

Prabodh Kumar Trivedi

List of Publications by Year in descending order

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123
papers

8,574
citations

34105

52
h-index

48315

88
g-index

131
all docs

131
docs citations

131
times ranked

7207
citing authors

#	ARTICLE	IF	CITATIONS
1	Effect of arsenic on growth, oxidative stress, and antioxidant system in rice seedlings. <i>Ecotoxicology and Environmental Safety</i> , 2009, 72, 1102-1110.	6.0	391
2	Glutathione S-Transferases: Role in Combating Abiotic Stresses Including Arsenic Detoxification in Plants. <i>Frontiers in Plant Science</i> , 2018, 9, 751.	3.6	300
3	Changes in activities of cell wall hydrolases during ethylene-induced ripening in banana: effect of 1-MCP, ABA and IAA. <i>Postharvest Biology and Technology</i> , 2004, 31, 119-126.	6.0	276
4	Ripening of fleshy fruit: Molecular insight and the role of ethylene. <i>Biotechnology Advances</i> , 2010, 28, 94-107.	11.7	276
5	Comparative transcriptome analysis of arsenate and arsenite stresses in rice seedlings. <i>Chemosphere</i> , 2009, 74, 688-702.	8.2	254
6	Modulation of Transcriptome and Metabolome of Tobacco by Arabidopsis Transcription Factor, <i>AtMYB12</i> , Leads to Insect Resistance. <i>Plant Physiology</i> , 2010, 152, 2258-2268.	4.8	216
7	Omics and biotechnology of arsenic stress and detoxification in plants: Current updates and prospective. <i>Environment International</i> , 2015, 74, 221-230.	10.0	208
8	Expression in <i>Arabidopsis</i> and cellular localization reveal involvement of rice <i>OsNRAMP1</i> , <i>OsNRAMP2</i> , and <i>OsNRAMP3</i> in arsenic transport and tolerance. <i>Plant, Cell and Environment</i> , 2014, 37, 140-152.	5.7	190
9	Expression of a rice Lambda class of glutathione S-transferase, <i>OsGSTL2</i> , in <i>Arabidopsis</i> provides tolerance to heavy metal and other abiotic stresses. <i>Journal of Hazardous Materials</i> , 2013, 248-249, 228-237.	12.4	184
10	Silicon mediates arsenic tolerance in rice (<i>Oryza sativa</i> L.) through lowering of arsenic uptake and improved antioxidant defence system. <i>Ecological Engineering</i> , 2013, 52, 96-103.	3.6	183
11	Sulfur mediated reduction of arsenic toxicity involves efficient thiol metabolism and the antioxidant defense system in rice. <i>Journal of Hazardous Materials</i> , 2015, 298, 241-251.	12.4	173
12	Thiol metabolism and antioxidant systems complement each other during arsenate detoxification in <i>Ceratophyllum demersum</i> L.. <i>Aquatic Toxicology</i> , 2008, 86, 205-215.	4.0	168
13	MicroRNA858 Is a Potential Regulator of Phenylpropanoid Pathway and Plant Development. <i>Plant Physiology</i> , 2016, 171, 944-959.	4.8	163
14	Transcriptomic and metabolomic shifts in rice roots in response to Cr (VI) stress. <i>BMC Genomics</i> , 2010, 11, 648.	2.8	147
15	Arsenic tolerances in rice (<i>Oryza sativa</i>) have a predominant role in transcriptional regulation of a set of genes including sulphur assimilation pathway and antioxidant system. <i>Chemosphere</i> , 2011, 82, 986-995.	8.2	146
16	Reduced arsenic accumulation in rice (<i>Oryza sativa</i> L.) shoot involves sulfur mediated improved thiol metabolism, antioxidant system and altered arsenic transporters. <i>Plant Physiology and Biochemistry</i> , 2016, 99, 86-96.	5.8	138
17	Recent advances in arsenic accumulation and metabolism in rice. <i>Molecular Breeding</i> , 2010, 26, 307-323.	2.1	134
18	Differential response of oxidative stress and thiol metabolism in contrasting rice genotypes for arsenic tolerance. <i>Ecotoxicology and Environmental Safety</i> , 2012, 79, 189-198.	6.0	129

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19	Nitric Oxide Alleviated Arsenic Toxicity by Modulation of Antioxidants and Thiol Metabolism in Rice (<i>Oryza sativa</i> L.). <i>Frontiers in Plant Science</i> , 2015, 6, 1272.	3.6	128
20	Artificial microRNA mediated gene silencing in plants: progress and perspectives. <i>Plant Molecular Biology</i> , 2014, 86, 1-18.	3.9	121
21	Arsenomics: omics of arsenic metabolism in plants. <i>Frontiers in Physiology</i> , 2012, 3, 275.	2.8	120
22	A protective role for nitric oxide and salicylic acid for arsenite phytotoxicity in rice (<i>Oryza sativa</i> L.). <i>Plant Physiology and Biochemistry</i> , 2017, 115, 163-173.	5.8	118
23	Thiol metabolism play significant role during cadmium detoxification by <i>Ceratophyllum demersum</i> L.. <i>Bioresource Technology</i> , 2009, 100, 2155-2161.	9.6	113
24	MaExp1, an ethylene-induced expansin from ripening banana fruit. <i>Plant Science</i> , 2004, 167, 1351-1358.	3.6	111
25	Salicylic acid modulates arsenic toxicity by reducing its root to shoot translocation in rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Overloc	3.6	110
26	Differential Expression of Rice Lambda Class GST Gene Family Members During Plant Growth, Development, and in Response to Stress Conditions. <i>Plant Molecular Biology Reporter</i> , 2013, 31, 569-580.	1.8	109
27	Unraveling Aspects of <i>Bacillus amyloliquefaciens</i> Mediated Enhanced Production of Rice under Biotic Stress of <i>Rhizoctonia solani</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 587.	3.6	109
28	Primary transcript of miR858 encodes regulatory peptide and controls flavonoid biosynthesis and development in <i>Arabidopsis</i> . <i>Nature Plants</i> , 2020, 6, 1262-1274.	9.3	103
29	Arsenate and arsenite exposure modulate antioxidants and amino acids in contrasting arsenic accumulating rice (<i>Oryza sativa</i> L.) genotypes. <i>Journal of Hazardous Materials</i> , 2013, 262, 1123-1131.	12.4	102
30	Selenium ameliorates arsenic induced oxidative stress through modulation of antioxidant enzymes and thiols in rice (<i>Oryza sativa</i> L.). <i>Ecotoxicology</i> , 2014, 23, 1153-1163.	2.4	102
31	Expression of phytochelatin synthase from aquatic macrophyte <i>Ceratophyllum demersum</i> L. enhances cadmium and arsenic accumulation in tobacco. <i>Plant Cell Reports</i> , 2012, 31, 1687-1699.	5.6	100
32	Heavy metals induce oxidative stress and genome-wide modulation in transcriptome of rice root. <i>Functional and Integrative Genomics</i> , 2014, 14, 401-417.	3.5	100
33	Expression of OsMATE1 and OsMATE2 alters development, stress responses and pathogen susceptibility in <i>Arabidopsis</i> . <i>Scientific Reports</i> , 2014, 4, 3964.	3.3	98
34	De Novo Assembly, Functional Annotation and Comparative Analysis of <i>Withania somnifera</i> Leaf and Root Transcriptomes to Identify Putative Genes Involved in the Withanolides Biosynthesis. <i>PLoS ONE</i> , 2013, 8, e62714.	2.5	95
35	Expression of <i>Arabidopsis</i> MYB transcription factor, AtMYB111, in tobacco requires light to modulate flavonol content. <i>Scientific Reports</i> , 2014, 4, 5018.	3.3	92
36	Differential expression and alternative splicing of rice sulphate transporter family members regulate sulphur status during plant growth, development and stress conditions. <i>Functional and Integrative Genomics</i> , 2011, 11, 259-273.	3.5	89

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37	Sulfur alleviates arsenic toxicity by reducing its accumulation and modulating proteome, amino acids and thiol metabolism in rice leaves. <i>Scientific Reports</i> , 2015, 5, 16205.	3.3	89
38	Transcriptome analysis of ripe and unripe fruit tissue of banana identifies major metabolic networks involved in fruit ripening process. <i>BMC Plant Biology</i> , 2014, 14, 316.	3.6	84
39	Heterologous expression of <i>Ceratophyllum demersum</i> phytochelatin synthase, CdPCS1, in rice leads to lower arsenic accumulation in grain. <i>Scientific Reports</i> , 2014, 4, 5784.	3.3	84
40	Co-expression of <i>Arabidopsis</i> transcription factor, <i>AtMYB12</i> , and soybean isoflavone synthase, <i>GmIFS1</i> , genes in tobacco leads to enhanced biosynthesis of isoflavones and flavonols resulting in osteoprotective activity. <i>Plant Biotechnology Journal</i> , 2014, 12, 69-80.	8.3	80
41	Constitutive expression of <i>Arabidopsis</i> MYB transcription factor, <i>AtMYB11</i> , in tobacco modulates flavonoid biosynthesis in favor of flavonol accumulation. <i>Plant Cell Reports</i> , 2015, 34, 1515-1528.	5.6	80
42	Genome-wide analysis of the AP2/ERF family in <i>Musa</i> species reveals divergence and neofunctionalisation during evolution. <i>Scientific Reports</i> , 2016, 6, 18878.	3.3	75
43	Differential expression of microRNAs by arsenate and arsenite stress in natural accessions of rice. <i>Metallomics</i> , 2015, 7, 174-187.	2.4	71
44	Genome-wide identification of rice class I metallothionein gene: tissue expression patterns and induction in response to heavy metal stress. <i>Functional and Integrative Genomics</i> , 2012, 12, 635-647.	3.5	70
45	Cloning and functional characterization of 3-hydroxy-3-methylglutaryl coenzyme A reductase gene from <i>Withania somnifera</i> : an important medicinal plant. <i>Protoplasma</i> , 2013, 250, 613-622.	2.1	70
46	Development of <i>AtMYB12</i> -expressing transgenic tobacco callus culture for production of rutin with biopesticidal potential. <i>Plant Cell Reports</i> , 2012, 31, 1867-1876.	5.6	66
47	<i>AtMYB12</i> expression in tomato leads to large scale differential modulation in transcriptome and flavonoid content in leaf and fruit tissues. <i>Scientific Reports</i> , 2015, 5, 12412.	3.3	66
48	Differential expression of farnesyl diphosphate synthase gene from <i>Withania somnifera</i> in different chemotypes and in response to elicitors. <i>Plant Growth Regulation</i> , 2011, 65, 93-100.	3.4	65
49	Expression of <i>Ceratophyllum demersum</i> phytochelatin synthase, CdPCS1, in <i>Escherichia coli</i> and <i>Arabidopsis</i> enhances heavy metal(loid)s accumulation. <i>Protoplasma</i> , 2013, 250, 1263-1272.	2.1	63
50	Arsenite Tolerance is Related to Proportional Thiolic Metabolite Synthesis in Rice (<i>Oryza sativa</i> L.). <i>Archives of Environmental Contamination and Toxicology</i> , 2013, 64, 235-242.	4.1	61
51	Isolation of High-Quality RNA from Apple (<i>Malus domestica</i>) Fruit. <i>Journal of Agricultural and Food Chemistry</i> , 2006, 54, 5227-5229.	5.2	58
52	Genome-Wide Analysis of the <i>Musa</i> WRKY Gene Family: Evolution and Differential Expression during Development and Stress. <i>Frontiers in Plant Science</i> , 2016, 7, 299.	3.6	55
53	Low Temperature-Enhanced Flavonol Synthesis Requires Light-Associated Regulatory Components in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2018, 59, 2099-2112.	3.1	55
54	<i>Agrobacterium tumefaciens</i> -mediated transformation of <i>Withania somnifera</i> (L.) Dunal: an important medicinal plant. <i>Plant Cell Reports</i> , 2010, 29, 133-141.	5.6	53

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55	Genome-wide Expression Analysis and Metabolite Profiling Elucidate Transcriptional Regulation of Flavonoid Biosynthesis and Modulation under Abiotic Stresses in Banana. <i>Scientific Reports</i> , 2016, 6, 31361.	3.3	52
56	WsSGTL1 gene from <i>Withania somnifera</i> , modulates glycosylation profile, antioxidant system and confers biotic and salt stress tolerance in transgenic tobacco. <i>Planta</i> , 2014, 239, 1217-1231.	3.2	51
57	Involvement of Small RNAs in Phosphorus and Sulfur Sensing, Signaling and Stress: Current Update. <i>Frontiers in Plant Science</i> , 2017, 8, 285.	3.6	50
58	Ethylene-induced ripening in banana evokes expression of defense and stress related genes in fruit tissue. <i>Postharvest Biology and Technology</i> , 2007, 46, 136-143.	6.0	49
59	Comparative Transcriptome Analysis Using High Papaverine Mutant of <i>Papaver somniferum</i> Reveals Pathway and Uncharacterized Steps of Papaverine Biosynthesis. <i>PLoS ONE</i> , 2013, 8, e65622.	2.5	48
60	Ethylene induced cotton leaf abscission is associated with higher expression of cellulase (GhCel1) and increased activities of ethylene biosynthesis enzymes in abscission zone. <i>Plant Physiology and Biochemistry</i> , 2008, 46, 54-63.	5.8	47
61	Genome-wide identification and expression analysis of the mitogen-activated protein kinase gene family from banana suggest involvement of specific members in different stages of fruit ripening. <i>Functional and Integrative Genomics</i> , 2014, 14, 161-175.	3.5	47
62	Arsenite tolerance in rice (<i>Oryza sativa</i> L.) involves coordinated role of metabolic pathways of thiols and amino acids. <i>Environmental Science and Pollution Research</i> , 2013, 20, 884-896.	5.3	46
63	Comparative transcriptome analysis of different chemotypes elucidates withanolide biosynthesis pathway from medicinal plant <i>Withania somnifera</i> . <i>Scientific Reports</i> , 2015, 5, 18611.	3.3	46
64	Synthetic phytochelatin complement a phytochelatin-deficient <i>Arabidopsis</i> mutant and enhance the accumulation of heavy metal(loid)s. <i>Biochemical and Biophysical Research Communications</i> , 2013, 434, 664-669.	2.1	44
65	Silencing of sterol glycosyltransferases modulates the withanolide biosynthesis and leads to compromised basal immunity of <i>Withania somnifera</i> . <i>Scientific Reports</i> , 2016, 6, 25562.	3.3	44
66	Expression of Rice CYP450-Like Gene (Os08g01480) in <i>Arabidopsis</i> Modulates Regulatory Network Leading to Heavy Metal and Other Abiotic Stress Tolerance. <i>PLoS ONE</i> , 2015, 10, e0138574.	2.5	43
67	Molecular components associated with the regulation of flavonoid biosynthesis. <i>Plant Science</i> , 2022, 317, 111196.	3.6	42
68	Comparative Transcriptional Profiling of Contrasting Rice Genotypes Shows Expression Differences during Arsenic Stress. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.09.0054.	2.8	41
69	Differential transcriptome modulation leads to variation in arsenic stress response in <i>Arabidopsis thaliana</i> accessions. <i>Journal of Hazardous Materials</i> , 2018, 351, 1-10.	12.4	41
70	Dietary plant miRNAs as an augmented therapy: cross-kingdom gene regulation. <i>RNA Biology</i> , 2018, 15, 1433-1439.	3.1	41
71	Arsenic accumulation in native plants of West Bengal, India: prospects for phytoremediation but concerns with the use of medicinal plants. <i>Environmental Monitoring and Assessment</i> , 2012, 184, 2617-2631.	2.7	37
72	Cloning and characterization of 2-C-methyl-d-erythritol-4-phosphate pathway genes for isoprenoid biosynthesis from Indian ginseng, <i>Withania somnifera</i> . <i>Protoplasma</i> , 2013, 250, 285-295.	2.1	37

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73	Heavy Metal Stress Signaling in Plants. , 2016, , 585-603.		37
74	Genome-Wide Identification and Expression Analysis of Homeodomain Leucine Zipper Subfamily IV (HDZ) Tj ETQq0,0,0 rgBT /Overlock 1	3.6	34
75	An improved Agrobacterium-mediated transformation of recalcitrant indica rice (<i>Oryza sativa</i> L.) cultivars. <i>Protoplasma</i> , 2013, 250, 631-636.	2.1	33
76	Differential sulphur assimilation mechanism regulates response of <i>Arabidopsis thaliana</i> natural variation towards arsenic stress under limiting sulphur condition. <i>Journal of Hazardous Materials</i> , 2017, 337, 198-207.	12.4	33
77	Prolyl-4-hydroxylase (AtP4H1) mediates and mimics low oxygen response in <i>Arabidopsis thaliana</i> . <i>Functional and Integrative Genomics</i> , 2009, 9, 525-535.	3.5	32
78	Light-regulated expression of terpene synthase gene, AtTPS03, is controlled by the bZIP transcription factor, HY5, in <i>Arabidopsis thaliana</i> . <i>Biochemical and Biophysical Research Communications</i> , 2020, 529, 437-443.	2.1	32
79	Characterization of isoflavone synthase gene from <i>Psoralea corylifolia</i> : a medicinal plant. <i>Plant Cell Reports</i> , 2010, 29, 747-755.	5.6	31
80	Arsenic accumulation and tolerance in rootless macrophyte <i>Najas indica</i> are mediated through antioxidants, amino acids and phytochelatins. <i>Aquatic Toxicology</i> , 2014, 157, 70-80.	4.0	30
81	Natural variations in expression of regulatory and detoxification related genes under limiting phosphate and arsenate stress in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 898.	3.6	30
82	MicroRNA 874-3p Exerts Skeletal Anabolic Effects Epigenetically during Weaning by Suppressing Hdac1 Expression. <i>Journal of Biological Chemistry</i> , 2016, 291, 3959-3966.	3.4	30
83	Arsenic-responsive high-affinity rice sulphate transporter, OsSultr1;1, provides abiotic stress tolerance under limiting sulphur condition. <i>Journal of Hazardous Materials</i> , 2019, 373, 753-762.	12.4	30
84	Tropine Forming Tropinone Reductase Gene from <i>Withania somnifera</i> (Ashwagandha): Biochemical Characteristics of the Recombinant Enzyme and Novel Physiological Overtones of Tissue-Wide Gene Expression Patterns. <i>PLoS ONE</i> , 2013, 8, e74777.	2.5	29
85	Preventive effects of withaferin A isolated from the leaves of an Indian medicinal plant <i>Withania somnifera</i> (L.): Comparisons with 17- β -estradiol and alendronate. <i>Nutrition</i> , 2015, 31, 205-213.	2.4	29
86	DEVELOPMENT AND OPTIMIZATION OF HPLC-PDA-MS-MS METHOD FOR SIMULTANEOUS QUANTIFICATION OF THREE CLASSES OF FLAVONOIDS IN LEGUME SEEDS, VEGETABLES, FRUITS, AND MEDICINAL PLANTS. <i>Journal of Liquid Chromatography and Related Technologies</i> , 2011, 34, 1729-1742.	1.0	27
87	Gene expression of pathogenesis-related protein during banana ripening and after treatment with 1-MCP. <i>Postharvest Biology and Technology</i> , 2010, 56, 64-70.	6.0	24
88	Genetically engineered flavonol enriched tomato fruit modulates chondrogenesis to increase bone length in growing animals. <i>Scientific Reports</i> , 2016, 6, 21668.	3.3	24
89	Sterol glycosyltransferases required for adaptation of <i>Withania somnifera</i> at high temperature. <i>Physiologia Plantarum</i> , 2017, 160, 297-311.	5.2	24
90	Effect of virus infection on the secondary metabolite production and phytohormone biosynthesis in plants. <i>3 Biotech</i> , 2020, 10, 547.	2.2	24

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91	Comprehensive analysis of regulatory elements of the promoters of rice sulfate transporter gene family and functional characterization of <i>OsSul1;1</i> promoter under different metal stress. <i>Plant Signaling and Behavior</i> , 2015, 10, e990843.	2.4	23
92	COP1 mediates light-dependent regulation of flavonol biosynthesis through HY5 in <i>Arabidopsis</i> . <i>Plant Science</i> , 2021, 303, 110760.	3.6	23
93	Comparative analysis of transcription factor gene families from <i>Papaver somniferum</i> : identification of regulatory factors involved in benzylisoquinoline alkaloid biosynthesis. <i>Protoplasma</i> , 2016, 253, 857-871.	2.1	21
94	Transcriptome and metabolite analyses in <i>Azadirachta indica</i> : identification of genes involved in biosynthesis of bioactive triterpenoids. <i>Scientific Reports</i> , 2017, 7, 5043.	3.3	21
95	Emerging tools and paradigm shift of gene editing in cereals, fruits, and horticultural crops for enhancing nutritional value and food security. <i>Food and Energy Security</i> , 2021, 10, e258.	4.3	21
96	Virus-Induced Silencing of Key Genes Leads to Differential Impact on Withanolide Biosynthesis in the Medicinal Plant, <i>Withania somnifera</i> . <i>Plant and Cell Physiology</i> , 2018, 59, 262-274.	3.1	19
97	Updates on plant long non-coding RNAs (lncRNAs): the regulatory components. <i>Plant Cell, Tissue and Organ Culture</i> , 2020, 140, 259-269.	2.3	19
98	Prevention of articular cartilage degeneration in a rat model of monosodium iodoacetate induced osteoarthritis by oral treatment with Withaferin A. <i>Biomedicine and Pharmacotherapy</i> , 2018, 99, 151-161.	5.6	16
99	Regulation of arsenic stress response by ethylene biosynthesis and signaling in <i>Arabidopsis thaliana</i> . <i>Environmental and Experimental Botany</i> , 2021, 185, 104408.	4.2	15
100	Organization and post-transcriptional processing of the <i>psb B</i> operon from chloroplasts of <i>Populus deltoides</i> . <i>Current Genetics</i> , 1999, 36, 165-172.	1.7	14
101	³ O-Methyltransferase, <i>Ps3OMT</i> , from opium poppy: involvement in papaverine biosynthesis. <i>Plant Cell Reports</i> , 2019, 38, 1235-1248.	5.6	14
102	Novel microRNAs regulating ripening-associated processes in banana fruit. <i>Plant Growth Regulation</i> , 2020, 90, 223-235.	3.4	14
103	Comparative interactions of withanolides and sterols with two members of sterol glycosyltransferases from <i>Withania somnifera</i> . <i>BMC Bioinformatics</i> , 2015, 16, 120.	2.6	13
104	Genome-wide identification and interactome analysis of members of two-component system in Banana. <i>BMC Genomics</i> , 2019, 20, 674.	2.8	13
105	Comprehensive assessment of the genes involved in withanolide biosynthesis from <i>Withania somnifera</i> : chemotype-specific and elicitor-responsive expression. <i>Functional and Integrative Genomics</i> , 2017, 17, 477-490.	3.5	12
106	SIMULTANEOUS SEPARATION AND QUANTIFICATION OF TARGETED GROUP OF COMPOUNDS IN <i>PSORALEA CORYLIFOLIA</i> L. USING HPLC-PDA-MS-MS. <i>Journal of Liquid Chromatography and Related Technologies</i> , 2012, 35, 2567-2583.	1.0	11
107	High frequency somatic embryogenesis, regeneration and correlation of alkaloid biosynthesis with gene expression in <i>Papaver somniferum</i> . <i>Plant Growth Regulation</i> , 2012, 68, 17-25.	3.4	10
108	HY5 regulates light-dependent expression and accumulation of miR858a-encoded peptide, miPEP858a. <i>Biochemical and Biophysical Research Communications</i> , 2022, 589, 204-208.	2.1	10

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109	MicroRNA858a, its encoded peptide, and phytoalexin regulate Arabidopsis growth and development. <i>Plant Physiology</i> , 2022, 189, 1397-1415.	4.8	10
110	Genes encoding members of 3-hydroxy-3-methylglutaryl coenzyme A reductase (HMGR) gene family from <i>Azadirachta indica</i> and correlation with azadirachtin biosynthesis. <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	2.1	9
111	Estrogen receptor activation in response to Azadirachtin A stimulates osteoblast differentiation and bone formation in mice. <i>Journal of Cellular Physiology</i> , 2019, 234, 23719-23735.	4.1	9
112	Ethylene regulates miRNA-mediated lignin biosynthesis and leaf serration in <i>Arabidopsis thaliana</i> . <i>Biochemical and Biophysical Research Communications</i> , 2022, 605, 51-55.	2.1	7
113	Genome wide identification of MADS box gene family in <i>Musa balbisiana</i> and their divergence during evolution. <i>Gene</i> , 2022, 836, 146666.	2.2	7
114	Genome-wide expression analysis reveals contrasting regulation of phosphate starvation response (PSR) in root and shoot of <i>Arabidopsis</i> and its association with biotic stress. <i>Environmental and Experimental Botany</i> , 2021, 188, 104483.	4.2	5
115	Genome-wide expression and variation in nucleotide sequences lead to differential response of <i>Arabidopsis thaliana</i> ecotypes towards arsenic stress under sulfur limiting condition. <i>Environmental and Experimental Botany</i> , 2022, 195, 104764.	4.2	5
116	Cloning and nucleotide sequence analysis of psbD/C operon from chloroplasts of <i>Populus deltoides</i> . <i>Journal of Genetics</i> , 1998, 77, 77-83.	0.7	4
117	Plastid gene expression is not associated with midday depression in CO ₂ assimilation and electron transport. <i>Plant Science</i> , 2000, 155, 187-192.	3.6	4
118	miR775 integrates light, sucrose and auxin associated pathways to regulate root growth in <i>Arabidopsis thaliana</i> . <i>Plant Science</i> , 2021, 313, 111073.	3.6	4
119	Short-chain dehydrogenase/reductase, PsDeHase, from opium poppy: putative involvement in papaverine biosynthesis. <i>Plant Cell, Tissue and Organ Culture</i> , 2020, 143, 431-440.	2.3	3
120	Secondary Metabolite Pathways in Medicinal Plants: Approaches in Reconstruction and Analysis. <i>Energy, Environment, and Sustainability</i> , 2019, , 339-364.	1.0	3
121	Genomics of Arsenic Stress Response in Plants. <i>Sustainable Development and Biodiversity</i> , 2019, , 231-248.	1.7	2
122	Photoinhibition of photosynthesis without net loss of photosystem II components in <i>Populus deltoides</i> . <i>Journal of Biosciences</i> , 1997, 22, 345-355.	1.1	1
123	Role of phytochelatin in cation translocation in plants. , 2022, , 401-415.		1