

Baohong Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

184
papers

14,277
citations

31976

53
h-index

21540

114
g-index

185
all docs

185
docs citations

185
times ranked

15910
citing authors

#	ARTICLE	IF	CITATIONS
1	microRNAs as oncogenes and tumor suppressors. <i>Developmental Biology</i> , 2007, 302, 1-12.	2.0	2,285
2	miRDeepFinder: a miRNA analysis tool for deep sequencing of plant small RNAs. <i>Plant Molecular Biology</i> , 2012, 80, 75-84.	3.9	1,159
3	Plant microRNA: A small regulatory molecule with big impact. <i>Developmental Biology</i> , 2006, 289, 3-16.	2.0	672
4	Conservation and divergence of plant microRNA genes. <i>Plant Journal</i> , 2006, 46, 243-259.	5.7	664
5	MicroRNAs and their regulatory roles in animals and plants. <i>Journal of Cellular Physiology</i> , 2007, 210, 279-289.	4.1	500
6	MicroRNA: a new target for improving plant tolerance to abiotic stress. <i>Journal of Experimental Botany</i> , 2015, 66, 1749-1761.	4.8	440
7	MicroRNAs in Control of Plant Development. <i>Journal of Cellular Physiology</i> , 2016, 231, 303-313.	4.1	276
8	Identification of soybean microRNAs and their targets. <i>Planta</i> , 2008, 229, 161-182.	3.2	259
9	Genome of wild olive and the evolution of oil biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9413-E9422.	7.1	233
10	Effects of Aluminum Oxide Nanoparticles on the Growth, Development, and microRNA Expression of Tobacco (<i>Nicotiana tabacum</i>). <i>PLoS ONE</i> , 2012, 7, e34783.	2.5	208
11	Identification of 188 conserved maize microRNAs and their targets. <i>FEBS Letters</i> , 2006, 580, 3753-3762.	2.8	201
12	Deep sequencing reveals important roles of microRNAs in response to drought and salinity stress in cotton. <i>Journal of Experimental Botany</i> , 2015, 66, 789-804.	4.8	198
13	Identification of cotton microRNAs and their targets. <i>Gene</i> , 2007, 397, 26-37.	2.2	190
14	Titanium dioxide nanoparticles affect the growth and microRNA expression of tobacco (<i>Nicotiana glauca</i>). <i>PLoS ONE</i> , 2013, 8, e61000.	3.5	190
15	MicroRNA-Based Biotechnology for Plant Improvement. <i>Journal of Cellular Physiology</i> , 2015, 230, 1-15.	4.1	188
16	Manipulating the Biosynthesis of Bioactive Compound Alkaloids for Next-Generation Metabolic Engineering in Opium Poppy Using CRISPR-Cas 9 Genome Editing Technology. <i>Scientific Reports</i> , 2016, 6, 30910.	3.3	180
17	Salt and Drought Stresses Induce the Aberrant Expression of microRNA Genes in Tobacco. <i>Molecular Biotechnology</i> , 2011, 49, 159-165.	2.4	171
18	Computational identification of microRNAs and their targets. <i>Computational Biology and Chemistry</i> , 2006, 30, 395-407.	2.3	164

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19	Identification and characterization of microRNAs and their targets in the bioenergy plant switchgrass (<i>Panicum virgatum</i>). <i>Planta</i> , 2010, 232, 417-434.	3.2	148
20	Small <scp>RNA</scp> and degradome deep sequencing reveals drought- and tissue-specific micromnas and their important roles in drought-sensitive and drought-tolerant tomato genotypes. <i>Plant Biotechnology Journal</i> , 2016, 14, 1727-1746.	8.3	146
21	CRISPR/Cas: A powerful tool for gene function study and crop improvement. <i>Journal of Advanced Research</i> , 2021, 29, 207-221.	9.5	136
22	Selection of Reliable Reference Genes in <i>Caenorhabditis elegans</i> for Analysis of Nanotoxicity. <i>PLoS ONE</i> , 2012, 7, e31849.	2.5	134
23	RDX Induces Aberrant Expression of MicroRNAs in Mouse Brain and Liver. <i>Environmental Health Perspectives</i> , 2009, 117, 231-240.	6.0	132
24	Mutagenicity evaluation of metal oxide nanoparticles by the bacterial reverse mutation assay. <i>Chemosphere</i> , 2010, 79, 113-116.	8.2	132
25	Nanoparticle-Plant Interactions: Two-Way Traffic. <i>Small</i> , 2019, 15, e1901794.	10.0	132
26	High-throughput deep sequencing shows that micro<scp>RNA</scp>s play important roles in switchgrass responses to drought and salinity stress. <i>Plant Biotechnology Journal</i> , 2014, 12, 354-366.	8.3	131
27	Response of miRNAs and their targets to salt and drought stresses in cotton (<i>Gossypium hirsutum</i> L.). <i>Gene</i> , 2013, 530, 26-32.	2.2	129
28	microRNAs: a new emerging class of players for disease diagnostics and gene therapy. <i>Journal of Cellular and Molecular Medicine</i> , 2008, 12, 3-21.	3.6	125
29	A high-efficiency CRISPR/Cas9 system for targeted mutagenesis in Cotton (<i>Gossypium hirsutum</i> L.). <i>Scientific Reports</i> , 2017, 7, 43902.	3.3	121
30	De novo sequencing and a comprehensive analysis of purple sweet potato (<i>Ipomoea batatas</i> L.) transcriptome. <i>Planta</i> , 2012, 236, 101-113.	3.2	118
31	High throughput sequencing technology reveals that the taxoid elicitor methyl jasmonate regulates microRNA expression in Chinese yew (<i>Taxus chinensis</i>). <i>Gene</i> , 2009, 436, 37-44.	2.2	112
32	Identification and characterization of microRNAs and their target genes in tobacco (<i>Nicotiana glauca</i>). <i>PLoS ONE</i> , 2011, 6, e26980.	3.2	110
33	Evaluation and identification of reliable reference genes for pharmacogenomics, toxicogenomics, and small RNA expression analysis. <i>Journal of Cellular Physiology</i> , 2011, 226, 2469-2477.	4.1	108
34	MicroRNA: A new player in stem cells. <i>Journal of Cellular Physiology</i> , 2006, 209, 266-269.	4.1	103
35	Genome-Wide Identification of R2R3-MYB Genes and Expression Analyses During Abiotic Stress in <i>Gossypium raimondii</i> . <i>Scientific Reports</i> , 2016, 6, 22980.	3.3	103
36	Genome-Wide Functional Analysis of the Cotton Transcriptome by Creating an Integrated EST Database. <i>PLoS ONE</i> , 2011, 6, e26980.	2.5	102

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37	Large-scale genome analysis reveals unique features of microRNAs. <i>Gene</i> , 2009, 443, 100-109.	2.2	101
38	Small RNA sequencing identifies miRNA roles in ovule and fibre development. <i>Plant Biotechnology Journal</i> , 2015, 13, 355-369.	8.3	98
39	CRISPR/Cas: a Nobel Prize award-winning precise genome editing technology for gene therapy and crop improvement. <i>Journal of Zhejiang University: Science B</i> , 2021, 22, 253-284.	2.8	97
40	Identification, characterization and expression analysis of MicroRNAs and their targets in the potato (<i>Solanum tuberosum</i>). <i>Gene</i> , 2011, 473, 8-22.	2.2	96
41	Evaluation and selection of reliable reference genes for gene expression under abiotic stress in cotton (<i>Gossypium hirsutum</i> L.). <i>Gene</i> , 2013, 530, 44-50.	2.2	91
42	Genome-wide identification and expression analysis of TCP transcription factors in <i>Gossypium raimondii</i> . <i>Scientific Reports</i> , 2014, 4, 6645.	3.3	90
43	Boron Stress Responsive MicroRNAs and Their Targets in Barley. <i>PLoS ONE</i> , 2013, 8, e59543.	2.5	89
44	Differential expression of microRNAs during fiber development between fuzzless-lintless mutant and its wild-type allotetraploid cotton. <i>Scientific Reports</i> , 2017, 7, 3.	3.3	88
45	CRISPR/Cas gene therapy. <i>Journal of Cellular Physiology</i> , 2021, 236, 2459-2481.	4.1	87
46	MicroRNA Expression Analysis in the Cellulosic Biofuel Crop Switchgrass (<i>Panicum virgatum</i>) under Abiotic Stress. <i>PLoS ONE</i> , 2012, 7, e32017.	2.5	87
47	Edible Plant Oil: Global Status, Health Issues, and Perspectives. <i>Frontiers in Plant Science</i> , 2020, 11, 1315.	3.6	83
48	CRISPR/Cas9: An RNA-guided highly precise synthetic tool for plant genome editing. <i>Journal of Cellular Physiology</i> , 2018, 233, 1844-1859.	4.1	82
49	A cotton miRNA is involved in regulation of plant response to salt stress. <i>Scientific Reports</i> , 2016, 6, 19736.	3.3	79
50	Target-align: a tool for plant microRNA target identification. <i>Bioinformatics</i> , 2010, 26, 3002-3003.	4.1	74
51	Development of a method for the determination of 9 currently used cotton pesticides by gas chromatography with electron capture detection. <i>Talanta</i> , 2008, 75, 1055-1060.	5.5	73
52	Integrated transcriptome, small RNA and degradome sequencing approaches provide insights into Ascochyta blight resistance in chickpea. <i>Plant Biotechnology Journal</i> , 2019, 17, 914-931.	8.3	66
53	An Efficient CRISPR/Cas9 Platform for Rapidly Generating Simultaneous Mutagenesis of Multiple Gene Homoeologs in Allotetraploid Oilseed Rape. <i>Frontiers in Plant Science</i> , 2018, 9, 442.	3.6	58
54	Genome-wide identification and characterization of SPL transcription factor family and their evolution and expression profiling analysis in cotton. <i>Scientific Reports</i> , 2018, 8, 762.	3.3	56

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73	MicroRNA target gene responses to lead-induced stress in cotton (<i>Gossypium hirsutum</i> L.). <i>Functional and Integrative Genomics</i> , 2014, 14, 507-515.	3.5	36
74	Triclosan Disrupts SKN-1/Nrf2-Mediated Oxidative Stress Response in <i>C. elegans</i> and Human Mesenchymal Stem Cells. <i>Scientific Reports</i> , 2017, 7, 12592.	3.3	36
75	Comprehensive analysis of TCP transcription factors and their expression during cotton (<i>Gossypium</i>) Tj ETQq1 1 0.784314 rgBT /Over	3.3	35
76	Potassium Deficiency Significantly Affected Plant Growth and Development as Well as microRNA-Mediated Mechanism in Wheat (<i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2020, 11, 1219.	3.6	35
77	Xylem sap in cotton contains proteins that contribute to environmental stress response and cell wall development. <i>Functional and Integrative Genomics</i> , 2015, 15, 17-26.	3.5	34
78	A critical and speculative review on microRNA technology in crop improvement: Current challenges and future directions. <i>Plant Science</i> , 2018, 274, 193-200.	3.6	33
79	Nicotine exposure and transgenerational impact: a prospective study on small regulatory microRNAs. <i>Scientific Reports</i> , 2014, 4, 7513.	3.3	32
80	MicroRNA expression profiles during cotton (<i>Gossypium hirsutum</i> L) fiber early development. <i>Scientific Reports</i> , 2017, 7, 44454.	3.3	32
81	A Comprehensive Approach to Identify Reliable Reference Gene Candidates to Investigate the Link between Alcoholism and Endocrinology in Sprague-Dawley Rats. <i>PLoS ONE</i> , 2014, 9, e94311.	2.5	32
82	MicroRNA, a new target for engineering new crop cultivars. <i>Bioengineered</i> , 2016, 7, 7-10.	3.2	31
83	<i>Caenorhabditis elegans</i> : A Model System for Anti-Cancer Drug Discovery and Therapeutic Target Identification. <i>Biomolecules and Therapeutics</i> , 2014, 22, 371-383.	2.4	31
84	MicroRNAs in model and complex organisms. <i>Functional and Integrative Genomics</i> , 2017, 17, 121-124.	3.5	30
85	Chilling and Heat Stress-Induced Physiological Changes and MicroRNA-Related Mechanism in Sweetpotato (<i>Ipomoea batatas</i> L.). <i>Frontiers in Plant Science</i> , 2020, 11, 687.	3.6	30
86	Toxicity of the explosive metabolites hexahydro-1,3,5-trinitroso-1,3,5-triazine (TNX) and hexahydro-1-nitroso-3,5-dinitro-1,3,5-triazine (MNX) to the earthworm <i>Eisenia fetida</i> . <i>Chemosphere</i> , 2006, 64, 86-95.	8.2	29
87	MicroRNA-target gene responses to root knot nematode (<i>Meloidogyne incognita</i>) infection in cotton (<i>Gossypium hirsutum</i> L.). <i>Genomics</i> , 2019, 111, 383-390.	2.9	29
88	Expression of MicroRNAs in Cotton. <i>Molecular Biotechnology</i> , 2009, 42, 269-274.	2.4	27
89	From Sequencing to Genome Editing for Cotton Improvement. <i>Trends in Biotechnology</i> , 2021, 39, 221-224.	9.3	27
90	MicroRNAs: key gene regulators with versatile functions. <i>Plant Molecular Biology</i> , 2012, 80, 1-1.	3.9	25

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91	Use of pressurized liquid extraction (PLE)/gas chromatography-electron capture detection (GC-ECD) for the determination of biodegradation intermediates of hexahydro-1,3,5-trinitro-1,3,5-triazine (RDX) in soils. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2005, 824, 277-282.	2.3	24
92	Global microRNA modification in cotton (<i>Gossypium hirsutum</i> L.). <i>Plant Biotechnology Journal</i> , 2015, 13, 492-500.	8.3	24
93	High throughput sequencing identifies chilling responsive genes in sweetpotato (<i>Ipomoea batatas</i>). <i>Trends in Plant Science</i> , 2020, 25, 719-722.	8.8	23
94	Characterizing viral microRNAs and its application on identifying new microRNAs in viruses. <i>Journal of Cellular Physiology</i> , 2007, 211, 10-18.	4.1	23
95	The infection and impact of <i>Azorhizobium caulinodans</i> ORS571 on wheat (<i>Triticum aestivum</i> L.). <i>PLoS ONE</i> , 2017, 12, e0187947.	2.5	23
96	Genome-wide identification, characterization, and expression analysis of superoxide dismutase (SOD) genes in foxtail millet (<i>Setaria italica</i> L.). <i>3 Biotech</i> , 2018, 8, 486.	2.2	23
97	Pectin Drives Cell Wall Morphogenesis without Turgor Pressure. <i>Trends in Plant Science</i> , 2020, 25, 719-722.	8.8	23
98	Chronic nicotine exposure systemically alters microRNA expression profiles during post-embryonic stages in <i>Caenorhabditis elegans</i> . <i>Journal of Cellular Physiology</i> , 2013, 229, n/a-n/a.	4.1	22
99	Identification and characterization of microRNAs in the plant parasitic root-knot nematode <i>Meloidogyne incognita</i> using deep sequencing. <i>Functional and Integrative Genomics</i> , 2016, 16, 127-142.	3.5	22
100	MicroRNAs in cotton: an open world needs more exploration. <i>Planta</i> , 2015, 241, 1303-1312.	3.2	21
101	Response of Root Growth and Development to Nitrogen and Potassium Deficiency as well as microRNA-Mediated Mechanism in Peanut (<i>Arachis hypogaea</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 695234.	3.6	21
102	Determination of reliable reference genes for multi-generational gene expression analysis on <i>C. elegans</i> exposed to abused drug nicotine. <i>Psychopharmacology</i> , 2013, 230, 77-88.	3.1	20
103	Transgenic Cotton: From Biotransformation Methods to Agricultural Application. <i>Methods in Molecular Biology</i> , 2013, 958, 3-15.	0.9	20
104	High throughput deep sequencing reveals the important roles of microRNAs during sweetpotato storage at chilling temperature. <i>Scientific Reports</i> , 2017, 7, 16578.	3.3	20
105	Direct modification of multiple gene homologs in <i>Brassica oleracea</i> and <i>Brassica napus</i> using doubled haploid inducer-mediated genome editing system. <i>Plant Biotechnology Journal</i> , 2021, 19, 1889-1891.	8.3	20
106	Isolation and molecular identification of endophytic diazotrophs from seeds and stems of three cereal crops. <i>PLoS ONE</i> , 2017, 12, e0187383.	2.5	20
107	Fungicide Difenoconazole Induced Biochemical and Developmental Toxicity in Wheat (<i>Triticum</i>). <i>Trends in Plant Science</i> , 2020, 25, 719-722.	8.8	20
108	Evaluating the bioavailability of explosive metabolites, hexahydro-1-nitroso-3,5-dinitro-1,3,5-triazine (MNX) and hexahydro-1,3,5-trinitroso-1,3,5-triazine (TNX), in soils using passive sampling devices. <i>Journal of Chromatography A</i> , 2006, 1101, 38-45.	3.7	19

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109	Cotton Transformation via Pollen Tube Pathway. <i>Methods in Molecular Biology</i> , 2013, 958, 71-77.	0.9	18
110	SpRY: Engineered CRISPR/Cas9 Harnesses New Genome-Editing Power. <i>Trends in Genetics</i> , 2020, 36, 546-548.	6.7	18
111	Effects of hexahydro-1,3,5-trinitro-1,3,5-triazine (RDX) metabolites on cricket (<i>Acheta domesticus</i>) survival and reproductive success. <i>Environmental Pollution</i> , 2006, 144, 540-544.	7.5	17
112	Organochlorine Pesticide Concentrations in Sediment and Amphibian Tissue in Playa Wetlands in the Southern High Plains, USA. <i>Bulletin of Environmental Contamination and Toxicology</i> , 2008, 80, 497-501.	2.7	17
113	Lack of K-Dependent Oxidative Stress in Cotton Roots Following Coronatine-Induced ROS Accumulation. <i>PLoS ONE</i> , 2015, 10, e0126476.	2.5	17
114	Identification and expression analysis of phosphatidyl ethanolamine-binding protein (PEBP) gene family in cotton. <i>Genomics</i> , 2019, 111, 1373-1380.	2.9	17
115	Virus-Based CRISPR/Cas9 Genome Editing in Plants. <i>Trends in Genetics</i> , 2020, 36, 810-813.	6.7	17
116	Integrated small RNA and mRNA expression profiles reveal miRNAs and their target genes in response to <i>Aspergillus flavus</i> growth in peanut seeds. <i>BMC Plant Biology</i> , 2020, 20, 215.	3.6	17
117	ChANN1 modulates the salinity tolerance by regulating ABA biosynthesis, ion homeostasis and phenylpropanoid pathway in cotton. <i>Environmental and Experimental Botany</i> , 2021, 185, 104427.	4.2	17
118	Differentiated expression of microRNAs may regulate genotype-dependent traits in cotton. <i>Gene</i> , 2014, 547, 233-238.	2.2	16
119	De Novo Transcriptome Assembly and Comparative Analysis Elucidate Complicated Mechanism Regulating <i>Astragalus chrysochlorus</i> Response to Selenium Stimuli. <i>PLoS ONE</i> , 2015, 10, e0135677.	2.5	16
120	Direct induction of cotton somatic embryogenesis. <i>Science Bulletin</i> , 1999, 44, 766-767.	1.7	15
121	Drug-dependent behaviors and nicotinic acetylcholine receptor expressions in <i>Caenorhabditis elegans</i> following chronic nicotine exposure. <i>NeuroToxicology</i> , 2015, 47, 27-36.	3.0	14
122	Role of microRNAs During Flower and Storage Root Development in Sweet Potato. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1731-1739.	1.8	14
123	Identification, characterization, and gene expression analysis of nucleotide binding site (NB)-type resistance gene homologues in switchgrass. <i>BMC Genomics</i> , 2016, 17, 892.	2.8	14
124	Effect of two major N-nitroso hexahydro-1,3,5-trinitro-1,3,5-triazine (RDX) metabolites on earthworm reproductive success. <i>Environmental Pollution</i> , 2008, 153, 658-667.	7.5	13
125	In silico identification of conserved microRNAs and their target transcripts from expressed sequence tags of three earthworm species. <i>Computational Biology and Chemistry</i> , 2010, 34, 313-319.	2.3	13
126	ZnO nanoparticles enhanced germ cell apoptosis in <i>Caenorhabditis elegans</i> , in comparison with ZnCl ₂ . <i>Toxicological Sciences</i> , 2016, 156, kfw258.	3.1	13

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127	Genome-Wide Identification and Analysis of Class III Peroxidases in Allotetraploid Cotton (<i>Gossypium</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	2.4	13
128	Protoplast Dissociation and Transcriptome Analysis Provides Insights to Salt Stress Response in Cotton. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2845.	4.1	13
129	Layered Double Hydroxide Nanosheets Improve the Adhesion of Fungicides to Leaves and the Antifungal Performance. <i>ACS Applied Nano Materials</i> , 2022, 5, 5316-5325.	5.0	13
130	Thermo-Responsive Quaternary Ammonium Chitosan Nanocapsules with On-Demand Controlled Pesticide Release and Maximally Synergistic Biological Activity. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 7653-7661.	5.2	13
131	Expression of microRNAs and their targets regulates floral development in tobacco (<i>Nicotiana</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.5	12
132	Selection and validation of reliable reference genes in <i>Gossypium raimondii</i> . <i>Biotechnology Letters</i> , 2015, 37, 1483-1493.	2.2	12
133	Migration of endophytic diazotroph <i>Azorhizobium caulinodans</i> ORS571 inside wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.5	12
134	Small RNA and degradome deep sequencing reveals important roles of microRNAs in cotton (<i>Gossypium hirsutum</i> L.) response to root-knot nematode <i>Meloidogyne incognita</i> infection. <i>Genomics</i> , 2021, 113, 1146-1156.	2.9	12
135	Coordination of root growth with root morphology, physiology and defense functions in response to root pruning in <i>Platyclusus orientalis</i> . <i>Journal of Advanced Research</i> , 2022, 36, 187-199.	9.5	12
136	Examination of the mutagenicity of RDX and its N-nitroso metabolites using the <i>Salmonella</i> reverse mutation assay. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2007, 629, 64-69.	1.7	11
137	Identification of Plant microRNAs Using Expressed Sequence Tag Analysis. <i>Methods in Molecular Biology</i> , 2011, 678, 13-25.	0.9	11
138	Genome-Wide Survey and Comparative Analysis of Long Terminal Repeat (LTR) Retrotransposon Families in Four <i>Gossypium</i> Species. <i>Scientific Reports</i> , 2018, 8, 9399.	3.3	11
139	Whole transcriptome analysis of three leaf stages in two cultivars and one of their F1 hybrid of <i>Camellia sinensis</i> L. with differing EGCG content. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	1.6	10
140	Genome Editing in Cotton Using CRISPR/Cas9 System. <i>Methods in Molecular Biology</i> , 2019, 1902, 95-104.	0.9	10
141	microRNA response in potato virus Y infected tobacco shows strain-specificity depending on host and symptom severity. <i>Virus Research</i> , 2019, 260, 20-32.	2.2	10
142	Transcriptome Analysis Provides Insights into Grain Filling in Foxtail Millet (<i>Setaria italica</i> L.). <i>International Journal of Molecular Sciences</i> , 2020, 21, 5031.	4.1	10
143	Genome-Wide Identification of ARF Transcription Factor Gene Family and Their Expression Analysis in Sweet Potato. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9391.	4.1	10
144	Biotechnological Perspectives to Combat the COVID-19 Pandemic: Precise Diagnostics and Inevitable Vaccine Paradigms. <i>Cells</i> , 2022, 11, 1182.	4.1	10

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145	Pollen Tube Pathway-Mediated Cotton Transformation. <i>Methods in Molecular Biology</i> , 2019, 1902, 67-73.	0.9	9
146	Selection of stable reference genes for gene expression analysis in sweet potato (<i>Ipomoea batatas</i> L.). <i>Molecular and Cellular Probes</i> , 2020, 53, 101610.	2.1	9
147	Environmentally friendly plant essential oil: Liquid gold for human health. <i>Advances in Agronomy</i> , 2021, , 289-337.	5.2	9
148	Uptake, bioaccumulation, and biodegradation of hexahydro-1,3,5-trinitro-1,3,5-triazine (RDX) and its reduced metabolites (MNX and TNX) by the earthworm (<i>Eisenia fetida</i>). <i>Chemosphere</i> , 2009, 76, 76-82.	8.2	8
149	Transgenic Cotton: From Biotransformation Methods to Agricultural Application. <i>Methods in Molecular Biology</i> , 2019, 1902, 3-16.	0.9	8
150	High throughput deep sequencing elucidates the important role of lncRNAs in Foxtail millet response to herbicides. <i>Genomics</i> , 2020, 112, 4463-4473.	2.9	8
151	CRISPR/Cas9 genome editing shows the important role of AZC_2928 gene in nitrogen-fixing bacteria of plants. <i>Functional and Integrative Genomics</i> , 2020, 20, 657-668.	3.5	8
152	Nicotine exposure caused significant transgenerational heritable behavioral changes in <i>Caenorhabditis elegans</i> . <i>EXCLI Journal</i> , 2013, 12, 793-806.	0.7	7
153	<i>Agrobacterium</i> -Mediated Transformation of Cotton. <i>Methods in Molecular Biology</i> , 2013, 958, 31-45.	0.9	6
154	Tobacco Rattle Virus-Induced Gene Silencing in Cotton. <i>Methods in Molecular Biology</i> , 2019, 1902, 105-119.	0.9	6
155	Reference gene selection for miRNA and mRNA normalization in potato in response to potato virus Y. <i>Molecular and Cellular Probes</i> , 2021, 55, 101691.	2.1	6
156	Non-Ionic Surfactants Antagonize Toxicity of Potential Phenolic Endocrine-Disrupting Chemicals, Including Triclosan in. <i>Molecules and Cells</i> , 2018, 41, 1052-1060.	2.6	6
157	Using Quantitative Real-Time PCR to Detect MicroRNA Expression Profile During Embryonic Stem Cell Differentiation. <i>Methods in Molecular Biology</i> , 2017, 1622, 255-265.	0.9	5
158	Subcritical Water Extraction of <i>Salvia miltiorrhiza</i> . <i>Molecules</i> , 2021, 26, 1634.	3.8	5
159	Metabolite Profile of Xylem Sap in Cotton Seedlings Is Changed by K Deficiency. <i>Frontiers in Plant Science</i> , 2020, 11, 592591.	3.6	5
160	New vision on the new era of genome study. <i>Functional and Integrative Genomics</i> , 2022, 22, 1-2.	3.5	5
161	Transcriptomic analysis reveals the significant effects of fertilization on the biosynthesis of sesquiterpenes in <i>Phoebe bournei</i> . <i>Genomics</i> , 2022, 114, 110375.	2.9	5
162	<i>Agrobacterium</i> -Mediated Genetic Transformation of Cotton. <i>Methods in Molecular Biology</i> , 2019, 1902, 19-33.	0.9	4

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163	CRISPR/Cas9: A Robust Genome-Editing Tool with Versatile Functions and Endless Application. International Journal of Molecular Sciences, 2020, 21, 5111.	4.1	4
164	DNA Methylation and RNA-Sequencing Analysis Show Epigenetic Function During Grain Filling in Foxtail Millet (<i>Setaria italica</i> L.). Frontiers in Plant Science, 2021, 12, 741415.	3.6	4
165	Construction and characterization of a bacterial artificial chromosome library for <i>Gossypium mustelinum</i> . PLoS ONE, 2018, 13, e0196847.	2.5	3
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