Ming Chen

List of Publications by Year
in descending order

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	Mapping the Mouse Cell Atlas by Microwell-Seq. Cell, 2018, 172, 1091-1107.e17.	28.9	1,068
2	Construction of a human cell landscape at single-cell level. Nature, 2020, 581, 303-309.	27.8	695
3	Non-Coding RNAs and their Integrated Networks. Journal of Integrative Bioinformatics, 2019, 16, .	1.5	382
4	Database Resources of the National Genomics Data Center, China National Center for Bioinformation in 2022. Nucleic Acids Research, 2022, 50, D27-D38.	14.5	364
5	Dissecting the Phenotypic Components of Crop Plant Growth and Drought Responses Based on High-Throughput Image Analysis Â. Plant Cell, 2015, 26, 4636-4655.	6.6	329
6	Tetraphenylpyrazine-based AIEgens: facile preparation and tunable light emission. Chemical Science, 2015, 6, 1932-1937.	7.4	259
7	Auxin-related gene families in abiotic stress response in Sorghum bicolor. Functional and Integrative Genomics, 2010, 10, 533-546.	3.5	240
8	Advanced phenotyping and phenotype data analysis for the study of plant growth and development. Frontiers in Plant Science, 2015, 6, 619.	3.6	238
9	Transcriptomic analysis of Chinese bayberry (Myrica rubra) fruit development and ripening using RNA-Seq. BMC Genomics, 2012, 13, 19.	2.8	199
10	Circular RNA: an emerging key player in RNA world. Briefings in Bioinformatics, 2017, 18, bbw045.	6.5	196
11	Big Data Analytics in Medicine and Healthcare. Journal of Integrative Bioinformatics, 2018, 15, .	1.5	188
12	DatabaseÂResources of the National Genomics Data Center, China National Center for Bioinformation in 2021. Nucleic Acids Research, 2021, 49, D18-D28.	14.5	168
13	Origin and evolutionary analysis of the plant-specific TIFY transcription factor family. Genomics, 2011, 98, 128-136.	2.9	167
14	Database Resources of the National Genomics Data Center in 2020. Nucleic Acids Research, 2020, 48, D24-D33.	14.5	165
15	PRIN: a predicted rice interactome network. BMC Bioinformatics, 2011, 12, 161.	2.6	157
16	Database Resources of the BIG Data Center in 2019. Nucleic Acids Research, 2019, 47, D8-D14.	14.5	157
17	Non-coding RNAs and Their Roles in Stress Response in Plants. Genomics, Proteomics and Bioinformatics, 2017, 15, 301-312.	6.9	150
18	MicroRNA-mediated signaling involved in plant root development. Biochemical and Biophysical Research Communications, 2010, 393, 345-349.	2.1	148

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19	Root hair–specific expansins modulate root hair elongation in rice. Plant Journal, 2011, 66, 725-734.	5.7	143
20	Expression profile of PIN, AUX/LAX and PGP auxin transporter gene families in *Sorghum bicolor* under phytohormone and abiotic stress. FEBS Journal, 2010, 277, 2954-2969.	4.7	139
21	Phosphate signaling in Arabidopsis and Oryza sativa. Plant Science, 2009, 176, 170-180.	3.6	127
22	Functional analysis of the structural domain of ARF proteins in rice (Oryza sativa L.). Journal of Experimental Botany, 2010, 61, 3971-3981.	4.8	125
23	Effect of hot air treatment on organic acid- and sugar-metabolism in Ponkan (Citrus reticulata) fruit. Scientia Horticulturae, 2012, 147, 118-125.	3.6	124
24	Near–Infrared Electron Acceptors with Fluorinated Regioisomeric Backbone for Highly Efficient Polymer Solar Cells. Advanced Materials, 2018, 30, e1803769.	21.0	116
25	CircFunBase: a database for functional circular RNAs. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	108
26	The two-component signal system in rice (Oryza sativa L.): A genome-wide study of cytokinin signal perception and transduction. Genomics, 2007, 89, 697-707.	2.9	106
27	The Regulatory Activities of Plant MicroRNAs: A More Dynamic Perspective. Plant Physiology, 2011, 157, 1583-1595.	4.8	92
28	The genomes of pecan and Chinese hickory provide insights into Carya evolution and nut nutrition. GigaScience, 2019, 8, .	6.4	88
29	Comparative Proteomic Analysis between the Domesticated Silkworm (*Bombyx mori*) Reared on Fresh Mulberry Leaves and on Artificial Diet. Journal of Proteome Research, 2008, 7, 5103-5111.	3.7	84
30	Genome-wide survey of rice microRNAs and microRNA–target pairs in the root of a novel auxin-resistant mutant. Planta, 2009, 230, 883-898.	3.2	84
31	Triphenylamine-functionalized tetraphenylpyrazine: facile preparation and multifaceted functionalities. Journal of Materials Chemistry C, 2016, 4, 2901-2908.	5.5	82
32	CircPro: an integrated tool for the identification of circRNAs with protein-coding potential. Bioinformatics, 2017, 33, 3314-3316.	4.1	82
33	PlantNATsDB: a comprehensive database of plant natural antisense transcripts. Nucleic Acids Research, 2012, 40, D1187-D1193.	14.5	76
34	The Differential Transcription Network between Embryo and Endosperm in the Early Developing Maize Seed Â Â Â. Plant Physiology, 2013, 162, 440-455.	4.8	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. BMC Cancer, 2018, 18, 46.	2.6	75
36	RNA regulatory networks in animals and plants: a long noncoding RNA perspective. Briefings in Functional Genomics, 2015, 14, 91-101.	2.7	74

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37	MTide: an integrated tool for the identification of miRNA–target interaction in plants. Bioinformatics, 2015, 31, 290-291.	4.1	73
38	MicroRNAs and Their Cross-Talks in Plant Development. Journal of Genetics and Genomics, 2013, 40, 161-170.	3.9	70
39	Dynamic control of enhancer activity drives stage-specific gene expression during flower morphogenesis. Nature Communications, 2019, 10, 1705.	12.8	70
40	Epigenetic performers in plants[†]. Development Growth and Differentiation, 2010, 52, 555-566.	1.5	65
41	CHI3L1 promotes tumor progression by activating TGF-β signaling pathway in hepatocellular carcinoma. Scientific Reports, 2018, 8, 15029.	3.3	57
42	Relationships Among Stop Codon Usage Bias, Its Context, Isochores, and Gene Expression Level in Various Eukaryotes. Journal of Molecular Evolution, 2005, 61, 437-444.	1.8	56
43	Are all the miRBase-registered microRNAs true?. RNA Biology, 2012, 9, 249-253.	3.1	56
44	Phenol–yne Click Polymerization: An Efficient Technique to Facilely Access Regio–and Stereoregular Poly(vinylene ether ketone)s. Chemistry - A European Journal, 2017, 23, 10725-10731.	3.3	56
45	Toward microRNA-mediated gene regulatory networks in plants. Briefings in Bioinformatics, 2011, 12, 645-659.	6.5	53
46	The mechanism of high contents of oil and oleic acid revealed by transcriptomic and lipidomic analysis during embryogenesis in Carya cathayensis Sarg.. BMC Genomics, 2016, 17, 113.	2.8	53
47	Identification and characterization of ncRNA-associated ceRNA networks in Arabidopsis leaf development. BMC Genomics, 2018, 19, 607.	2.8	52
48	Predicting plant biomass accumulation from image-derived parameters. GigaScience, 2018, 7, .	6.4	51
49	Genome-scale metabolic model in guiding metabolic engineering of microbial improvement. Applied Microbiology and Biotechnology, 2013, 97, 519-539.	3.6	50
50	PceRBase: a database of plant competing endogenous RNA. Nucleic Acids Research, 2017, 45, D1009-D1014.	14.5	50
51	Characterization and Function of Circular RNAs in Plants. Frontiers in Molecular Biosciences, 2020, 7, 91.	3.5	50
52	BNArray: an R package for constructing gene regulatory networks from microarray data by using Bayesian network. Bioinformatics, 2006, 22, 2952-2954.	4.1	49
53	High-throughput degradome sequencing can be used to gain insights into microRNA precursor metabolism. Journal of Experimental Botany, 2010, 61, 3833-3837.	4.8	46
54	PSI: A Comprehensive and Integrative Approach for Accurate Plant Subcellular Localization Prediction. PLoS ONE, 2013, 8, e75826.	2.5	46

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55	RNA editing of nuclear transcripts in Arabidopsis thaliana. BMC Genomics, 2010, 11, S12.	2.8	44
56	PlantCircNet: a database for plant circRNA–miRNA–mRNA regulatory networks. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	44
57	Tracing cell-type evolution by cross-species comparison of cell atlases. Cell Reports, 2021, 34, 108803.	6.4	44
58	PmiRKB: a plant microRNA knowledge base. Nucleic Acids Research, 2011, 39, D181-D187.	14.5	43
59	Codon usage patterns in Chinese bayberry (Myrica rubra) based on RNA-Seq data. BMC Genomics, 2013, 14, 732.	2.8	42
60	CompareSVM: supervised, Support Vector Machine (SVM) inference of gene regularity networks. BMC Bioinformatics, 2014, 15, 395.	2.6	42
61	BioPepDB: an integrated data platform for food-derived bioactive peptides. International Journal of Food Sciences and Nutrition, 2018, 69, 963-968.	2.8	42
62	The anterior insular cortex unilaterally controls feeding in response to aversive visceral stimuli in mice. Nature Communications, 2020, 11, 640.	12.8	42
63	Genome-wide view of natural antisense transcripts in Arabidopsis thaliana. DNA Research, 2015, 22, 233-243.	3.4	41
64	Postsynaptic RIM1 modulates synaptic function by facilitating membrane delivery of recycling NMDARs in hippocampal neurons. Nature Communications, 2018, 9, 2267.	12.8	40
65	PmliPred: a method based on hybrid model and fuzzy decision for plant miRNA–lncRNA interaction prediction. Bioinformatics, 2020, 36, 2986-2992.	4.1	40
66	Use of transcriptome sequencing to understand the pistillate flowering in hickory (Carya cathayensis) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.8	39
67	Unveiling the Different Emission Behavior of Polytriazoles Constructed from Pyrazine-Based AIE Monomers by Click Polymerization. ACS Applied Materials & Interfaces, 2018, 10, 12181-12188.	8.0	38
68	Proteomic and Bioinformatic Analysis on Endocrine Organs of Domesticated Silkworm, Bombyx mori L. for a Comprehensive Understanding of Their Roles and Relations. Journal of Proteome Research, 2009, 8, 2620-2632.	3.7	36
69	Insights into the increasing virulence of the swine-origin pandemic H1N1/2009 influenza virus. Scientific Reports, 2013, 3, 1601.	3.3	36
70	Plant siRNAs from introns mediate DNA methylation of host genes. Rna, 2011, 17, 1012-1024.	3.5	35
71	ChIP-Hub provides an integrative platform for exploring plant regulome. Nature Communications, 2022, 13, .	12.8	35
72	Mechanisms of microRNA-mediated auxin signaling inferred from the rice mutant osaxr. Plant Signaling and Behavior, 2010, 5, 252-254.	2.4	34

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73	Anionic conjugated polytriazole: direct preparation, aggregation-enhanced emission, and highly efficient Al^{3+} sensing. Polymer Chemistry, 2016, 7, 5835-5839.	3.9	34
74	A medical bioinformatics approach for metabolic disorders: Biomedical data prediction, modeling, and systematic analysis. Journal of Biomedical Informatics, 2006, 39, 147-159.	4.3	32
75	Construction of MicroRNA- and MicroRNA*-mediated regulatory networks in plants. RNA Biology, 2011, 8, 1124-1148.	3.1	32
76	Expression Profiling and Regulation of Genes Related to Silkworm Posterior Silk Gland Development and Fibroin Synthesis. Journal of Proteome Research, 2011, 10, 3551-3564.	3.7	31
77	CancerNet: a database for decoding multilevel molecular interactions across diverse cancer types. Oncogenesis, 2015, 4, e177-e177.	4.9	31
78	The roles of cross-talk epigenetic patterns in *Arabidopsis thaliana*. Briefings in Functional Genomics, 2016, 15, 278-287.	2.7	31
79	N-type pyrazine and triazole-based luminogens with aggregation-enhanced emission characteristics. Chemical Communications, 2015, 51, 10710-10713.	4.1	30
80	Quantitative Petri net model of gene regulated metabolic networks in the cell. In Silico Biology, 2003, 3, 347-65.	0.9	29
81	Distinctive features of immunostaining and mutational load in primary pulmonary enteric adenocarcinoma: implications for differential diagnosis and immunotherapy. Journal of Translational Medicine, 2018, 16, 81.	4.4	28
82	LIN28 coordinately promotes nucleolar/ribosomal functions and represses the 2C-like transcriptional program in pluripotent stem cells. Protein and Cell, 2022, 13, 490-512.	11.0	28
83	A reversed framework for the identification of microRNA-target pairs in plants. Briefings in Bioinformatics, 2013, 14, 293-301.	6.5	27
84	Dissecting the chromatin interactome of microRNA genes. Nucleic Acids Research, 2014, 42, 3028-3043.	14.5	27
85	DeepTrio: a ternary prediction system for protein–protein interaction using mask multiple parallel convolutional neural networks. Bioinformatics, 2022, 38, 694-702.	4.1	27
86	Data-mining Techniques for Image-based Plant Phenotypic Traits Identification and Classification. Scientific Reports, 2019, 9, 19526.	3.3	26
87	Small RNAs in angiosperms: sequence characteristics, distribution and generation. Bioinformatics, 2010, 26, 1391-1394.	4.1	25
88	Digital Biomass Accumulation Using High-Throughput Plant Phenotype Data Analysis. Journal of Integrative Bioinformatics, 2017, 14, .	1.5	25
89	The Genome of a Mongolian Individual Reveals the Genetic Imprints of Mongolians on Modern Human Populations. Genome Biology and Evolution, 2014, 6, 3122-3136.	2.5	24
90	Versatile interactions and bioinformatics analysis of noncoding RNAs. Briefings in Bioinformatics, 2019, 20, 1781-1794.	6.5	24

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91	PlncRNADB: A Repository of Plant lncRNAs and lncRNA-RBP Protein Interactions. Current Bioinformatics, 2019, 14, 621-627.	1.5	24
92	rRNA biogenesis regulates mouse 2C-like state by 3D structure reorganization of peri-nucleolar heterochromatin. Nature Communications, 2021, 12, 6365.	12.8	24
93	PathAligner. Applied Bioinformatics, 2004, 3, 241-252.	1.6	21
94	Dissecting LncRNA Roles in Renal Cell Carcinoma Metastasis and Characterizing Genomic Heterogeneity by Single-Cell RNA-seq. Molecular Cancer Research, 2018, 16, 1879-1888.	3.4	21
95	A Hybrid Prediction Method for Plant lncRNA-Protein Interaction. Cells, 2019, 8, 521.	4.1	21
96	Identification of epistasis loci underlying rice flowering time by controlling population stratification and polygenic effect. DNA Research, 2019, 26, 119-130.	3.4	21
97	Shotgun proteomics approach to characterizing the embryonic proteome of the silkworm, <i>Bombyx mori</i>, at labrum appearance stage. Insect Molecular Biology, 2009, 18, 649-660.	2.0	20
98	Shotgun proteomic analysis on the embryos of silkworm Bombyx mori at the end of organogenesis. Insect Biochemistry and Molecular Biology, 2010, 40, 293-302.	2.7	20
99	Computational Identification of Protein-Protein Interactions in Rice Based on the Predicted Rice Interactome Network. Genomics, Proteomics and Bioinformatics, 2011, 9, 128-137.	6.9	20
100	Proteome Analysis of Silkworm, <i>Bombyx mori</i>, Larval Gonads: Characterization of Proteins Involved in Sexual Dimorphism and Gametogenesis. Journal of Proteome Research, 2013, 12, 2422-2438.	3.7	20
101	Inhibition of ERα/ERK/P62 cascades induces â€œautophagic switchâ€•in the estrogen receptor-positive breast cancer cells exposed to gemcitabine. Oncotarget, 2016, 7, 48501-48516.	1.8	20
102	A reference single-cell regulomic and transcriptomic map of cynomolgus monkeys. Nature Communications, 2022, 13, .	12.8	20
103	Shotgun strategy-based proteome profiling analysis on the head of silkworm Bombyx mori. Amino Acids, 2010, 39, 751-761.	2.7	19
104	FPD: A comprehensive phosphorylation database in fungi. Fungal Biology, 2017, 121, 869-875.	2.5	19
105	An Integrative Bioinformatics Framework for Genome-scale Multiple Level Network Reconstruction of Rice. Journal of Integrative Bioinformatics, 2013, 10, 94-102.	1.5	18
106	Gene Expression Nebulas (GEN): a comprehensive data portal integrating transcriptomic profiles across multiple species at both bulk and single-cell levels. Nucleic Acids Research, 2022, 50, D1016-D1024.	14.5	18
107	Role of the <scp>typeâ€‘B</scp> authentic response regulator gene family in fragrant rice under alkaline salt stress. Physiologia Plantarum, 2022, 174, e13696.	5.2	18
108	Bioinformatics resources facilitate understanding and harnessing clinical research of SARS-CoV-2. Briefings in Bioinformatics, 2021, 22, 714-725.	6.5	17

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109	Shotgun proteomic analysis of the fat body during metamorphosis of domesticated silkworm (Bombyx) Tj ETQq1 1.0 784314 rgBT /O	2.7	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, .	3.0	16
112	Expression-Based Functional Investigation of the Organ-Specific MicroRNAs in Arabidopsis. PLoS ONE, 2012, 7, e50870.	2.5	16
113	Construction of gene regulatory networks mediated by vegetative and reproductive stageâ€specific small <scp>RNA</scp>s in rice (<i><scp>O</scp>ryza sativa</i>). New Phytologist, 2013, 197, 441-453.	7.3	15
114	Fas Signaling Promotes Gastric Cancer Metastasis through STAT3-Dependent Upregulation of Fascin. PLoS ONE, 2015, 10, e0125132.	2.5	15
115	Genes and Pathways Induced in Early Response to Defoliation in Rice Seedlings. Current Issues in Molecular Biology, 2009, , .	2.4	15
116	Biogenesis, Functions, Interactions, and Resources of Non-Coding RNAs in Plants. International Journal of Molecular Sciences, 2022, 23, 3695.	4.1	15
117	Pathway knockout and redundancy in metabolic networks. Journal of Theoretical Biology, 2011, 270, 63-69.	1.7	14
118	miRNA Digger: a comprehensive pipeline for genome-wide novel miRNA mining. Scientific Reports, 2016, 6, 18901.	3.3	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.	2.4	14
120	Proteinâ€"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
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.	3.5	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.	0.9	13
123	CircPlant: An Integrated Tool for circRNA Detection and Functional Prediction in Plants. Genomics, Proteomics and Bioinformatics, 2020, 18, 352-358.	6.9	13
124	Petri net models for the semi-automatic construction of large scale biological networks. Natural Computing, 2011, 10, 1077-1097.	3.0	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.	3.5	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.	5.6	12

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127	A comprehensive description and evolutionary analysis of 9 Loliginidae mitochondrial genomes. Hydrobiologia, 2018, 808, 115-124.	2.0	12
128	The HTPmod Shiny application enables modeling and visualization of large-scale biological data. Communications Biology, 2018, 1, 89.	4.4	12
129	An integrative bioinformatics framework for genome-scale multiple level network reconstruction of rice. Journal of Integrative Bioinformatics, 2013, 10, 223.	1.5	12
130	Genome-Wide Analysis of the Soybean TIFY Family and Identification of GmTIFY10e and GmTIFY10g Response to Salt Stress. Frontiers in Plant Science, 2022, 13, 845314.	3.6	12
131	Functional characterization of plant small RNAs based on next-generation sequencing data. Computational Biology and Chemistry, 2010, 34, 308-312.	2.3	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 TFs' binding sites in the genome according to the ChIP-seq data. Russian Journal of Genetics: Applied Research, 2017, 7, 513-522.	0.4	11
134	OverCOVID: an integrative web portal for SARS-CoV-2 bioinformatics resources. Journal of Integrative Bioinformatics, 2021, 18, 9-17.	1.5	11
135	Genomic survey of sequence features for ultraviolet tolerance in haloarchaea (family) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 4	2.9	10
136	InvA Protein Is a Nudix Hydrolase Required for Infection by Pathogenic Leptospira in Cell Lines and Animals*. Journal of Biological Chemistry, 2011, 286, 36852-36863.	3.4	10
137	Microarray analysis of differentially expressed genes engaged in fruit development between Prunus mume and Prunus armeniaca. Journal of Plant Physiology, 2012, 169, 1776-1788.	3.5	10
138	Toward a next-generation atlas of RNA secondary structure. Briefings in Bioinformatics, 2016, 17, 63-77.	6.5	10
139	Biological Big Bytes: Integrative Analysis of Large Biological Datasets. Journal of Integrative Bioinformatics, 2017, 14, .	1.5	10
140	Web-Based Information Retrieval System for the Prediction of Metabolic Pathways. IEEE Transactions on Nanobioscience, 2004, 3, 192-199.	3.3	9
141	Methodological framework for functional characterization of plant microRNAs. Journal of Experimental Botany, 2010, 61, 2271-2280.	4.8	9
142	Identification of novel microRNA-like-coding sites on the long-stem microRNA precursors in Arabidopsis. Gene, 2013, 527, 477-483.	2.2	9
143	Plant Biology at Belyaev Conference – 2017. BMC Plant Biology, 2017, 17, 257.	3.6	9
144	Computational investigation of small RNAs in the establishment of root nodules and arbuscular mycorrhiza in leguminous plants. Science China Life Sciences, 2018, 61, 706-717.	4.9	9

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145	Medical genomics at Belyaev Conference – 2017. BMC Medical Genomics, 2018, 11, 11.	1.5	9
146	Genome-Wide Analysis of the Distinct Types of Chromatin Interactions inArabidopsis thaliana. Plant and Cell Physiology, 2016, 58, pcw194.	3.1	8
147	Exploring the mechanisms of genome-wide long-range interactions: interpreting chromosome organization. Briefings in Functional Genomics, 2016, 15, 385-395.	2.7	8
148	A practical guide for DNase-seq data analysis: from data management to common applications. Briefings in Bioinformatics, 2019, 20, 1865-1877.	6.5	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.	5.5	7
150	Computational Identification of miRNAs and Temperature-Responsive lncRNAs From Mango (Mangifera) Tj ETQq0 0 0 rgBT /Overlock 10	2.3	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.	3.8	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, .	3.0	6
153	STCDB: Signal Transduction Classification Database. Nucleic Acids Research, 2004, 32, 456D-458.	14.5	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.	2.9	5
156	Integrative Bioinformatics: History and Future. Journal of Integrative Bioinformatics, 2019, 16, .	1.5	5
157	A Petri nets-based framework for whole-cell modeling. BioSystems, 2021, 210, 104533.	2.0	5
158	VIRS: A visual tool for identifying restriction sites in multiple DNA sequences. Biotechnology Progress, 2009, 25, 1525-1527.	2.6	4
159	Detection of Thrombin with an Aptamer-Based Macromolecule Biosensor Using Bacterial Ghost System. ACS Synthetic Biology, 2014, 3, 963-965.	3.8	4
160	DEF: an automated dead-end filling approach based on quasi-endosymbiosis. Bioinformatics, 2017, 33, 405-413.	4.1	4
161	Endo-1,4-Î²-glucanase gene involved into the rapid elongation of Phyllostachys heterocycla var. pubescens. Trees - Structure and Function, 2016, 30, 1259-1274.	1.9	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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163	Medical genomics at the Systems Biology and Bioinformatics (SBB-2019) school. BMC Medical Genomics, 2020, 13, 127.	1.5	4
164	Sequence repetitiveness quantification and <i>de novo</i> repeat detection by weighted k-mer coverage. Briefings in Bioinformatics, 2021, 22, .	6.5	4
165	Database Resources for Functional Circular RNAs. Methods in Molecular Biology, 2021, 2284, 457-466.	0.9	4
166	Genetic polymorphisms and related risk factors of ischemic stroke in a Mongolian population in China. Vavilovskii Zhurnal Genetiki I Selektsii, 2017, 21, 581-587.	1.1	4
167	Computer and statistical analysis of transcription factor binding and chromatin modifications by ChIP-seq data in embryonic stem cell. Journal of Integrative Bioinformatics, 2012, 9, 211.	1.5	4
168	Plant Biology and Biotechnology: Focus on Genomics and Bioinformatics. International Journal of Molecular Sciences, 2022, 23, 6759.	4.1	4
169	CloneAssistant 1.0: A stand-alone software for automated cloning primer design. Journal of Biotechnology, 2010, 150, 294-298.	3.8	3
170	Open problems in Petri net modeling and simulation of biological systems. IT - Information Technology, 2014, 56, .	0.9	3
171	RNA Scaffold: Designed to Co-localize Enzymes. Methods in Molecular Biology, 2015, 1316, 105-112.	0.9	3
172	DaTo: an atlas of biological databases and tools. Journal of Integrative Bioinformatics, 2016, 13, 297.	1.5	3
173	Construction and analysis of microRNA–transcription factor regulation network in arabidopsis. IET Systems Biology, 2014, 8, 76-86.	1.5	2
174	A Generalized Approach for Measuring Relationships Among Genes. Journal of Integrative Bioinformatics, 2017, 14, .	1.5	2
175	A novel riboswitch classification based on imbalanced sequences achieved by machine learning. PLoS Computational Biology, 2020, 16, e1007760.	3.2	2
176	In situ dissecting the evolution of gene duplication with different histone modification patterns based on high-throughput data analysis in Arabidopsis thaliana. PeerJ, 2021, 9, e10426.	2.0	2
177	Genome-wide discovery of hidden genes mediating known drug-disease association using KDDANet. Npj Genomic Medicine, 2021, 6, 50.	3.8	2
178	Systematic Annotation and Bioinformatics Analyses of Large-Scale Oryza sativa Proteome. Current Protein and Peptide Science, 2011, 12, 621-630.	1.4	2
179	Simulating the Dynamic Intra-Tumor Heterogeneity and Therapeutic Responses. Cancers, 2022, 14, 1645.	3.7	2
180	Reassessment of Reliability and Reproducibility for Triple-Negative Breast Cancer Subtyping. Cancers, 2022, 14, 2571.	3.7	2

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181	Systems Biology Brings Life Sciences Closer. Genomics, Proteomics and Bioinformatics, 2005, 3, 194-196.	6.9	1
182	RiceDB: A Web-Based Integrated Database for Annotating Rice Microarray. Rice Science, 2007, 14, 256-264.	3.9	1
183	MicroRNAs in Plant Roots: Current Understanding and Future Perspectives. RNA Technologies, 2011, , 269-284.	0.3	1
184	MyBioNet: interactively visualize, edit and merge biological networks on the Web. Bioinformatics, 2011, 27, 3321-3322.	4.1	1
185	Editorial (Thematic Issue: Protein Systems Biology: Method, Regulation, and Network). Current Protein and Peptide Science, 2014, 15, 519-521.	1.4	1
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