Prabodh Kumar Trivedi

List of Publications by Year
in descending order

123	8,574	34105 52	48315 88
papers	citations	h-index	g-index

131	131	131	7207
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	HY5 regulates light-dependent expression and accumulation of miR858a-encoded peptide, miPEP858a. Biochemical and Biophysical Research Communications, 2022, 589, 204-208.	2.1	10
2	Genome-wide expression and variation in nucleotide sequences lead to differential response of Arabidopsis thaliana ecotypes towards arsenic stress under sulfur limiting condition. Environmental and Experimental Botany, 2022, 195, 104764.	4.2	5
3	Role of phytochelatin in cation translocation in plants. , 2022, , 401-415.		1
4	Molecular components associated with the regulation of flavonoid biosynthesis. Plant Science, 2022, 317, 111196.	3.6	42
5	MicroRNA858a, its encoded peptide, and phytosulfokine regulate Arabidopsis growth and development. Plant Physiology, 2022, 189, 1397-1415.	4.8	10
6	Ethylene regulates miRNA-mediated lignin biosynthesis and leaf serration in Arabidopsis thaliana. Biochemical and Biophysical Research Communications, 2022, 605, 51-55.	2.1	7
7	Genome wide identification of MADS box gene family in Musa balbisiana and their divergence during evolution. Gene, 2022, 836, 146666.	2.2	7
8	COP1 mediates light-dependent regulation of flavonol biosynthesis through HY5 in Arabidopsis. Plant Science, 2021, 303, 110760.	3.6	23
9	Emerging tools and paradigm shift of gene editing in cereals, fruits, and horticultural crops for enhancing nutritional value and food security. Food and Energy Security, 2021, 10, e258.	4.3	21
10	Regulation of arsenic stress response by ethylene biosynthesis and signaling in Arabidopsis thaliana. Environmental and Experimental Botany, 2021, 185, 104408.	4.2	15
11	Genome-wide expression analysis reveals contrasting regulation of phosphate starvation response (PSR) in root and shoot of Arabidopsis and its association with biotic stress. Environmental and Experimental Botany, 2021, 188, 104483.	4.2	5
12	miR775 integrates light, sucrose and auxin associated pathways to regulate root growth in Arabidopsis thaliana. Plant Science, 2021, 313, 111073.	3.6	4
13	Updates on plant long non-coding RNAs (lncRNAs): the regulatory components. Plant Cell, Tissue and Organ Culture, 2020, 140, 259-269.	2.3	19
14	Effect of virus infection on the secondary metabolite production and phytohormone biosynthesis in plants. 3 Biotech, 2020, 10, 547.	2.2	24
15	Primary transcript of miR858 encodes regulatory peptide and controls flavonoid biosynthesis and development in Arabidopsis. Nature Plants, 2020, 6, 1262-1274.	9.3	103
16	Short-chain dehydrogenase/reductase, PsDeHase, from opium poppy: putative involvement in papaverine biosynthesis. Plant Cell, Tissue and Organ Culture, 2020, 143, 431-440.	2.3	3
17	Light-regulated expression of terpene synthase gene, AtTPS03, is controlled by the bZIP transcription factor, HY5, in Arabidopsis thaliana. Biochemical and Biophysical Research Communications, 2020, 529, 437-443.	2.1	32
18	Novel microRNAs regulating ripening-associated processes in banana fruit. Plant Growth Regulation, 2020, 90, 223-235.	3.4	14

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19	Genome-wide identification and interactome analysis of members of two-component system in Banana. BMC Genomics, 2019, 20, 674.	2.8	13
20	Estrogen receptor activation in response to Azadirachtin A stimulates osteoblast differentiation and bone formation in mice. Journal of Cellular Physiology, 2019, 234, 23719-23735.	4.1	9
21	3â€²O-Methyltransferase, Ps3â€²OMT, from opium poppy: involvement in papaverine biosynthesis. Plant Cell Reports, 2019, 38, 1235-1248.	5.6	14
22	Genomics of Arsenic Stress Response in Plants. Sustainable Development and Biodiversity, 2019, , 231-248.	1.7	2
23	Arsenic-responsive high-affinity rice sulphate transporter, OsSultr1;1, provides abiotic stress tolerance under limiting sulphur condition. Journal of Hazardous Materials, 2019, 373, 753-762.	12.4	30
24	Secondary Metabolite Pathways in Medicinal Plants: Approaches in Reconstruction and Analysis. Energy, Environment, and Sustainability, 2019, , 339-364.	1.0	3
25	Differential transcriptome modulation leads to variation in arsenic stress response in Arabidopsis thaliana accessions. Journal of Hazardous Materials, 2018, 351, 1-10.	12.4	41
26	Prevention of articular cartilage degeneration in a rat model of monosodium iodoacetate induced osteoarthritis by oral treatment with Withaferin A. Biomedicine and Pharmacotherapy, 2018, 99, 151-161.	5.6	16
27	Virus-Induced Silencing of Key Genes Leads to Differential Impact on Withanolide Biosynthesis in the Medicinal Plant, Withania somnifera. Plant and Cell Physiology, 2018, 59, 262-274.	3.1	19
28	Dietary plant miRNAs as an augmented therapy: cross-kingdom gene regulation. RNA Biology, 2018, 15, 1433-1439.	3.1	41
29	Glutathione S-Transferases: Role in Combating Abiotic Stresses Including Arsenic Detoxification in Plants. Frontiers in Plant Science, 2018, 9, 751.	3.6	300
30	Low Temperature-Enhanced Flavonol Synthesis Requires Light-Associated Regulatory Components in Arabidopsis thaliana. Plant and Cell Physiology, 2018, 59, 2099-2112.	3.1	55
31	A protective role for nitric oxide and salicylic acid for arsenite phytotoxicity in rice (Oryza sativa L.). Plant Physiology and Biochemistry, 2017, 115, 163-173.	5.8	118
32	Genes encoding members of 3-hydroxy-3-methylglutaryl coenzyme A reductase (HMGR) gene family from Azadirachta indica and correlation with azadirachtin biosynthesis. Acta Physiologiae Plantarum, 2017, 39, 1.	2.1	9
33	Differential sulphur assimilation mechanism regulates response of Arabidopsis thaliana natural variation towards arsenic stress under limiting sulphur condition. Journal of Hazardous Materials, 2017, 337, 198-207.	12.4	33
34	Comprehensive assessment of the genes involved in withanolide biosynthesis from Withania somnifera: chemotype-specific and elicitor-responsive expression. Functional and Integrative Genomics, 2017, 17, 477-490.	3.5	12
35	Sterol glycosyltransferases required for adaptation of Withania somnifera at high temperature. Physiologia Plantarum, 2017, 160, 297-311.	5.2	24
36	Transcriptome and metabolite analyses in Azadirachta indica: identification of genes involved in biosynthesis of bioactive triterpenoids. Scientific Reports, 2017, 7, 5043.	3.3	21

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37	Involvement of Small RNAs in Phosphorus and Sulfur Sensing, Signaling and Stress: Current Update. Frontiers in Plant Science, 2017, 8, 285.	3.6	50
38	Genome-Wide Identification and Expression Analysis of Homeodomain Leucine Zipper Subfamily IV (HDZ) Tj ETQq0 0 0 rgBT /Overlock 1	3.6	34
39	Genome-Wide Analysis of the Musa WRKY Gene Family: Evolution and Differential Expression during Development and Stress. Frontiers in Plant Science, 2016, 7, 299.	3.6	55
40	Unraveling Aspects of Bacillus amyloliquefaciens Mediated Enhanced Production of Rice under Biotic Stress of Rhizoctonia solani. Frontiers in Plant Science, 2016, 7, 587.	3.6	109
41	Genome-wide analysis of the AP2/ERF family in Musa species reveals divergence and neofunctionalisation during evolution. Scientific Reports, 2016, 6, 18878.	3.3	75
42	Silencing of sterol glycosyltransferases modulates the withanolide biosynthesis and leads to compromised basal immunity of Withania somnifera. Scientific Reports, 2016, 6, 25562.	3.3	44
43	MicroRNA858 Is a Potential Regulator of Phenylpropanoid Pathway and Plant Development. Plant Physiology, 2016, 171, 944-959.	4.8	163
44	Genome-wide Expression Analysis and Metabolite Profiling Elucidate Transcriptional Regulation of Flavonoid Biosynthesis and Modulation under Abiotic Stresses in Banana. Scientific Reports, 2016, 6, 31361.	3.3	52
45	Genetically engineered flavonol enriched tomato fruit modulates chondrogenesis to increase bone length in growing animals. Scientific Reports, 2016, 6, 21668.	3.3	24
46	Heavy Metal Stress Signaling in Plants. , 2016, , 585-603.		37
47	Reduced arsenic accumulation in rice (Oryza sativa L.) shoot involves sulfur mediated improved thiol metabolism, antioxidant system and altered arsenic transporters. Plant Physiology and Biochemistry, 2016, 99, 86-96.	5.8	138
48	MicroRNA 874-3p Exerts Skeletal Anabolic Effects Epigenetically during Weaning by Suppressing Hdac1 Expression. Journal of Biological Chemistry, 2016, 291, 3959-3966.	3.4	30
49	Comparative analysis of transcription factor gene families from Papaver somniferum: identification of regulatory factors involved in benzylisoquinoline alkaloid biosynthesis. Protoplasma, 2016, 253, 857-871.	2.1	21
50	Comparative transcriptome analysis of different chemotypes elucidates withanolide biosynthesis pathway from medicinal plant Withania somnifera. Scientific Reports, 2015, 5, 18611.	3.3	46
51	Sulfur alleviates arsenic toxicity by reducing its accumulation and modulating proteome, amino acids and thiol metabolism in rice leaves. Scientific Reports, 2015, 5, 16205.	3.3	89
52	Comparative Transcriptional Profiling of Contrasting Rice Genotypes Shows Expression Differences during Arsenic Stress. Plant Genome, 2015, 8, eplantgenome2014.09.0054.	2.8	41
53	Expression of Rice CYP450-Like Gene (Os08g01480) in Arabidopsis Modulates Regulatory Network Leading to Heavy Metal and Other Abiotic Stress Tolerance. PLoS ONE, 2015, 10, e0138574.	2.5	43
54	Salicylic acid modulates arsenic toxicity by reducing its root to shoot translocation in rice (Oryza) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.6	110

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55	Natural variations in expression of regulatory and detoxification related genes under limiting phosphate and arsenate stress in Arabidopsis thaliana. Frontiers in Plant Science, 2015, 6, 898.	3.6	30
56	Constitutive expression of Arabidopsis MYB transcription factor, AtMYB11, in tobacco modulates flavonoid biosynthesis in favor of flavonol accumulation. Plant Cell Reports, 2015, 34, 1515-1528.	5.6	80
57	Sulfur mediated reduction of arsenic toxicity involves efficient thiol metabolism and the antioxidant defense system in rice. Journal of Hazardous Materials, 2015, 298, 241-251.	12.4	173
58	AtMYB12 expression in tomato leads to large scale differential modulation in transcriptome and flavonoid content in leaf and fruit tissues. Scientific Reports, 2015, 5, 12412.	3.3	66
59	Comparative interactions of withanolides and sterols with two members of sterol glycosyltransferases from Withania somnifera. BMC Bioinformatics, 2015, 16, 120.	2.6	13
60	Comprehensive analysis of regulatory elements of the promoters of rice sulfate transporter gene family and functional characterization ofOsSul1;1promoter under different metal stress. Plant Signaling and Behavior, 2015, 10, e990843.	2.4	23
61	Differential expression of microRNAs by arsenate and arsenite stress in natural accessions of rice. Metallomics, 2015, 7, 174-187.	2.4	71
62	Omics and biotechnology of arsenic stress and detoxification in plants: Current updates and prospective. Environment International, 2015, 74, 221-230.	10.0	208
63	Preventive effects of withaferin A isolated from the leaves of an Indian medicinal plant Withania somnifera (L.): Comparisons with 17-Î²-estradiol and alendronate. Nutrition, 2015, 31, 205-213.	2.4	29
64	Nitric Oxide Alleviated Arsenic Toxicity by Modulation of Antioxidants and Thiol Metabolism in Rice (Oryza sativa L.). Frontiers in Plant Science, 2015, 6, 1272.	3.6	128
65	Transcriptome analysis of ripe and unripe fruit tissue of banana identifies major metabolic networks involved in fruit ripening process. BMC Plant Biology, 2014, 14, 316.	3.6	84
66	Expression in <scp>A</scp>rabidopsis and cellular localization reveal involvement of rice <scp>NRAMP</scp>, <scp>OsNRAMP</scp>1, in arsenic transport and tolerance. Plant, Cell and Environment, 2014, 37, 140-152.	5.7	190
67	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. Functional and Integrative Genomics, 2014, 14, 161-175.	3.5	47
68	WsSGTL1 gene from Withania somnifera, modulates glycosylation profile, antioxidant system and confers biotic and salt stress tolerance in transgenic tobacco. Planta, 2014, 239, 1217-1231.	3.2	51
69	Heavy metals induce oxidative stress and genome-wide modulation in transcriptome of rice root. Functional and Integrative Genomics, 2014, 14, 401-417.	3.5	100
70	Arsenic accumulation and tolerance in rootless macrophyte Najas indica are mediated through antioxidants, amino acids and phytochelatins. Aquatic Toxicology, 2014, 157, 70-80.	4.0	30
71	Artificial microRNA mediated gene silencing in plants: progress and perspectives. Plant Molecular Biology, 2014, 86, 1-18.	3.9	121
72	Selenium ameliorates arsenic induced oxidative stress through modulation of antioxidant enzymes and thiols in rice (Oryza sativa L.). Ecotoxicology, 2014, 23, 1153-1163.	2.4	102

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73	Coâ€expression of Arabidopsis transcription factor, At<scp>MYB</scp>12, and soybean isoflavone synthase, Gm<scp>IFS</scp>1, genes in tobacco leads to enhanced biosynthesis of isoflavones and flavonols resulting in osteoprotective activity. Plant Biotechnology Journal, 2014, 12, 69-80.	8.3	80
74	Expression of OsMATE1 and OsMATE2 alters development, stress responses and pathogen susceptibility in Arabidopsis. Scientific Reports, 2014, 4, 3964.	3.3	98
75	Expression of Arabidopsis MYB transcription factor, AtMYB111, in tobacco requires light to modulate flavonol content. Scientific Reports, 2014, 4, 5018.	3.3	92
76	Heterologous expression of Ceratophyllum demersum phytochelatin synthase, CdPCS1, in rice leads to lower arsenic accumulation in grain. Scientific Reports, 2014, 4, 5784.	3.3	84
77	Cloning and characterization of 2-C-methyl-d-erythritol-4-phosphate pathway genes for isoprenoid biosynthesis from Indian ginseng, Withania somnifera. Protoplasma, 2013, 250, 285-295.	2.1	37
78	Expression of Ceratophyllum demersum phytochelatin synthase, CdPCS1, in Escherichia coli and Arabidopsis enhances heavy metal(loid)s accumulation. Protoplasma, 2013, 250, 1263-1272.	2.1	63
79	Synthetic phytochelatins complement a phytochelatin-deficient Arabidopsis mutant and enhance the accumulation of heavy metal(loid)s. Biochemical and Biophysical Research Communications, 2013, 434, 664-669.	2.1	44
80	Arsenite tolerance in rice (Oryza sativa L.) involves coordinated role of metabolic pathways of thiols and amino acids. Environmental Science and Pollution Research, 2013, 20, 884-896.	5.3	46
81	Arsenate and arsenite exposure modulate antioxidants and amino acids in contrasting arsenic accumulating rice (Oryza sativa L.) genotypes. Journal of Hazardous Materials, 2013, 262, 1123-1131.	12.4	102
82	An improved Agrobacterium-mediated transformation of recalcitrant indica rice (Oryza sativa L.) cultivars. Protoplasma, 2013, 250, 631-636.	2.1	33
83	Differential Expression of Rice Lambda Class GST Gene Family Members During Plant Growth, Development, and in Response to Stress Conditions. Plant Molecular Biology Reporter, 2013, 31, 569-580.	1.8	109
84	Cloning and functional characterization of 3-hydroxy-3-methylglutaryl coenzyme A reductase gene from Withania somnifera: an important medicinal plant. Protoplasma, 2013, 250, 613-622.	2.1	70
85	Expression of a rice Lambda class of glutathione S-transferase, OsGSTL2, in Arabidopsis provides tolerance to heavy metal and other abiotic stresses. Journal of Hazardous Materials, 2013, 248-249, 228-237.	12.4	184
86	Arsenite Tolerance is Related to Proportional Thiolic Metabolite Synthesis in Rice (Oryza sativa L.). Archives of Environmental Contamination and Toxicology, 2013, 64, 235-242.	4.1	61
87	Silicon mediates arsenic tolerance in rice (Oryza sativa L.) through lowering of arsenic uptake and improved antioxidant defence system. Ecological Engineering, 2013, 52, 96-103.	3.6	183
88	Comparative Transcriptome Analysis Using High Papaverine Mutant of Papaver somniferum Reveals Pathway and Uncharacterized Steps of Papaverine Biosynthesis. PLoS ONE, 2013, 8, e65622.	2.5	48
89	Tropine Forming Tropinone Reductase Gene from Withania somnifera (Ashwagandha): Biochemical Characteristics of the Recombinant Enzyme and Novel Physiological Overtones of Tissue-Wide Gene Expression Patterns. PLoS ONE, 2013, 8, e74777.	2.5	29
90	De Novo Assembly, Functional Annotation and Comparative Analysis of Withania somnifera Leaf and Root Transcriptomes to Identify Putative Genes Involved in the Withanolides Biosynthesis. PLoS ONE, 2013, 8, e62714.	2.5	95

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91	Arsenomics: omics of arsenic metabolism in plants. Frontiers in Physiology, 2012, 3, 275.	2.8	120
92	SIMULTANEOUS SEPARATION AND QUANTIFICATION OF TARGETED GROUP OF COMPOUNDS IN PSORALEA CORYLIFOLIA L. USING HPLC-PDA-MS-MS. Journal of Liquid Chromatography and Related Technologies, 2012, 35, 2567-2583.	1.0	11
93	Expression of phytochelatin synthase from aquatic macrophyte Ceratophyllum demersum L. enhances cadmium and arsenic accumulation in tobacco. Plant Cell Reports, 2012, 31, 1687-1699.	5.6	100
94	Development of AtMYB12-expressing transgenic tobacco callus culture for production of rutin with biopesticidal potential. Plant Cell Reports, 2012, 31, 1867-1876.	5.6	66
95	Genome-wide identification of rice class I metallothionein gene: tissue expression patterns and induction in response to heavy metal stress. Functional and Integrative Genomics, 2012, 12, 635-647.	3.5	70
96	High frequency somatic embryogenesis, regeneration and correlation of alkaloid biosynthesis with gene expression in Papaver somniferum. Plant Growth Regulation, 2012, 68, 17-25.	3.4	10
97	Differential response of oxidative stress and thiol metabolism in contrasting rice genotypes for arsenic tolerance. Ecotoxicology and Environmental Safety, 2012, 79, 189-198.	6.0	129
98	Arsenic accumulation in native plants of West Bengal, India: prospects for phytoremediation but concerns with the use of medicinal plants. Environmental Monitoring and Assessment, 2012, 184, 2617-2631.	2.7	37
99	Arsenic tolerances in rice (Oryza sativa) have a predominant role in transcriptional regulation of a set of genes including sulphur assimilation pathway and antioxidant system. Chemosphere, 2011, 82, 986-995.	8.2	146
100	Differential expression of farnesyl diphosphate synthase gene from Withania somnifera in different chemotypes and in response to elicitors. Plant Growth Regulation, 2011, 65, 93-100.	3.4	65
101	Differential expression and alternative splicing of rice sulphate transporter family members regulate sulphur status during plant growth, development and stress conditions. Functional and Integrative Genomics, 2011, 11, 259-273.	3.5	89
102	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. Journal of Liquid Chromatography and Related Technologies, 2011, 34, 1729-1742.	1.0	27
103	Agrobacterium tumefaciens-mediated transformation of Withania somnifera (L.) Dunal: an important medicinal plant. Plant Cell Reports, 2010, 29, 133-141.	5.6	53
104	Characterization of isoflavone synthase gene from Psoralea corylifolia: a medicinal plant. Plant Cell Reports, 2010, 29, 747-755.	5.6	31
105	Recent advances in arsenic accumulation and metabolism in rice. Molecular Breeding, 2010, 26, 307-323.	2.1	134
106	Gene expression of pathogenesis-related protein during banana ripening and after treatment with 1-MCP. Postharvest Biology and Technology, 2010, 56, 64-70.	6.0	24
107	Transcriptomic and metabolomic shifts in rice roots in response to Cr (VI) stress. BMC Genomics, 2010, 11, 648.	2.8	147
108	Ripening of fleshy fruit: Molecular insight and the role of ethylene. Biotechnology Advances, 2010, 28, 94-107.	11.7	276

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109	Modulation of Transcriptome and Metabolome of Tobacco by Arabidopsis Transcription Factor, AtMYB12, Leads to Insect Resistance. Plant Physiology, 2010, 152, 2258-2268.	4.8	216
110	Prolyl-4-hydroxylase (AtP4H1) mediates and mimics low oxygen response in Arabidopsis thaliana. Functional and Integrative Genomics, 2009, 9, 525-535.	3.5	32
111	Thiol metabolism play significant role during cadmium detoxification by Ceratophyllum demersum L.. Bioresource Technology, 2009, 100, 2155-2161.	9.6	113
112	Effect of arsenic on growth, oxidative stress, and antioxidant system in rice seedlings. Ecotoxicology and Environmental Safety, 2009, 72, 1102-1110.	6.0	391
113	Comparative transcriptome analysis of arsenate and arsenite stresses in rice seedlings. Chemosphere, 2009, 74, 688-702.	8.2	254
114	Ethylene induced cotton leaf abscission is associated with higher expression of cellulase (GhCel1) and increased activities of ethylene biosynthesis enzymes in abscission zone. Plant Physiology and Biochemistry, 2008, 46, 54-63.	5.8	47
115	Thiol metabolism and antioxidant systems complement each other during arsenate detoxification in Ceratophyllum demersum L.. Aquatic Toxicology, 2008, 86, 205-215.	4.0	168
116	Ethylene-induced ripening in banana evokes expression of defense and stress related genes in fruit tissue. Postharvest Biology and Technology, 2007, 46, 136-143.	6.0	49
117	Isolation of High-Quality RNA from Apple (Malus domestica) Fruit. Journal of Agricultural and Food Chemistry, 2006, 54, 5227-5229.	5.2	58
118	Changes in activities of cell wall hydrolases during ethylene-induced ripening in banana: effect of 1-MCP, ABA and IAA. Postharvest Biology and Technology, 2004, 31, 119-126.	6.0	276
119	MaExp1, an ethylene-induced expansin from ripening banana fruit. Plant Science, 2004, 167, 1351-1358.	3.6	111
120	Plastid gene expression is not associated with midday depression in CO2 assimilation and electron transport. Plant Science, 2000, 155, 187-192.	3.6	4
121	Organization and post-transcriptional processing of the psb B operon from chloroplasts of Populus deltoides. Current Genetics, 1999, 36, 165-172.	1.7	14
122	Cloning and nucleotide sequence analysis ofpsbD/C operon from chloroplasts ofPopulus deltoides. Journal of Genetics, 1998, 77, 77-83.	0.7	4
123	Photoinhibition of photosynthesis without net loss of photosystem II components inPopulus deltoides. Journal of Biosciences, 1997, 22, 345-355.	1.1	1