

Ajit Ghosh

List of Publications by Year in descending order

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Version: 2024-02-01

38
papers

1,221
citations

471509

17
h-index

377865

34
g-index

39
all docs

39
docs citations

39
times ranked

1166
citing authors

#	ARTICLE	IF	CITATIONS
1	Methylglyoxal " a signaling molecule in plant abiotic stress responses. <i>Free Radical Biology and Medicine</i> , 2018, 122, 96-109.	2.9	117
2	A unique N ² -independent and methylglyoxal-inducible rice glyoxalase I possesses a single active site and functions in abiotic stress response. <i>Plant Journal</i> , 2014, 78, 951-963.	5.7	113
3	A glutathione responsive rice glyoxalase II, OsGLYII ² , functions in salinity adaptation by maintaining better photosynthesis efficiency and antioxidant pool. <i>Plant Journal</i> , 2014, 80, 93-105.	5.7	102
4	Presence of unique glyoxalase III proteins in plants indicates the existence of shorter route for methylglyoxal detoxification. <i>Scientific Reports</i> , 2016, 6, 18358.	3.3	100
5	Glyoxalases and stress tolerance in plants. <i>Biochemical Society Transactions</i> , 2014, 42, 485-490.	3.4	97
6	Manipulation of glyoxalase pathway confers tolerance to multiple stresses in rice. <i>Plant, Cell and Environment</i> , 2018, 41, 1186-1200.	5.7	95
7	Genome-wide identification and expression analysis of glutathione S-transferase gene family in tomato: Gaining an insight to their physiological and stress-specific roles. <i>PLoS ONE</i> , 2017, 12, e0187504.	2.5	84
8	Genome-wide identification of glutathione S-transferase gene family in pepper, its classification, and expression profiling under different anatomical and environmental conditions. <i>Scientific Reports</i> , 2019, 9, 9101.	3.3	74
9	Genome-wide analysis and expression profiling of glyoxalase gene families in soybean (<i>Glycine max</i>) indicate their development and abiotic stress specific response. <i>BMC Plant Biology</i> , 2016, 16, 87.	3.6	68
10	Comprehensive analysis and transcript profiling of <i>Arabidopsis thaliana</i> and <i>Oryza sativa</i> catalase gene family suggests their specific roles in development and stress responses. <i>Plant Physiology and Biochemistry</i> , 2018, 123, 54-64.	5.8	49
11	Comprehensive genome-wide analysis of Glutathione S-transferase gene family in potato (<i>Solanum</i>) Tj ETQq1 1 0.784314 rgBT /Over conditions. <i>Gene</i> , 2018, 639, 149-162.	2.2	44
12	A nuclear-localized rice glyoxalase I enzyme, OsGLYI ⁸ , functions in the detoxification of methylglyoxal in the nucleus. <i>Plant Journal</i> , 2017, 89, 565-576.	5.7	36
13	Synthesis, characterization, density functional study and antimicrobial evaluation of a series of bischelated complexes with a dithiocarbamate Schiff base ligand. <i>Arabian Journal of Chemistry</i> , 2017, 10, 172-184.	4.9	27
14	Evolutionary variation and expression profiling of Isopentenyl transferase gene family in <i>Arabidopsis thaliana</i> L. and <i>Oryza sativa</i> L.. <i>Plant Gene</i> , 2018, 15, 15-27.	2.3	26
15	Genome-Wide Identification of Glyoxalase Genes in <i>Medicago truncatula</i> and Their Expression Profiling in Response to Various Developmental and Environmental Stimuli. <i>Frontiers in Plant Science</i> , 2017, 8, 836.	3.6	25
16	Genome-wide identification and expression profiling of glutathione S-transferase family under multiple abiotic and biotic stresses in <i>Medicago truncatula</i> L.. <i>PLoS ONE</i> , 2021, 16, e0247170.	2.5	23
17	Advances on plant extracts and phytochemicals with acetylcholinesterase inhibition activity for possible treatment of Alzheimer's disease. <i>Phytomedicine Plus</i> , 2022, 2, 100184.	2.0	22
18	Evolution, family expansion, and functional diversification of plant aldehyde dehydrogenases. <i>Gene</i> , 2022, 829, 146522.	2.2	13

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19	Genome-wide dissection and expression profiling of unique glyoxalase III genes in soybean reveal the differential pattern of transcriptional regulation. <i>Scientific Reports</i> , 2018, 8, 4848.	3.3	12
20	SSR markers linked to mite (<i>Polyphagotarsonemus latus</i> Banks) resistance in jute (<i>Corchorus</i>) Tj ETQq0 0 0 rgBT /Overlock 1Q Tf 50 702	0.8	8
21	Identification and characterization of jute LTR retrotransposons. <i>Mobile Genetic Elements</i> , 2011, 1, 18-28.	1.8	8
22	Genome-wide analysis and transcript profiling identify several abiotic and biotic stress-responsive Glutathione S-transferase genes in soybean. <i>Plant Gene</i> , 2020, 23, 100239.	2.3	8
23	Identification and expression profiling of proline metabolizing genes in <i>Arabidopsis thaliana</i> and <i>Oryza sativa</i> to reveal their stress-specific transcript alteration. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 1469-1485.	3.1	8
24	Genome-wide identification, evolution, and transcript profiling of Aldehyde dehydrogenase superfamily in potato during development stages and stress conditions. <i>Scientific Reports</i> , 2021, 11, 18284.	3.3	8
25	Aldehyde dehydrogenase superfamily in sorghum: genome-wide identification, evolution, and transcript profiling during development stages and stress conditions. <i>BMC Plant Biology</i> , 2022, 22, .	3.6	8
26	Genome-wide in silico identification and characterization of Simple Sequence Repeats in diverse completed SARS-CoV-2 genomes. <i>Gene Reports</i> , 2021, 23, 101020.	0.8	6
27	Glyoxalase <scp>III</scp> enhances salinity tolerance through reactive oxygen species scavenging and reduced glycation. <i>Physiologia Plantarum</i> , 2022, 174, e13693.	5.2	6
28	Gene modification by fast-track recombineering for cellular localization and isolation of components of plant protein complexes. <i>Plant Journal</i> , 2019, 100, 411-429.	5.7	5
29	Leaf Disc Stress Tolerance Assay for Tobacco. <i>Bio-protocol</i> , 2015, 5, .	0.4	5
30	Glyoxalase Pathway and Drought Stress Tolerance in Plants. , 2016, , 379-399.		4
31	Impact of Lockdown Measures and Meteorological Parameters on the COVID-19 Incidence and Mortality Rate in Bangladesh. <i>Infectious Microbes & Diseases</i> , 2021, 3, 41-48.	1.3	4
32	Identification and molecular characterization of a receptor-like protein kinase gene from <i>Corchorus capsularis</i> . <i>Turkish Journal of Biology</i> , 0, , .	0.8	4
33	Genome wide analysis of the heavy-metal-associated (HMA) gene family in tomato and expression profiles under different stresses. <i>Gene</i> , 2022, 835, 146664.	2.2	4
34	Molecular evolution of SUN-domain containing proteins in diverse plant species and their expression profiling in response to developmental and perturbation stimuli. <i>Phytochemistry</i> , 2019, 157, 28-42.	2.9	3
35	Investigating the possible origin and transmission routes of SARS-CoV-2 genomes and variants of concern in Bangladesh. <i>Infection, Genetics and Evolution</i> , 2021, 95, 105057.	2.3	2
36	Development of Multi-epitope Based Subunit Vaccine Against Crimean-Congo Hemorrhagic Fever Virus Using Reverse Vaccinology Approach. <i>International Journal of Peptide Research and Therapeutics</i> , 2022, 28, .	1.9	2

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37	Stress Tolerance Assay at the Seed Germination Stage for Tobacco. Bio-protocol, 2015, 5, .	0.4	0
38	Plant Gene Modification by BAC Recombineering. Methods in Molecular Biology, 2022, 2479, 71-84.	0.9	0