

Ming Chen

List of Publications by Year in descending order

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202
papers

10,586
citations

43973

48
h-index

42291

92
g-index

223
all docs

223
docs citations

223
times ranked

16169
citing authors

#	ARTICLE	IF	CITATIONS
1	Mapping the Mouse Cell Atlas by Microwell-Seq. <i>Cell</i> , 2018, 172, 1091-1107.e17.	13.5	1,068
2	Construction of a human cell landscape at single-cell level. <i>Nature</i> , 2020, 581, 303-309.	13.7	695
3	Non-Coding RNAs and their Integrated Networks. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.0	382
4	Database Resources of the National Genomics Data Center, China National Center for Bioinformation in 2022. <i>Nucleic Acids Research</i> , 2022, 50, D27-D38.	6.5	364
5	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.	3.1	329
6	Tetraphenylpyrazine-based AIEgens: facile preparation and tunable light emission. <i>Chemical Science</i> , 2015, 6, 1932-1937.	3.7	259
7	Auxin-related gene families in abiotic stress response in <i>Sorghum bicolor</i> . <i>Functional and Integrative Genomics</i> , 2010, 10, 533-546.	1.4	240
8	Advanced phenotyping and phenotype data analysis for the study of plant growth and development. <i>Frontiers in Plant Science</i> , 2015, 6, 619.	1.7	238
9	Transcriptomic analysis of Chinese bayberry (<i>Myrica rubra</i>) fruit development and ripening using RNA-Seq. <i>BMC Genomics</i> , 2012, 13, 19.	1.2	199
10	Circular RNA: an emerging key player in RNA world. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw045.	3.2	196
11	Big Data Analytics in Medicine and Healthcare. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.0	188
12	Database Resources of the National Genomics Data Center, China National Center for Bioinformation in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D18-D28.	6.5	168
13	Origin and evolutionary analysis of the plant-specific TIFY transcription factor family. <i>Genomics</i> , 2011, 98, 128-136.	1.3	167
14	Database Resources of the National Genomics Data Center in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D24-D33.	6.5	165
15	PRIN: a predicted rice interactome network. <i>BMC Bioinformatics</i> , 2011, 12, 161.	1.2	157
16	Database Resources of the BIG Data Center in 2019. <i>Nucleic Acids Research</i> , 2019, 47, D8-D14.	6.5	157
17	Non-coding RNAs and Their Roles in Stress Response in Plants. <i>Genomics, Proteomics and Bioinformatics</i> , 2017, 15, 301-312.	3.0	150
18	MicroRNA-mediated signaling involved in plant root development. <i>Biochemical and Biophysical Research Communications</i> , 2010, 393, 345-349.	1.0	148

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19	Root hair-specific expansins modulate root hair elongation in rice. <i>Plant Journal</i> , 2011, 66, 725-734.	2.8	143
20	Expression profile of PIN, AUX/LAX and PGP auxin transporter gene families in <i>Sorghum bicolor</i> under phytohormone and abiotic stress. <i>FEBS Journal</i> , 2010, 277, 2954-2969.	2.2	139
21	Phosphate signaling in <i>Arabidopsis</i> and <i>Oryza sativa</i> . <i>Plant Science</i> , 2009, 176, 170-180.	1.7	127
22	Functional analysis of the structural domain of ARF proteins in rice (<i>Oryza sativa</i> L.). <i>Journal of Experimental Botany</i> , 2010, 61, 3971-3981.	2.4	125
23	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.	1.7	124
24	Near-Infrared Electron Acceptors with Fluorinated Regioisomeric Backbone for Highly Efficient Polymer Solar Cells. <i>Advanced Materials</i> , 2018, 30, e1803769.	11.1	116
25	CircFunBase: a database for functional circular RNAs. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	108
26	The two-component signal system in rice (<i>Oryza sativa</i> L.): A genome-wide study of cytokinin signal perception and transduction. <i>Genomics</i> , 2007, 89, 697-707.	1.3	106
27	The Regulatory Activities of Plant MicroRNAs: A More Dynamic Perspective. <i>Plant Physiology</i> , 2011, 157, 1583-1595.	2.3	92
28	The genomes of pecan and Chinese hickory provide insights into <i>Carya</i> evolution and nut nutrition. <i>GigaScience</i> , 2019, 8, .	3.3	88
29	Comparative Proteomic Analysis between the Domesticated Silkworm (<i>Bombyx mori</i>) Reared on Fresh Mulberry Leaves and on Artificial Diet. <i>Journal of Proteome Research</i> , 2008, 7, 5103-5111.	1.8	84
30	Genome-wide survey of rice microRNAs and microRNA target pairs in the root of a novel auxin-resistant mutant. <i>Planta</i> , 2009, 230, 883-898.	1.6	84
31	Triphenylamine-functionalized tetraphenylpyrazine: facile preparation and multifaceted functionalities. <i>Journal of Materials Chemistry C</i> , 2016, 4, 2901-2908.	2.7	82
32	CircPro: an integrated tool for the identification of circRNAs with protein-coding potential. <i>Bioinformatics</i> , 2017, 33, 3314-3316.	1.8	82
33	PlantNATsDB: a comprehensive database of plant natural antisense transcripts. <i>Nucleic Acids Research</i> , 2012, 40, D1187-D1193.	6.5	76
34	The Differential Transcription Network between Embryo and Endosperm in the Early Developing Maize Seed. <i>Plant Physiology</i> , 2013, 162, 440-455.	2.3	76
35	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.	1.1	75
36	RNA regulatory networks in animals and plants: a long noncoding RNA perspective. <i>Briefings in Functional Genomics</i> , 2015, 14, 91-101.	1.3	74

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37	MTide: an integrated tool for the identification of miRNA–target interaction in plants. <i>Bioinformatics</i> , 2015, 31, 290-291.	1.8	73
38	MicroRNAs and Their Cross-Talks in Plant Development. <i>Journal of Genetics and Genomics</i> , 2013, 40, 161-170.	1.7	70
39	Dynamic control of enhancer activity drives stage-specific gene expression during flower morphogenesis. <i>Nature Communications</i> , 2019, 10, 1705.	5.8	70
40	Epigenetic performers in plants. <i>Development Growth and Differentiation</i> , 2010, 52, 555-566.	0.6	65
41	CHI3L1 promotes tumor progression by activating TGF- β 2 signaling pathway in hepatocellular carcinoma. <i>Scientific Reports</i> , 2018, 8, 15029.	1.6	57
42	Relationships Among Stop Codon Usage Bias, Its Context, Isochores, and Gene Expression Level in Various Eukaryotes. <i>Journal of Molecular Evolution</i> , 2005, 61, 437-444.	0.8	56
43	Are all the miRBase-registered microRNAs true?. <i>RNA Biology</i> , 2012, 9, 249-253.	1.5	56
44	Phenol–yne Click Polymerization: An Efficient Technique to Facilely Access Regio– and Stereoregular Poly(vinylene ether ketone)s. <i>Chemistry - A European Journal</i> , 2017, 23, 10725-10731.	1.7	56
45	Toward microRNA-mediated gene regulatory networks in plants. <i>Briefings in Bioinformatics</i> , 2011, 12, 645-659.	3.2	53
46	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.	1.2	53
47	Identification and characterization of ncRNA-associated ceRNA networks in <i>Arabidopsis</i> leaf development. <i>BMC Genomics</i> , 2018, 19, 607.	1.2	52
48	Predicting plant biomass accumulation from image-derived parameters. <i>GigaScience</i> , 2018, 7, .	3.3	51
49	Genome-scale metabolic model in guiding metabolic engineering of microbial improvement. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 519-539.	1.7	50
50	PceRBase: a database of plant competing endogenous RNA. <i>Nucleic Acids Research</i> , 2017, 45, D1009-D1014.	6.5	50
51	Characterization and Function of Circular RNAs in Plants. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 91.	1.6	50
52	BNArray: an R package for constructing gene regulatory networks from microarray data by using Bayesian network. <i>Bioinformatics</i> , 2006, 22, 2952-2954.	1.8	49
53	High-throughput degradome sequencing can be used to gain insights into microRNA precursor metabolism. <i>Journal of Experimental Botany</i> , 2010, 61, 3833-3837.	2.4	46
54	PSI: A Comprehensive and Integrative Approach for Accurate Plant Subcellular Localization Prediction. <i>PLoS ONE</i> , 2013, 8, e75826.	1.1	46

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55	RNA editing of nuclear transcripts in <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2010, 11, S12.	1.2	44
56	PlantCircNet: a database for plant circRNA-miRNA-mRNA regulatory networks. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	44
57	Tracing cell-type evolution by cross-species comparison of cell atlases. <i>Cell Reports</i> , 2021, 34, 108803.	2.9	44
58	PmiRKB: a plant microRNA knowledge base. <i>Nucleic Acids Research</i> , 2011, 39, D181-D187.	6.5	43
59	Codon usage patterns in Chinese bayberry (<i>Myrica rubra</i>) based on RNA-Seq data. <i>BMC Genomics</i> , 2013, 14, 732.	1.2	42
60	CompareSVM: supervised, Support Vector Machine (SVM) inference of gene regularity networks. <i>BMC Bioinformatics</i> , 2014, 15, 395.	1.2	42
61	BioPepDB: an integrated data platform for food-derived bioactive peptides. <i>International Journal of Food Sciences and Nutrition</i> , 2018, 69, 963-968.	1.3	42
62	The anterior insular cortex unilaterally controls feeding in response to aversive visceral stimuli in mice. <i>Nature Communications</i> , 2020, 11, 640.	5.8	42
63	Genome-wide view of natural antisense transcripts in <i>Arabidopsis thaliana</i> . <i>DNA Research</i> , 2015, 22, 233-243.	1.5	41
64	Postsynaptic RIM1 modulates synaptic function by facilitating membrane delivery of recycling NMDARs in hippocampal neurons. <i>Nature Communications</i> , 2018, 9, 2267.	5.8	40
65	PmliPred: a method based on hybrid model and fuzzy decision for plant miRNA-lncRNA interaction prediction. <i>Bioinformatics</i> , 2020, 36, 2986-2992.	1.8	40
66	Use of transcriptome sequencing to understand the pistillate flowering in hickory (<i>Carya cathayensis</i>) Tj ETQq0 0 0,rgBT /Overlock 10 Tf	1.2	39
67	Unveiling the Different Emission Behavior of Polytriazoles Constructed from Pyrazine-Based AIE Monomers by Click Polymerization. <i>ACS Applied Materials & Interfaces</i> , 2018, 10, 12181-12188.	4.0	38
68	Proteomic and Bioinformatic Analysis on Endocrine Organs of Domesticated Silkworm, <i>Bombyx mori</i> L. for a Comprehensive Understanding of Their Roles and Relations. <i>Journal of Proteome Research</i> , 2009, 8, 2620-2632.	1.8	36
69	Insights into the increasing virulence of the swine-origin pandemic H1N1/2009 influenza virus. <i>Scientific Reports</i> , 2013, 3, 1601.	1.6	36
70	Plant siRNAs from introns mediate DNA methylation of host genes. <i>Rna</i> , 2011, 17, 1012-1024.	1.6	35
71	ChIP-Hub provides an integrative platform for exploring plant regulome. <i>Nature Communications</i> , 2022, 13, .	5.8	35
72	Mechanisms of microRNA-mediated auxin signaling inferred from the rice mutant <i>osaxr</i> . <i>Plant Signaling and Behavior</i> , 2010, 5, 252-254.	1.2	34

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73	Anionic conjugated polytriazole: direct preparation, aggregation-enhanced emission, and highly efficient Al ³⁺ sensing. <i>Polymer Chemistry</i> , 2016, 7, 5835-5839.	1.9	34
74	A medical bioinformatics approach for metabolic disorders: Biomedical data prediction, modeling, and systematic analysis. <i>Journal of Biomedical Informatics</i> , 2006, 39, 147-159.	2.5	32
75	Construction of MicroRNA- and MicroRNA*-mediated regulatory networks in plants. <i>RNA Biology</i> , 2011, 8, 1124-1148.	1.5	32
76	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.	1.8	31
77	CancerNet: a database for decoding multilevel molecular interactions across diverse cancer types. <i>Oncogenesis</i> , 2015, 4, e177-e177.	2.1	31
78	The roles of cross-talk epigenetic patterns in <i>Arabidopsis thaliana</i> . <i>Briefings in Functional Genomics</i> , 2016, 15, 278-287.	1.3	31
79	N-type pyrazine and triazole-based luminogens with aggregation-enhanced emission characteristics. <i>Chemical Communications</i> , 2015, 51, 10710-10713.	2.2	30
80	Quantitative Petri net model of gene regulated metabolic networks in the cell. <i>In Silico Biology</i> , 2003, 3, 347-65.	0.4	29
81	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.	1.8	28
82	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.	4.8	28
83	A reversed framework for the identification of microRNA-target pairs in plants. <i>Briefings in Bioinformatics</i> , 2013, 14, 293-301.	3.2	27
84	Dissecting the chromatin interactome of microRNA genes. <i>Nucleic Acids Research</i> , 2014, 42, 3028-3043.	6.5	27
85	DeepTrio: a ternary prediction system for protein-protein interaction using mask multiple parallel convolutional neural networks. <i>Bioinformatics</i> , 2022, 38, 694-702.	1.8	27
86	Data-mining Techniques for Image-based Plant Phenotypic Traits Identification and Classification. <i>Scientific Reports</i> , 2019, 9, 19526.	1.6	26
87	Small RNAs in angiosperms: sequence characteristics, distribution and generation. <i>Bioinformatics</i> , 2010, 26, 1391-1394.	1.8	25
88	Digital Biomass Accumulation Using High-Throughput Plant Phenotype Data Analysis. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, .	1.0	25
89	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.	1.1	24
90	Versatile interactions and bioinformatics analysis of noncoding RNAs. <i>Briefings in Bioinformatics</i> , 2019, 20, 1781-1794.	3.2	24

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91	PlncRNADB: A Repository of Plant lncRNAs and lncRNA-RBP Protein Interactions. <i>Current Bioinformatics</i> , 2019, 14, 621-627.	0.7	24
92	rRNA biogenesis regulates mouse 2C-like state by 3D structure reorganization of peri-nucleolar heterochromatin. <i>Nature Communications</i> , 2021, 12, 6365.	5.8	24
93	PathAligner. <i>Applied Bioinformatics</i> , 2004, 3, 241-252.	1.7	21
94	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.	1.5	21
95	A Hybrid Prediction Method for Plant lncRNA-Protein Interaction. <i>Cells</i> , 2019, 8, 521.	1.8	21
96	Identification of epistasis loci underlying rice flowering time by controlling population stratification and polygenic effect. <i>DNA Research</i> , 2019, 26, 119-130.	1.5	21
97	Shotgun proteomics approach to characterizing the embryonic proteome of the silkworm, <i>Bombyx mori</i> , at labrum appearance stage. <i>Insect Molecular Biology</i> , 2009, 18, 649-660.	1.0	20
98	Shotgun proteomic analysis on the embryos of silkworm <i>Bombyx mori</i> at the end of organogenesis. <i>Insect Biochemistry and Molecular Biology</i> , 2010, 40, 293-302.	1.2	20
99	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.	3.0	20
100	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.	1.8	20
101	Inhibition of ER1±/ERK/P62 cascades induces "autophagic switch" in the estrogen receptor-positive breast cancer cells exposed to gemcitabine. <i>Oncotarget</i> , 2016, 7, 48501-48516.	0.8	20
102	A reference single-cell regulomic and transcriptomic map of cynomolgus monkeys. <i>Nature Communications</i> , 2022, 13, .	5.8	20
103	Shotgun strategy-based proteome profiling analysis on the head of silkworm <i>Bombyx mori</i> . <i>Amino Acids</i> , 2010, 39, 751-761.	1.2	19
104	FPD: A comprehensive phosphorylation database in fungi. <i>Fungal Biology</i> , 2017, 121, 869-875.	1.1	19
105	An Integrative Bioinformatics Framework for Genome-scale Multiple Level Network Reconstruction of Rice. <i>Journal of Integrative Bioinformatics</i> , 2013, 10, 94-102.	1.0	18
106	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.	6.5	18
107	Role of the <sc>type"€B</sc> authentic response regulator gene family in fragrant rice under alkaline salt stress. <i>Physiologia Plantarum</i> , 2022, 174, e13696.	2.6	18
108	Bioinformatics resources facilitate understanding and harnessing clinical research of SARS-CoV-2. <i>Briefings in Bioinformatics</i> , 2021, 22, 714-725.	3.2	17

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109	Shotgun proteomic analysis of the fat body during metamorphosis of domesticated silkworm (<i>Bombyx</i>) Tj ETQq1 1,0,784314 rgBT /O	1.2	16
110	Bridging Genomics and Phenomics. , 2014, , 299-333.		16
111	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, .	1.4	16
112	Expression-Based Functional Investigation of the Organ-Specific MicroRNAs in Arabidopsis. PLoS ONE, 2012, 7, e50870.	1.1	16
113	Construction of gene regulatory networks mediated by vegetative and reproductive stage-specific small <sc>RNA</sc>s in rice (<i><sc>O</sc>ryza sativa</i>). New Phytologist, 2013, 197, 441-453.	3.5	15
114	Fas Signaling Promotes Gastric Cancer Metastasis through STAT3-Dependent Upregulation of Fascin. PLoS ONE, 2015, 10, e0125132.	1.1	15
115	Genes and Pathways Induced in Early Response to Defoliation in Rice Seedlings. Current Issues in Molecular Biology, 2009, , .	1.0	15
116	Biogenesis, Functions, Interactions, and Resources of Non-Coding RNAs in Plants. International Journal of Molecular Sciences, 2022, 23, 3695.	1.8	15
117	Pathway knockout and redundancy in metabolic networks. Journal of Theoretical Biology, 2011, 270, 63-69.	0.8	14
118	miRNA Digger: a comprehensive pipeline for genome-wide novel miRNA mining. Scientific Reports, 2016, 6, 18901.	1.6	14
119	Identification of the long non-coding RNA LET as a novel tumor suppressor in gastric cancer. Molecular Medicine Reports, 2017, 15, 2229-2234.	1.1	14
120	Protein-protein interaction network with machine learning models and multiomics data reveal potential neurodegenerative disease-related proteins. Human Molecular Genetics, 2020, 29, 1378-1387.	1.4	14
121	Genome-wide analysis of long non-coding RNAs responsive to multiple nutrient stresses in Arabidopsis thaliana. Functional and Integrative Genomics, 2021, 21, 17-30.	1.4	14
122	Modeling of Cell-to-Cell Communication Processes with Petri Nets Using the Example of Quorum Sensing. In Silico Biology, 2010, 10, 27-48.	0.4	13
123	CircPlant: An Integrated Tool for circRNA Detection and Functional Prediction in Plants. Genomics, Proteomics and Bioinformatics, 2020, 18, 352-358.	3.0	13
124	Petri net models for the semi-automatic construction of large scale biological networks. Natural Computing, 2011, 10, 1077-1097.	1.8	12
125	Bioinformatics prediction of miRNAs in the Prunus persica genome with validation of their precise sequences by miR-RACE. Journal of Plant Physiology, 2013, 170, 80-92.	1.6	12
126	Single nucleotide polymorphisms in DNA repair genes and the risk of laryngeal cancer: A meta-analysis. Biomedicine and Pharmacotherapy, 2016, 78, 92-100.	2.5	12

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127	A comprehensive description and evolutionary analysis of 9 Loliginidae mitochondrial genomes. <i>Hydrobiologia</i> , 2018, 808, 115-124.	1.0	12
128	The HTPmod Shiny application enables modeling and visualization of large-scale biological data. <i>Communications Biology</i> , 2018, 1, 89.	2.0	12
129	An integrative bioinformatics framework for genome-scale multiple level network reconstruction of rice. <i>Journal of Integrative Bioinformatics</i> , 2013, 10, 223.	1.0	12
130	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.	1.7	12
131	Functional characterization of plant small RNAs based on next-generation sequencing data. <i>Computational Biology and Chemistry</i> , 2010, 34, 308-312.	1.1	11
132	Hybrid-Dimensional Visualization and Interaction - Integrating 2D and 3D Visualization with Semi-Immersive Navigation Techniques. , 2015, , .		11
133	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
134	OverCOVID: an integrative web portal for SARS-CoV-2 bioinformatics resources. <i>Journal of Integrative Bioinformatics</i> , 2021, 18, 9-17.	1.0	11
135	Genomic survey of sequence features for ultraviolet tolerance in haloarchaea (family) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 4	1.3	10
136	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.	1.6	10
137	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.	1.6	10
138	Toward a next-generation atlas of RNA secondary structure. <i>Briefings in Bioinformatics</i> , 2016, 17, 63-77.	3.2	10
139	Biological Big Bytes: Integrative Analysis of Large Biological Datasets. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, .	1.0	10
140	Web-Based Information Retrieval System for the Prediction of Metabolic Pathways. <i>IEEE Transactions on Nanobioscience</i> , 2004, 3, 192-199.	2.2	9
141	Methodological framework for functional characterization of plant microRNAs. <i>Journal of Experimental Botany</i> , 2010, 61, 2271-2280.	2.4	9
142	Identification of novel microRNA-like-coding sites on the long-stem microRNA precursors in <i>Arabidopsis</i> . <i>Gene</i> , 2013, 527, 477-483.	1.0	9
143	Plant Biology at Belyaev Conference â€™ 2017. <i>BMC Plant Biology</i> , 2017, 17, 257.	1.6	9
144	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.	2.3	9

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145	Medical genomics at Belyaev Conference 2017. BMC Medical Genomics, 2018, 11, 11.	0.7	9
146	Genome-Wide Analysis of the Distinct Types of Chromatin Interactions in <i>Arabidopsis thaliana</i> . Plant and Cell Physiology, 2016, 58, pcw194.	1.5	8
147	Exploring the mechanisms of genome-wide long-range interactions: interpreting chromosome organization. Briefings in Functional Genomics, 2016, 15, 385-395.	1.3	8
148	A practical guide for DNase-seq data analysis: from data management to common applications. Briefings in Bioinformatics, 2019, 20, 1865-1877.	3.2	7
149	Enhanced HSC-like cell generation from mouse pluripotent stem cells in a 3D induction system cocultured with stromal cells. Stem Cell Research and Therapy, 2021, 12, 353.	2.4	7
150	Computational Identification of miRNAs and Temperature-Responsive lncRNAs From Mango (<i>Mangifera</i>) Tj ETQq0 0.0 rgBT /Qverlock 10	1.1	7
151	Discovering Putative Peptides Encoded from Noncoding RNAs in Ribosome Profiling Data of <i>Arabidopsis thaliana</i> . ACS Synthetic Biology, 2018, 7, 655-663.	1.9	6
152	mPPI: a database extension to visualize structural interactome in a one-to-many manner. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	6
153	STCDB: Signal Transduction Classification Database. Nucleic Acids Research, 2004, 32, 456D-458.	6.5	5
154	A Computational Approach for Recognition of Electronic Microscope Plant Pollen Images. , 2008, , .		5
155	A Systematic Petri Net Approach for Multiple-Scale Modeling and Simulation of Biochemical Processes. Applied Biochemistry and Biotechnology, 2011, 164, 338-352.	1.4	5
156	Integrative Bioinformatics: History and Future. Journal of Integrative Bioinformatics, 2019, 16, .	1.0	5
157	A Petri nets-based framework for whole-cell modeling. BioSystems, 2021, 210, 104533.	0.9	5
158	VIRS: A visual tool for identifying restriction sites in multiple DNA sequences. Biotechnology Progress, 2009, 25, 1525-1527.	1.3	4
159	Detection of Thrombin with an Aptamer-Based Macromolecule Biosensor Using Bacterial Ghost System. ACS Synthetic Biology, 2014, 3, 963-965.	1.9	4
160	DEF: an automated dead-end filling approach based on quasi-endosymbiosis. Bioinformatics, 2017, 33, 405-413.	1.8	4
161	Endo-1,4- β -glucanase gene involved into the rapid elongation of <i>Phyllostachys heterocycla</i> var. <i>pubescens</i> . Trees - Structure and Function, 2016, 30, 1259-1274.	0.9	4
162	Complete mitochondrial genome of the <i>Loligo beka</i> . Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4278-4279.	0.7	4

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