Pankaj Barah

List of Publications by Year in descending order

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933447 752698 1,119 25 10 20 citations g-index h-index papers 29 29 29 2170 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	SNMRS: An advanced measure for Co-expression network analysis. Computers in Biology and Medicine, 2022, 143, 105222.	7.0	1
2	Transcriptomic data of MCF-7 breast cancer cells treated with G1, a G-protein coupled estrogen receptor (GPER) agonist. Data in Brief, 2022, 41, 107948.	1.0	O
3	Time-course transcriptome analysis identifies rewiring patterns of transcriptional regulatory networks in rice under Rhizoctonia solani infection. Gene, 2022, 828, 146468.	2.2	5
4	Identifying Signal-Crosstalk Mechanism in Maize Plants during Combined Salinity and Boron Stress Using Integrative Systems Biology Approaches. BioMed Research International, 2022, 2022, 1-17.	1.9	6
5	Integrative network-based approaches identified systems-level molecular signatures associated with gallbladder cancer pathogenesis from gallstone diseases. Journal of Biosciences, 2022, 47, .	1.1	O
6	Identification of Systems Level Molecular Signatures from Glioblastoma Multiforme Derived Extracellular Vesicles. Journal of Molecular Neuroscience, 2021, 71, 1156-1167.	2.3	4
7	Identification of potential Parkinson's disease biomarkers using computational biology approaches. Network Modeling Analysis in Health Informatics and Bioinformatics, 2021, 10, 1.	2.1	O
8	An Integrative Systems Biology Approach Identifies Molecular Signatures Associated with Gallbladder Cancer Pathogenesis. Journal of Clinical Medicine, 2021, 10, 3520.	2.4	3
9	Identifying critical genes in esophageal squamous cell carcinoma using an ensemble approach. Informatics in Medicine Unlocked, 2020, 18, 100277.	3.4	3
10	Integrative network analysis identifies differential regulation of neuroimmune system in Schizophrenia and Bipolar disorder. Brain, Behavior, & Immunity - Health, 2020, 2, 100023.	2.5	9
11	Temperature differentially modulates the transcriptome response in Oryza sativa to Xanthomonas oryzae pv. oryzae infection. Genomics, 2020, 112, 4842-4852.	2.9	11
12	Comparison of Methods for Differential Co-expression Analysis for Disease Biomarker Prediction. Computers in Biology and Medicine, 2019, 113, 103380.	7.0	57
13	Evolutionary Trajectories of IDHWT Glioblastomas Reveal a Common Path of Early Tumorigenesis Instigated Years ahead of Initial Diagnosis. Cancer Cell, 2019, 35, 692-704.e12.	16.8	172
14	Arginylation regulates adipogenesis by regulating expression of PPAR \hat{I}^3 at transcript and protein level. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2019, 1864, 596-607.	2.4	9
15	Integrative Approaches to Understand the Mastery in Manipulation of Host Cytokine Networks by Protozoan Parasites with Emphasis on Plasmodium and Leishmania Species. Frontiers in Immunology, 2018, 9, 296.	4.8	13
16	Transcriptional regulatory networks in <i>Arabidopsis thaliana</i> during single and combined stresses. Nucleic Acids Research, 2016, 44, 3147-3164.	14.5	62
17	Multidimensional approaches for studying plant defence against insects: from ecology to omics and synthetic biology. Journal of Experimental Botany, 2015, 66, 479-493.	4.8	60
18	Endangered species damned by dams. Nature, 2014, 515, 37-37.	27.8	1

#	Article	IF	Citations
19	Transcriptome Responses to Combinations of Stresses in Arabidopsis Â. Plant Physiology, 2013, 161, 1783-1794.	4.8	478
20	Genome scale transcriptional response diversity among ten ecotypes of Arabidopsis thaliana during heat stress. Frontiers in Plant Science, 2013, 4, 532.	3.6	43
21	Genome-scale cold stress response regulatory networks in ten Arabidopsis thalianaecotypes. BMC Genomics, 2013, 14, 722.	2.8	73
22	Molecular Signatures in Arabidopsis thaliana in Response to Insect Attack and Bacterial Infection. PLoS ONE, 2013, 8, e58987.	2.5	67
23	Systems Biology: A Promising Tool to Study Abiotic Stress Responses. , 2011, , 163-172.		10
24	Systems Biology: A Promising Tool to Study Abiotic Stress Responses., 2011,, 163-172.		6
25	Analysis of protein folds using protein contact networks. Pramana - Journal of Physics, 2008, 71, 369-378.	1.8	24