Amit Rai

List of Publications by Year
in descending order

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28 papers	1,705 citations	489802 18 h-index	563245 28 g-index
29 all docs	29 docs citations	29 times ranked	3268 citing authors

#	Article	IF	Citations
1	Chromosome-level genome assembly of Ophiorrhiza pumila reveals the evolution of camptothecin biosynthesis. Nature Communications, 2021, 12, 405.	5.8	77
2	A multi-objective hybrid machine learning approach-based optimization for enhanced biomass and bioactive phycobiliproteins production in Nostoc sp. CCC-403. Bioresource Technology, 2021, 329, 124908.	4.8	33
3	Gene-Metabolite Network Analysis Revealed Tissue-Specific Accumulation of Therapeutic Metabolites in Mallotus japonicus. International Journal of Molecular Sciences, 2021, 22, 8835.	1.8	3
4	Metabolomics and complementary techniques to investigate the plant phytochemical cosmos. Natural Product Reports, 2021, 38, 1729-1759.	5.2	46
5	Multiomics-based characterization of specialized metabolites biosynthesis in Cornus Officinalis. DNA Research, 2020, 27, .	1.5	8
6	Resource partitioning strategies during toxin production in Microcystis aeruginosa revealed by integrative omics analysis. Algal Research, 2019, 42, 101582.	2.4	6
7	Metabolic diversification of nitrogenâ€containing metabolites by the expression of a heterologous lysine decarboxylase gene in Arabidopsis. Plant Journal, 2019, 100, 505-521.	2.8	11
8	A new era in plant functional genomics. Current Opinion in Systems Biology, 2019, 15, 58-67.	1.3	26
9	A cheminformatics approach to characterize metabolomes in stable-isotope-labeled organisms. Nature Methods, 2019, 16, 295-298.	9.0	194
10	Perspective: functional genomics towards new biotechnology in medicinal plants. Plant Biotechnology Reports, 2018, 12, 69-75.	0.9	17
11	De Novo Transcriptome Assembly and Characterization of Lithospermum officinale to Discover Putative Genes Involved in Specialized Metabolites Biosynthesis. Planta Medica, 2018, 84, 920-934.	0.7	25
12	Comparative transcriptome analyses of three medicinal Forsythia species and prediction of candidate genes involved in secondary metabolisms. Journal of Natural Medicines, 2018, 72, 867-881.	1.1	15
13	Integrated omics analysis of specialized metabolism in medicinal plants. Plant Journal, 2017, 90, 764-787.	2.8	185
14	De novo transcriptome assembly and characterization of nine tissues of Lonicera japonica to identify potential candidate genes involved in chlorogenic acid, luteolosides, and secoiridoid biosynthesis pathways. Journal of Natural Medicines, 2017, 71, 1-15.	1.1	60
15	De Novo RNA Sequencing and Expression Analysis of Aconitum carmichaelii to Analyze Key Genes Involved in the Biosynthesis of Diterpene Alkaloids. Molecules, 2017, 22, 2155.	1.7	38
16	An MYB transcription factor regulating specialized metabolisms in <i>Ophiorrhiza pumila</i>. Plant Biotechnology, 2016, 33, 1-9.	0.5	35
17	RNA-seq Transcriptome Analysis of Panax japonicus, and Its Comparison with Other Panax Species to Identify Potential Genes Involved in the Saponins Biosynthesis. Frontiers in Plant Science, 2016, 7, 481.	1.7	62
18	Function of AP2/ERF Transcription Factors Involved in the Regulation of Specialized Metabolism in Ophiorrhiza pumila Revealed by Transcriptomics and Metabolomics. Frontiers in Plant Science, 2016, 7, 1861.	1.7	54

#	Article	IF	Citations
19	High-throughput sequencing and de novo transcriptome assembly of Swertia japonica to identify genes involved in the biosynthesis of therapeutic metabolites. Plant Cell Reports, 2016, 35, 2091-2111.	2.8	38
20	Coordinate Regulation of Metabolite Glycosylation and Stress Hormone Biosynthesis by TT8 in Arabidopsis. Plant Physiology, 2016, 171, 2499-2515.	2.3	45
21	De Novo Deep Transcriptome Analysis of Medicinal Plants for Gene Discovery in Biosynthesis of Plant Natural Products. Methods in Enzymology, 2016, 576, 19-45.	0.4	31
22	Omics data input for metabolic modeling. Current Opinion in Biotechnology, 2016, 37, 127-134.	3.3	42
23	Characterization and functional analysis of eugenol O-methyltransferase gene reveal metabolite shifts, chemotype specific differential expression and developmental regulation in Ocimum tenuiflorum L.. Molecular Biology Reports, 2014, 41, 1857-1870.	1.0	23
24	Plant Metabolomics: From Experimental Design to Knowledge Extraction. Methods in Molecular Biology, 2013, 1069, 279-312.	0.4	7
25	A bacterial quercetin oxidoreductase QuoA-mediated perturbation in the phenylpropanoid metabolic network increases lignification with a concomitant decrease in phenolamides in Arabidopsis. Journal of Experimental Botany, 2013, 64, 5183-5194.	2.4	13
26	Glycine Decarboxylase Activity Drives Non-Small Cell Lung Cancer Tumor-Initiating Cells and Tumorigenesis. Cell, 2012, 148, 259-272.	13.5	593
27	Glycine Decarboxylase Activity Drives Non-Small Cell Lung Cancer Tumor-Initiating Cells and Tumorigenesis. Cell, 2012, 148, 1066.	13.5	12
28	Modifications of ampicillin structure and its implication: an in-silico approach. International Journal of Bioinformatics Research and Applications, 2009, 5, 616.	0.1	0