

# Baohong Zhang

## List of Publications by Year in descending order

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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	Computational Tools and Resources for CRISPR/Cas Genome Editing. <i>Genomics, Proteomics and Bioinformatics</i> , 2023, 21, 108-126.	6.9	51
2	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
3	New vision on the new era of genome study. <i>Functional and Integrative Genomics</i> , 2022, 22, 1-2.	3.5	5
4	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
5	Biotechnological Perspectives to Combat the COVID-19 Pandemic: Precise Diagnostics and Inevitable Vaccine Paradigms. <i>Cells</i> , 2022, 11, 1182.	4.1	10
6	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
7	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
8	Conservation and Divergence of Phosphoenolpyruvate Carboxylase Gene Family in Cotton. <i>Plants</i> , 2022, 11, 1482.	3.5	1
9	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
10	From Sequencing to Genome Editing for Cotton Improvement. <i>Trends in Biotechnology</i> , 2021, 39, 221-224.	9.3	27
11	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
12	Foxtail Millet: A New Model for C4 Plants. <i>Trends in Plant Science</i> , 2021, 26, 199-201.	8.8	50
13	CRISPR/Cas gene therapy. <i>Journal of Cellular Physiology</i> , 2021, 236, 2459-2481.	4.1	87
14	Targeted Breeding in Cotton Using CRISPR/Cas9 Genome Editing. , 2021, , 313-327.		1
15	Identification of Stable Reference Genes for Toxicogenomic and Gene Expression Analysis. <i>Methods in Molecular Biology</i> , 2021, 2326, 67-94.	0.9	1
16	Biochemical and Physiological Toxicity of Nanoparticles in Plant. <i>Methods in Molecular Biology</i> , 2021, 2326, 225-239.	0.9	1
17	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
18	Subcritical Water Extraction of <i>Salvia miltiorrhiza</i> . <i>Molecules</i> , 2021, 26, 1634.	3.8	5

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19	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
20	GhANN1 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
21	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
22	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
23	DNA Methylation and RNA-Sequencing Analysis Show Epigenetic Function During Grain Filling in Foxtail Millet ( <i>Setaria italica</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 741415.	3.6	4
24	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
25	Direct modification of multiple gene homoeologs 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
26	Environmentally friendly plant essential oil: Liquid gold for human health. <i>Advances in Agronomy</i> , 2021, , 289-337.	5.2	9
27	Impact of Nanoparticles on Plant Growth, Development, and Biomass. <i>Methods in Molecular Biology</i> , 2021, 2326, 217-224.	0.9	1
28	Fungicide Difenconazole Induced Biochemical and Developmental Toxicity in Wheat ( <i>Triticum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 38	3.5	20
29	A critical look on CRISPR-based genome editing in plants. <i>Journal of Cellular Physiology</i> , 2020, 235, 666-682.	4.1	39
30	CRISPR/Cas9: A Robust Genome-Editing Tool with Versatile Functions and Endless Application. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5111.	4.1	4
31	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
32	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
33	Edible Plant Oil: Global Status, Health Issues, and Perspectives. <i>Frontiers in Plant Science</i> , 2020, 11, 1315.	3.6	83
34	Virus-Based CRISPR/Cas9 Genome Editing in Plants. <i>Trends in Genetics</i> , 2020, 36, 810-813.	6.7	17
35	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
36	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

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37	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
38	Impact of potassium deficiency on cotton growth, development and potential microRNA-mediated mechanism. <i>Plant Physiology and Biochemistry</i> , 2020, 153, 72-80.	5.8	43
39	Pectin Drives Cell Wall Morphogenesis without Turgor Pressure. <i>Trends in Plant Science</i> , 2020, 25, 719-722.	8.8	23
40	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
41	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
42	SpRY: Engineered CRISPR/Cas9 Harnesses New Genome-Editing Power. <i>Trends in Genetics</i> , 2020, 36, 546-548.	6.7	18
43	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
44	High throughput sequencing identifies chilling responsive genes in sweetpotato ( <i>Ipomoea batatas</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.9	24
45	Nanoparticle-Plant Interactions: Two-Way Traffic. <i>Small</i> , 2019, 15, e1901794.	10.0	132
46	Genome-Wide Identification and Analysis of Class III Peroxidases in Allotetraploid Cotton ( <i>Gossypium</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.4	13
47	Small RNA Sequencing Reveals Regulatory Roles of MicroRNAs in the Development of <i>Meloidogyne incognita</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 5466.	4.1	3
48	A Grafting Technique for Efficiently Transplanting Transgenic Regenerated Plants of Cotton. <i>Methods in Molecular Biology</i> , 2019, 1902, 195-198.	0.9	0
49	Pollen Tube Pathway-Mediated Cotton Transformation. <i>Methods in Molecular Biology</i> , 2019, 1902, 67-73.	0.9	9
50	Overexpression of miRNA in Cotton via <i>Agrobacterium</i> -Mediated Transformation. <i>Methods in Molecular Biology</i> , 2019, 1902, 223-231.	0.9	1
51	Genome Editing in Cotton Using CRISPR/Cas9 System. <i>Methods in Molecular Biology</i> , 2019, 1902, 95-104.	0.9	10
52	Transgenic Cotton: From Biotransformation Methods to Agricultural Application. <i>Methods in Molecular Biology</i> , 2019, 1902, 3-16.	0.9	8
53	<i>Agrobacterium</i> -Mediated Genetic Transformation of Cotton. <i>Methods in Molecular Biology</i> , 2019, 1902, 19-33.	0.9	4
54	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

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55	Integrated transcriptome, small <scp>RNA</scp> and degradome sequencing approaches provide insights into Ascochyta blight resistance in chickpea. <i>Plant Biotechnology Journal</i> , 2019, 17, 914-931.	8.3	66
56	Identification and expression analysis of phosphatidyl ethanolamine-binding protein (PEBP) gene family in cotton. <i>Genomics</i> , 2019, 111, 1373-1380.	2.9	17
57	Tobacco Rattle Virus-Induced Gene Silencing in Cotton. <i>Methods in Molecular Biology</i> , 2019, 1902, 105-119.	0.9	6
58	Nanoparticle titanium dioxide affects the growth and microRNA expression of switchgrass ( <i>Panicum</i> ) Tj ETQq0 0 0 ggBT /Overlock 10 Tf	2.9	42
59	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
60	A Simple and Rapid Method for Determining Transgenic Cotton Plants Using a Marker Gene. <i>Methods in Molecular Biology</i> , 2019, 1902, 187-194.	0.9	0
61	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
62	CRISPR/Cas9: An RNAâ€gguided highly precise synthetic tool for plant genome editing. <i>Journal of Cellular Physiology</i> , 2018, 233, 1844-1859.	4.1	82
63	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
64	Construction and characterization of a bacterial artificial chromosome library for <i>Gossypium mustelinum</i> . <i>PLoS ONE</i> , 2018, 13, e0196847.	2.5	3
65	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
66	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
67	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
68	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
69	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
70	MicroRNAs in model and complex organisms. <i>Functional and Integrative Genomics</i> , 2017, 17, 121-124.	3.5	30
71	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
72	MicroRNA expression profiles during cotton ( <i>Gossypium hirsutum</i> L) fiber early development. <i>Scientific Reports</i> , 2017, 7, 44454.	3.3	32

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73	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
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	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
76	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
77	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
78	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
79	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
80	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
81	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
82	MicroRNAs in Control of Plant Development. <i>Journal of Cellular Physiology</i> , 2016, 231, 303-313.	4.1	276
83	Comprehensive analysis of TCP transcription factors and their expression during cotton ( <i>Gossypium</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.3	35
84	Proteome quantification of cotton xylem sap suggests the mechanisms of potassium-deficiency-induced changes in plant resistance to environmental stresses. <i>Scientific Reports</i> , 2016, 6, 21060.	3.3	40
85	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
86	A cotton miRNA is involved in regulation of plant response to salt stress. <i>Scientific Reports</i> , 2016, 6, 19736.	3.3	79
87	ZnO nanoparticles enhanced germ cell apoptosis in <i>Caenorhabditis elegans</i> , in comparison with ZnCl <sub>2</sub> . <i>Toxicological Sciences</i> , 2016, 156, kfw258.	3.1	13
88	Small <sc>RNA</sc> and degradome deep sequencing reveals drought- and tissue-specific microRNAs and their important roles in drought-sensitive and drought-tolerant tomato genotypes. <i>Plant Biotechnology Journal</i> , 2016, 14, 1727-1746.	8.3	146
89	Small <sc>RNA</sc> and degradome sequencing reveals important micro<sc>RNA</sc> function in <i><sc>A</sc>stragalus chrysochlorus</i> response to selenium stimuli. <i>Plant Biotechnology Journal</i> , 2016, 14, 543-556.	8.3	43
90	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

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91	MicroRNA, a new target for engineering new crop cultivars. <i>Bioengineered</i> , 2016, 7, 7-10.	3.2	31
92	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
93	Contribution and distribution of inorganic ions and organic compounds to the osmotic adjustment in <i>Halostachys caspica</i> response to salt stress. <i>Scientific Reports</i> , 2015, 5, 13639.	3.3	40
94	Lack of K-Dependent Oxidative Stress in Cotton Roots Following Coronatine-Induced ROS Accumulation. <i>PLoS ONE</i> , 2015, 10, e0126476.	2.5	17
95	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
96	Manipulating microRNAs for improved biomass and biofuels from plant feedstocks. <i>Plant Biotechnology Journal</i> , 2015, 13, 337-354.	8.3	37
97	Editorial. <i>Plant Biotechnology Journal</i> , 2015, 13, 281-281.	8.3	0
98	microRNA evolution and expression analysis in polyploidized cotton genome. <i>Plant Biotechnology Journal</i> , 2015, 13, 421-434.	8.3	44
99	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
100	MicroRNA: a new target for improving plant tolerance to abiotic stress. <i>Journal of Experimental Botany</i> , 2015, 66, 1749-1761.	4.8	440
101	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
102	Small RNA sequencing identifies miRNA roles in ovule and fibre development. <i>Plant Biotechnology Journal</i> , 2015, 13, 355-369.	8.3	98
103	Selection and validation of reliable reference genes in <i>Gossypium raimondii</i> . <i>Biotechnology Letters</i> , 2015, 37, 1483-1493.	2.2	12
104	MicroRNAs in cotton: an open world needs more exploration. <i>Planta</i> , 2015, 241, 1303-1312.	3.2	21
105	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
106	Genome-wide identification of auxin response factor (ARF) genes and its tissue-specific prominent expression in <i>Gossypium raimondii</i> . <i>Functional and Integrative Genomics</i> , 2015, 15, 481-493.	3.5	41
107	Revisiting Chaos Theorem to Understand the Nature of miRNAs in Response to Drugs of Abuse. <i>Journal of Cellular Physiology</i> , 2015, 230, 2857-2868.	4.1	0
108	MicroRNA-Based Biotechnology for Plant Improvement. <i>Journal of Cellular Physiology</i> , 2015, 230, 1-15.	4.1	188

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109	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
110	Global microRNA modification in cotton ( <i>Gossypium hirsutum</i> L.). <i>Plant Biotechnology Journal</i> , 2015, 13, 492-500.	8.3	24
111	Species-Specific Expansion and Molecular Evolution of the 3-hydroxy-3-methylglutaryl Coenzyme A Reductase (HMGR) Gene Family in Plants. <i>PLoS ONE</i> , 2014, 9, e94172.	2.5	50
112	High-throughput deep sequencing shows that microRNAs play important roles in switchgrass responses to drought and salinity stress. <i>Plant Biotechnology Journal</i> , 2014, 12, 354-366.	8.3	131
113	Expression of microRNAs and their targets regulates floral development in tobacco ( <i>Nicotiana glauca</i> ). <i>PLoS ONE</i> , 2014, 9, e94172.	3.5	12
114	Titanium dioxide nanoparticles affect the growth and microRNA expression of tobacco ( <i>Nicotiana glauca</i> ). <i>PLoS ONE</i> , 2014, 9, e94172.	3.5	190
115	Differentiated expression of microRNAs may regulate genotype-dependent traits in cotton. <i>Gene</i> , 2014, 547, 233-238.	2.2	16
116	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
117	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
118	Nicotine exposure and transgenerational impact: a prospective study on small regulatory microRNAs. <i>Scientific Reports</i> , 2014, 4, 7513.	3.3	32
119	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
120	<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
121	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
122	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
123	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
124	Agrobacterium-Mediated Transformation of Cotton. <i>Methods in Molecular Biology</i> , 2013, 958, 31-45.	0.9	6
125	A Simple and Rapid Method for Determining Transgenic Cotton Plants. <i>Methods in Molecular Biology</i> , 2013, 958, 153-160.	0.9	1
126	Cotton Transformation via Pollen Tube Pathway. <i>Methods in Molecular Biology</i> , 2013, 958, 71-77.	0.9	18



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127	Transgenic Cotton: From Biotransformation Methods to Agricultural Application. <i>Methods in Molecular Biology</i> , 2013, 958, 3-15.	0.9	20
128	Overexpression of miR 156 in Cotton via <i>Agrobacterium</i> -Mediated Transformation. <i>Methods in Molecular Biology</i> , 2013, 958, 189-197.	0.9	0
129	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
130	MicroRNA, Breast Cancer and Green Tea Polyphenon-60. , 2013, , 821-828.		0
131	Evaluation and selection of reliable reference genes for gene expression under abiotic stress in cotton ( <i>Gossypium hirsutum</i> L.). , 2013, 530, 44-44.		1
132	Boron Stress Responsive MicroRNAs and Their Targets in Barley. <i>PLoS ONE</i> , 2013, 8, e59543.	2.5	89
133	Nicotine exposure caused significant transgenerational heritable behavioral changes in <i>Caenorhabditis elegans</i> . <i>EXCLI Journal</i> , 2013, 12, 793-806.	0.7	7
134	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
135	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
136	MicroRNAs: key gene regulators with versatile functions. <i>Plant Molecular Biology</i> , 2012, 80, 1-1.	3.9	25
137	Selection of Reliable Reference Genes in <i>Caenorhabditis elegans</i> for Analysis of Nanotoxicity. <i>PLoS ONE</i> , 2012, 7, e31849.	2.5	134
138	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
139	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
140	Identification of Plant microRNAs Using Expressed Sequence Tag Analysis. <i>Methods in Molecular Biology</i> , 2011, 678, 13-25.	0.9	11
141	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
142	MicroRNAs in Cotton. <i>RNA Technologies</i> , 2011, , 301-312.	0.3	0
143	Genome-Wide Functional Analysis of the Cotton Transcriptome by Creating an Integrated EST Database. <i>PLoS ONE</i> , 2011, 6, e26980.	2.5	102
144	Transcriptome-wide identification and stress properties of the 14-3-3 gene family in cotton ( <i>Gossypium</i> ) Tj ETQq0 Q,0 rgBT /Overlock 10	3.5	44

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145	Salt and Drought Stresses Induce the Aberrant Expression of microRNA Genes in Tobacco. <i>Molecular Biotechnology</i> , 2011, 49, 159-165.	2.4	171
146	5-fluorouracil drug alters the microRNA expression profiles in MCF-7 breast cancer cells. <i>Journal of Cellular Physiology</i> , 2011, 226, 1868-1878.	4.1	53
147	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
148	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
149	Identification and characterization of microRNAs and their target genes in tobacco ( <i>Nicotiana glauca</i> ). <i>Journal of Cellular Physiology</i> , 2010, 225, 296-301.	3.2	110
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