolar/ribosomal functions and represses the 2C-like transcriptional program in pluripotent stem cells. <i>Protein and Cell</i> , 2022, 13, 490-512.	11.0	28
2	Gene Expression Nebulas (GEN): a comprehensive data portal integrating transcriptomic profiles across multiple species at both bulk and single-cell levels. <i>Nucleic Acids Research</i> , 2022, 50, D1016-D1024.	14.5	18
3	Database Resources of the National Genomics Data Center, China National Center for Bioinformation in 2022. <i>Nucleic Acids Research</i> , 2022, 50, D27-D38.	14.5	364
4	DeepTrio: a ternary prediction system for protein-protein interaction using mask multiple parallel convolutional neural networks. <i>Bioinformatics</i> , 2022, 38, 694-702.	4.1	27
5	Editorial: Petri nets for cellular process modelling. <i>BioSystems</i> , 2022, 212, 104603.	2.0	0
6	Genome-Wide Analysis of the Soybean TIFY Family and Identification of GmTIFY10e and GmTIFY10g Response to Salt Stress. <i>Frontiers in Plant Science</i> , 2022, 13, 845314.	3.6	12
7	Simulating the Dynamic Intra-Tumor Heterogeneity and Therapeutic Responses. <i>Cancers</i> , 2022, 14, 1645.	3.7	2
8	Biogenesis, Functions, Interactions, and Resources of Non-Coding RNAs in Plants. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3695.	4.1	15
9	Role of the <i>OsWRKY40</i> authentic response regulator gene family in fragrant rice under alkaline salt stress. <i>Physiologia Plantarum</i> , 2022, 174, e13696.	5.2	18
10	Reassessment of Reliability and Reproducibility for Triple-Negative Breast Cancer Subtyping. <i>Cancers</i> , 2022, 14, 2571.	3.7	2
11	ChIP-Hub provides an integrative platform for exploring plant regulome. <i>Nature Communications</i> , 2022, 13, .	12.8	35
12	Plant Biology and Biotechnology: Focus on Genomics and Bioinformatics. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6759.	4.1	4
13	LBD: a manually curated database of experimentally validated lymphoma biomarkers. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	3.0	1
14	A reference single-cell regulomic and transcriptomic map of cynomolgus monkeys. <i>Nature Communications</i> , 2022, 13, .	12.8	20
15	Sequence repetitiveness quantification and <i>de novo</i> repeat detection by weighted k-mer coverage. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	4
16	Database Resources of the National Genomics Data Center, China National Center for Bioinformation in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D18-D28.	14.5	168
17	Genome-wide analysis of long non-coding RNAs responsive to multiple nutrient stresses in <i>Arabidopsis thaliana</i> . <i>Functional and Integrative Genomics</i> , 2021, 21, 17-30.	3.5	14
18	In situ dissecting the evolution of gene duplication with different histone modification patterns based on high-throughput data analysis in <i>Arabidopsis thaliana</i> . <i>PeerJ</i> , 2021, 9, e10426.	2.0	2

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19	Circular RNA. <i>Methods in Molecular Biology</i> , 2021, 2362, 109-118.	0.9	1
20	Database Resources for Functional Circular RNAs. <i>Methods in Molecular Biology</i> , 2021, 2284, 457-466.	0.9	4
21	Tracing cell-type evolution by cross-species comparison of cell atlases. <i>Cell Reports</i> , 2021, 34, 108803.	6.4	44
22	OverCOVID: an integrative web portal for SARS-CoV-2 bioinformatics resources. <i>Journal of Integrative Bioinformatics</i> , 2021, 18, 9-17.	1.5	11
23	Genome-wide discovery of hidden genes mediating known drug-disease association using KDDANet. <i>Npj Genomic Medicine</i> , 2021, 6, 50.	3.8	2
24	Enhanced HSC-like cell generation from mouse pluripotent stem cells in a 3D induction system cocultured with stromal cells. <i>Stem Cell Research and Therapy</i> , 2021, 12, 353.	5.5	7
25	Computational Identification of miRNAs and Temperature-Responsive lncRNAs From Mango ( <i>Mangifera</i> ) Tj ETQq1 1,0,784314 rgBT /Cve 2.3	2.3	7
26	mPPI: a database extension to visualize structural interactome in a one-to-many manner. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	3.0	6
27	A Petri nets-based framework for whole-cell modeling. <i>BioSystems</i> , 2021, 210, 104533.	2.0	5
28	Bioinformatics resources facilitate understanding and harnessing clinical research of SARS-CoV-2. <i>Briefings in Bioinformatics</i> , 2021, 22, 714-725.	6.5	17
29	Detection and Location of Model-Plant Mismatch in Multiple Input Multiple Output Systems under Model Predictive Controller Using Granger Causality Method. <i>Processes</i> , 2021, 9, 1976.	2.8	0
30	rRNA biogenesis regulates mouse 2C-like state by 3D structure reorganization of peri-nucleolar heterochromatin. <i>Nature Communications</i> , 2021, 12, 6365.	12.8	24
31	Database Resources of the National Genomics Data Center in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D24-D33.	14.5	165
32	Medical genomics at the Systems Biology and Bioinformatics (SBB-2019) school. <i>BMC Medical Genomics</i> , 2020, 13, 127.	1.5	4
33	A novel riboswitch classification based on imbalanced sequences achieved by machine learning. <i>PLoS Computational Biology</i> , 2020, 16, e1007760.	3.2	2
34	CircPlant: An Integrated Tool for circRNA Detection and Functional Prediction in Plants. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 352-358.	6.9	13
35	Characterization and Function of Circular RNAs in Plants. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 91.	3.5	50
36	Construction of a human cell landscape at single-cell level. <i>Nature</i> , 2020, 581, 303-309.	27.8	695

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37	PncStress: a manually curated database of experimentally validated stress-responsive non-coding RNAs in plants. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	16
38	The anterior insular cortex unilaterally controls feeding in response to aversive visceral stimuli in mice. Nature Communications, 2020, 11, 640.	12.8	42
39	PmliPred: a method based on hybrid model and fuzzy decision for plant miRNA–lncRNA interaction prediction. Bioinformatics, 2020, 36, 2986-2992.	4.1	40
40	Protein–protein interaction network with machine learning models and multiomics data reveal potential neurodegenerative disease-related proteins. Human Molecular Genetics, 2020, 29, 1378-1387.	2.9	14
41	Bioinformatics of genome regulation and structure – 2020 papers collection. Journal of Integrative Bioinformatics, 2020, 17, .	1.5	1
42	Versatile interactions and bioinformatics analysis of noncoding RNAs. Briefings in Bioinformatics, 2019, 20, 1781-1794.	6.5	24
43	A practical guide for DNase-seq data analysis: from data management to common applications. Briefings in Bioinformatics, 2019, 20, 1865-1877.	6.5	7
44	Non-Coding RNAs and their Integrated Networks. Journal of Integrative Bioinformatics, 2019, 16, .	1.5	382
45	A Hybrid Prediction Method for Plant lncRNA-Protein Interaction. Cells, 2019, 8, 521.	4.1	21
46	The genomes of pecan and Chinese hickory provide insights into Carya evolution and nut nutrition. GigaScience, 2019, 8, .	6.4	88
47	Dynamic control of enhancer activity drives stage-specific gene expression during flower morphogenesis. Nature Communications, 2019, 10, 1705.	12.8	70
48	CircFunBase: a database for functional circular RNAs. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	108
49	Integrative Bioinformatics: History and Future. Journal of Integrative Bioinformatics, 2019, 16, .	1.5	5
50	Data-mining Techniques for Image-based Plant Phenotypic Traits Identification and Classification. Scientific Reports, 2019, 9, 19526.	3.3	26
51	Identification of epistasis loci underlying rice flowering time by controlling population stratification and polygenic effect. DNA Research, 2019, 26, 119-130.	3.4	21
52	Identification of novel microRNAs in rice ( <i>Oryza sativa</i> ) based on the cleavage signals in precursors. Plant Biosystems, 2019, 153, 506-513.	1.6	1
53	Database Resources of the BIG Data Center in 2019. Nucleic Acids Research, 2019, 47, D8-D14.	14.5	157
54	Special Issue on Plant Bioinformatics. Current Bioinformatics, 2019, 14, 564-565.	1.5	1

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55	PlncRNADB: A Repository of Plant lncRNAs and lncRNA-RBP Protein Interactions. <i>Current Bioinformatics</i> , 2019, 14, 621-627.	1.5	24
56	Analyzing the genes related to Alzheimer's disease via a network and pathway-based approach. , 2019, , 40-40.		0
57	Mapping the Mouse Cell Atlas by Microwell-Seq. <i>Cell</i> , 2018, 172, 1091-1107.e17.	28.9	1,068
58	Unveiling the Different Emission Behavior of Polytriazoles Constructed from Pyrazine-Based AIE Monomers by Click Polymerization. <i>ACS Applied Materials &amp; Interfaces</i> , 2018, 10, 12181-12188.	8.0	38
59	Discovering Putative Peptides Encoded from Noncoding RNAs in Ribosome Profiling Data of <i>Arabidopsis thaliana</i> . <i>ACS Synthetic Biology</i> , 2018, 7, 655-663.	3.8	6
60	Predicting plant biomass accumulation from image-derived parameters. <i>GigaScience</i> , 2018, 7, .	6.4	51
61	Computational investigation of small RNAs in the establishment of root nodules and arbuscular mycorrhiza in leguminous plants. <i>Science China Life Sciences</i> , 2018, 61, 706-717.	4.9	9
62	Medical genomics at Belyaev Conference " 2017. <i>BMC Medical Genomics</i> , 2018, 11, 11.	1.5	9
63	Distinctive features of immunostaining and mutational load in primary pulmonary enteric adenocarcinoma: implications for differential diagnosis and immunotherapy. <i>Journal of Translational Medicine</i> , 2018, 16, 81.	4.4	28
64	BioPepDB: an integrated data platform for food-derived bioactive peptides. <i>International Journal of Food Sciences and Nutrition</i> , 2018, 69, 963-968.	2.8	42
65	A comprehensive description and evolutionary analysis of 9 Loliginidae mitochondrial genomes. <i>Hydrobiologia</i> , 2018, 808, 115-124.	2.0	12
66	CHI3L1 promotes tumor progression by activating TGF- $\beta$ 2 signaling pathway in hepatocellular carcinoma. <i>Scientific Reports</i> , 2018, 8, 15029.	3.3	57
67	Near-Infrared Electron Acceptors with Fluorinated Regioisomeric Backbone for Highly Efficient Polymer Solar Cells. <i>Advanced Materials</i> , 2018, 30, e1803769.	21.0	116
68	The HTPmod Shiny application enables modeling and visualization of large-scale biological data. <i>Communications Biology</i> , 2018, 1, 89.	4.4	12
69	Gene-expression signature regulated by the KEAP1-NRF2-CUL3 axis is associated with a poor prognosis in head and neck squamous cell cancer. <i>BMC Cancer</i> , 2018, 18, 46.	2.6	75
70	Big Data Analytics in Medicine and Healthcare. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.5	188
71	Identification and characterization of ncRNA-associated ceRNA networks in <i>Arabidopsis</i> leaf development. <i>BMC Genomics</i> , 2018, 19, 607.	2.8	52
72	Dissecting lncRNA Roles in Renal Cell Carcinoma Metastasis and Characterizing Genomic Heterogeneity by Single-Cell RNA-seq. <i>Molecular Cancer Research</i> , 2018, 16, 1879-1888.	3.4	21

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73	Postsynaptic RIM1 modulates synaptic function by facilitating membrane delivery of recycling NMDARs in hippocampal neurons. <i>Nature Communications</i> , 2018, 9, 2267.	12.8	40
74	Brief introduction of bioinformatics education in Đhina. , 2018, , 10-11.		0
75	Roles of non-coding RNAs in stress response in plants. , 2018, , 23-23.		0
76	Quantifying genome sequence repeatability by repeater. , 2018, , 26-26.		0
77	Systems biology approaches for analysis of dementia with Lewy bodies in mouse models. , 2018, , 16-16.		0
78	Genome-wide analysis of long non-coding RNAs responsive to multiple nutrient stresses in <i>Arabidopsis thaliana</i> . , 2018, , 66-66.		0
79	Computer studies of miRNA in abiotic stress response in plants. , 2018, , 30-30.		0
80	DEF: an automated dead-end filling approach based on quasi-endosymbiosis. <i>Bioinformatics</i> , 2017, 33, 405-413.	4.1	4
81	Circular RNA: an emerging key player in RNA world. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw045.	6.5	196
82	Computer analysis of colocalization of the TFsâ€™ binding sites in the genome according to the ChIP-seq data. <i>Russian Journal of Genetics: Applied Research</i> , 2017, 7, 513-522.	0.4	11
83	Non-coding RNAs and Their Roles in Stress Response in Plants. <i>Genomics, Proteomics and Bioinformatics</i> , 2017, 15, 301-312.	6.9	150
84	Digital Biomass Accumulation Using High-Throughput Plant Phenotype Data Analysis. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, .	1.5	25
85	Phenolâ€™ne Click Polymerization: An Efficient Technique to Facilely Access Regioâ€™and Stereoregular Poly(vinylene ether ketone)s. <i>Chemistry - A European Journal</i> , 2017, 23, 10725-10731.	3.3	56
86	FPD: A comprehensive phosphorylation database in fungi. <i>Fungal Biology</i> , 2017, 121, 869-875.	2.5	19
87	Frontispiece: Phenolâ€™ne Click Polymerization: An Efficient Technique to Facilely Access Regioâ€™and Stereoregular Poly(vinylene ether ketone)s. <i>Chemistry - A European Journal</i> , 2017, 23, .	3.3	0
88	CircPro: an integrated tool for the identification of circRNAs with protein-coding potential. <i>Bioinformatics</i> , 2017, 33, 3314-3316.	4.1	82
89	PceRBase: a database of plant competing endogenous RNA. <i>Nucleic Acids Research</i> , 2017, 45, D1009-D1014.	14.5	50
90	Biological Big Bytes: Integrative Analysis of Large Biological Datasets. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, .	1.5	10

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91	Identification of the long non-coding RNA LET as a novel tumor suppressor in gastric cancer. <i>Molecular Medicine Reports</i> , 2017, 15, 2229-2234.	2.4	14
92	PlantCircNet: a database for plant circRNA-miRNA-mRNA regulatory networks. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	44
93	Plant Biology at Belyaev Conference 2017. <i>BMC Plant Biology</i> , 2017, 17, 257.	3.6	9
94	A Generalized Approach for Measuring Relationships Among Genes. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, .	1.5	2
95	Genetic polymorphisms and related risk factors of ischemic stroke in a Mongolian population in China. <i>Vavilovskii Zhurnal Genetiki I Seleksii</i> , 2017, 21, 581-587.	1.1	4
96	miRNA Digger: a comprehensive pipeline for genome-wide novel miRNA mining. <i>Scientific Reports</i> , 2016, 6, 18901.	3.3	14
97	Genome-Wide Analysis of the Distinct Types of Chromatin Interactions in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2016, 58, pcw194.	3.1	8
98	Anionic conjugated polytriazole: direct preparation, aggregation-enhanced emission, and highly efficient Al <sup>3+</sup> sensing. <i>Polymer Chemistry</i> , 2016, 7, 5835-5839.	3.9	34
99	The mechanism of high contents of oil and oleic acid revealed by transcriptomic and lipidomic analysis during embryogenesis in <i>Carya cathayensis</i> Sarg.. <i>BMC Genomics</i> , 2016, 17, 113.	2.8	53
100	Exploring the mechanisms of genome-wide long-range interactions: interpreting chromosome organization. <i>Briefings in Functional Genomics</i> , 2016, 15, 385-395.	2.7	8
101	Endo-1,4-β-glucanase gene involved into the rapid elongation of <i>Phyllostachys heterocycla</i> var. <i>pubescens</i> . <i>Trees - Structure and Function</i> , 2016, 30, 1259-1274.	1.9	4
102	Single nucleotide polymorphisms in DNA repair genes and the risk of laryngeal cancer: A meta-analysis. <i>Biomedicine and Pharmacotherapy</i> , 2016, 78, 92-100.	5.6	12
103	Triphenylamine-functionalized tetraphenylpyrazine: facile preparation and multifaceted functionalities. <i>Journal of Materials Chemistry C</i> , 2016, 4, 2901-2908.	5.5	82
104	Complete mitochondrial genome of the <i>Loligo beka</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4278-4279.	0.7	4
105	The roles of cross-talk epigenetic patterns in <i>Arabidopsis thaliana</i> . <i>Briefings in Functional Genomics</i> , 2016, 15, 278-287.	2.7	31
106	Toward a next-generation atlas of RNA secondary structure. <i>Briefings in Bioinformatics</i> , 2016, 17, 63-77.	6.5	10
107	Inhibition of ERK1/2/ERK/P62 cascades induces autophagic switch in the estrogen receptor-positive breast cancer cells exposed to gemcitabine. <i>Oncotarget</i> , 2016, 7, 48501-48516.	1.8	20
108	Computer analysis of co-localization of transcription factor binding sites in genome by ChIP-seq data. <i>Vavilovskii Zhurnal Genetiki I Seleksii</i> , 2016, 20, 770-778.	1.1	1

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109	DaTo: an atlas of biological databases and tools. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, 297.	1.5	3
110	Advanced phenotyping and phenotype data analysis for the study of plant growth and development. <i>Frontiers in Plant Science</i> , 2015, 6, 619.	3.6	238
111	Hybrid-Dimensional Visualization and Interaction - Integrating 2D and 3D Visualization with Semi-Immersive Navigation Techniques. , 2015, , .		11
112	CancerNet: a database for decoding multilevel molecular interactions across diverse cancer types. <i>Oncogenesis</i> , 2015, 4, e177-e177.	4.9	31
113	Tetraphenylpyrazine-based AIEgens: facile preparation and tunable light emission. <i>Chemical Science</i> , 2015, 6, 1932-1937.	7.4	259
114	N-type pyrazine and triazole-based luminogens with aggregation-enhanced emission characteristics. <i>Chemical Communications</i> , 2015, 51, 10710-10713.	4.1	30
115	Genome-wide view of natural antisense transcripts in <i>Arabidopsis thaliana</i> . <i>DNA Research</i> , 2015, 22, 233-243.	3.4	41
116	RNA Scaffold: Designed to Co-localize Enzymes. <i>Methods in Molecular Biology</i> , 2015, 1316, 105-112.	0.9	3
117	Dissecting the Phenotypic Components of Crop Plant Growth and Drought Responses Based on High-Throughput Image Analysis. <i>Plant Cell</i> , 2015, 26, 4636-4655.	6.6	329
118	RNA regulatory networks in animals and plants: a long noncoding RNA perspective. <i>Briefings in Functional Genomics</i> , 2015, 14, 91-101.	2.7	74
119	MTide: an integrated tool for the identification of miRNA-target interaction in plants. <i>Bioinformatics</i> , 2015, 31, 290-291.	4.1	73
120	Fas Signaling Promotes Gastric Cancer Metastasis through STAT3-Dependent Upregulation of Fascin. <i>PLoS ONE</i> , 2015, 10, e0125132.	2.5	15
121	Editorial (Thematic Issue: Protein Systems Biology: Method, Regulation, and Network). <i>Current Protein and Peptide Science</i> , 2014, 15, 519-521.	1.4	1
122	Open problems in Petri net modeling and simulation of biological systems. <i>IT - Information Technology</i> , 2014, 56, .	0.9	3
123	CompareSVM: supervised, Support Vector Machine (SVM) inference of gene regularity networks. <i>BMC Bioinformatics</i> , 2014, 15, 395.	2.6	42
124	Dissecting the chromatin interactome of microRNA genes. <i>Nucleic Acids Research</i> , 2014, 42, 3028-3043.	14.5	27
125	Bridging Genomics and Phenomics. , 2014, , 299-333.		16
126	The Genome of a Mongolian Individual Reveals the Genetic Imprints of Mongolians on Modern Human Populations. <i>Genome Biology and Evolution</i> , 2014, 6, 3122-3136.	2.5	24



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127	Detection of Thrombin with an Aptamer-Based Macromolecule Biosensor Using Bacterial Ghost System. <i>ACS Synthetic Biology</i> , 2014, 3, 963-965.	3.8	4
128	Construction and analysis of microRNA- $\epsilon$ transcription factor regulation network in arabidopsis. <i>IET Systems Biology</i> , 2014, 8, 76-86.	1.5	2
129	Uncovering DCL1-dependent small RNA loci on plant genomes: a structure-based approach. <i>Journal of Experimental Botany</i> , 2014, 65, 395-400.	4.8	1
130	The Organelle-focused Proteomes and Interactomes in Rice. <i>Current Protein and Peptide Science</i> , 2014, 15, 583-590.	1.4	1
131	Genome-scale metabolic model in guiding metabolic engineering of microbial improvement. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 519-539.	3.6	50
132	Identification of novel microRNA-like-coding sites on the long-stem microRNA precursors in Arabidopsis. <i>Gene</i> , 2013, 527, 477-483.	2.2	9
133	Use of transcriptome sequencing to understand the pistillate flowering in hickory ( <i>Carya cathayensis</i> ) Tj ETQq1 1 0.784314 rgBT /Overde	2.8	39
134	Bioinformatics prediction of miRNAs in the <i>Prunus persica</i> genome with validation of their precise sequences by miR-RACE. <i>Journal of Plant Physiology</i> , 2013, 170, 80-92.	3.5	12
135	A reversed framework for the identification of microRNA-target pairs in plants. <i>Briefings in Bioinformatics</i> , 2013, 14, 293-301.	6.5	27
136	Construction of gene regulatory networks mediated by vegetative and reproductive stage-specific small <i>scp</i> RNA in rice ( <i>Oryza sativa</i> ). <i>New Phytologist</i> , 2013, 197, 441-453.	7.3	15
137	MicroRNAs and Their Cross-Talks in Plant Development. <i>Journal of Genetics and Genomics</i> , 2013, 40, 161-170.	3.9	70
138	Proteome Analysis of Silkworm, <i>Bombyx mori</i> , Larval Gonads: Characterization of Proteins Involved in Sexual Dimorphism and Gametogenesis. <i>Journal of Proteome Research</i> , 2013, 12, 2422-2438.	3.7	20
139	The Differential Transcription Network between Embryo and Endosperm in the Early Developing Maize Seed $\hat{A} \hat{A}$ . <i>Plant Physiology</i> , 2013, 162, 440-455.	4.8	76
140	An Integrative Bioinformatics Framework for Genome-scale Multiple Level Network Reconstruction of Rice. <i>Journal of Integrative Bioinformatics</i> , 2013, 10, 94-102.	1.5	18
141	Insights into the increasing virulence of the swine-origin pandemic H1N1/2009 influenza virus. <i>Scientific Reports</i> , 2013, 3, 1601.	3.3	36
142	Codon usage patterns in Chinese bayberry ( <i>Myrica rubra</i> ) based on RNA-Seq data. <i>BMC Genomics</i> , 2013, 14, 732.	2.8	42
143	PSI: A Comprehensive and Integrative Approach for Accurate Plant Subcellular Localization Prediction. <i>PLoS ONE</i> , 2013, 8, e75826.	2.5	46
144	An integrative bioinformatics framework for genome-scale multiple level network reconstruction of rice. <i>Journal of Integrative Bioinformatics</i> , 2013, 10, 223.	1.5	12

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145	PlantNATsDB: a comprehensive database of plant natural antisense transcripts. <i>Nucleic Acids Research</i> , 2012, 40, D1187-D1193.	14.5	76
146	Are all the miRBase-registered microRNAs true?. <i>RNA Biology</i> , 2012, 9, 249-253.	3.1	56
147	Microarray analysis of differentially expressed genes engaged in fruit development between <i>Prunus mume</i> and <i>Prunus armeniaca</i> . <i>Journal of Plant Physiology</i> , 2012, 169, 1776-1788.	3.5	10
148	Transcriptomic analysis of Chinese bayberry ( <i>Myrica rubra</i> ) fruit development and ripening using RNA-Seq. <i>BMC Genomics</i> , 2012, 13, 19.	2.8	199
149	Effect of hot air treatment on organic acid- and sugar-metabolism in Ponkan ( <i>Citrus reticulata</i> ) fruit. <i>Scientia Horticulturae</i> , 2012, 147, 118-125.	3.6	124
150	Expression-Based Functional Investigation of the Organ-Specific MicroRNAs in Arabidopsis. <i>PLoS ONE</i> , 2012, 7, e50870.	2.5	16
151	Computer and statistical analysis of transcription factor binding and chromatin modifications by ChIP-seq data in embryonic stem cell. <i>Journal of Integrative Bioinformatics</i> , 2012, 9, 211.	1.5	4
152	The Regulatory Activities of Plant MicroRNAs: A More Dynamic Perspective. <i>Plant Physiology</i> , 2011, 157, 1583-1595.	4.8	92
153	Plant siRNAs from introns mediate DNA methylation of host genes. <i>Rna</i> , 2011, 17, 1012-1024.	3.5	35
154	Expression Profiling and Regulation of Genes Related to Silkworm Posterior Silk Gland Development and Fibroin Synthesis. <i>Journal of Proteome Research</i> , 2011, 10, 3551-3564.	3.7	31
155	PRIN: a predicted rice interactome network. <i>BMC Bioinformatics</i> , 2011, 12, 161.	2.6	157
156	Toward microRNA-mediated gene regulatory networks in plants. <i>Briefings in Bioinformatics</i> , 2011, 12, 645-659.	6.5	53
157	MicroRNAs in Plant Roots: Current Understanding and Future Perspectives. <i>RNA Technologies</i> , 2011, , 269-284.	0.3	1
158	Origin and evolutionary analysis of the plant-specific TIFY transcription factor family. <i>Genomics</i> , 2011, 98, 128-136.	2.9	167
159	Computational Identification of Protein-Protein Interactions in Rice Based on the Predicted Rice Interactome Network. <i>Genomics, Proteomics and Bioinformatics</i> , 2011, 9, 128-137.	6.9	20
160	Root hair-specific expansins modulate root hair elongation in rice. <i>Plant Journal</i> , 2011, 66, 725-734.	5.7	143
161	Petri net models for the semi-automatic construction of large scale biological networks. <i>Natural Computing</i> , 2011, 10, 1077-1097.	3.0	12
162	A Systematic Petri Net Approach for Multiple-Scale Modeling and Simulation of Biochemical Processes. <i>Applied Biochemistry and Biotechnology</i> , 2011, 164, 338-352.	2.9	5

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163	Pathway knockout and redundancy in metabolic networks. <i>Journal of Theoretical Biology</i> , 2011, 270, 63-69.	1.7	14
164	PmiRKB: a plant microRNA knowledge base. <i>Nucleic Acids Research</i> , 2011, 39, D181-D187.	14.5	43
165	InvA Protein Is a Nudix Hydrolase Required for Infection by Pathogenic <i>Leptospira</i> in Cell Lines and Animals*. <i>Journal of Biological Chemistry</i> , 2011, 286, 36852-36863.	3.4	10
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