## Togawa Rc

List of Publications by Year in descending order

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Τος γινα Ρς

#	Article	IF	CITATIONS
1	Global transcriptome analysis of two wild relatives of peanut under drought and fungi infection. BMC Genomics, 2012, 13, 387.	2.8	83
2	Transcription profile of soybean-root-knot nematode interaction reveals a key role of phythormones in the resistance reaction. BMC Genomics, 2013, 14, 322.	2.8	56
3	Transcriptome Analysis in Cotton Boll Weevil (Anthonomus grandis) and RNA Interference in Insect Pests. PLoS ONE, 2013, 8, e85079.	2.5	52
4	Worker Honeybee Brain Proteome. Journal of Proteome Research, 2012, 11, 1485-1493.	3.7	48
5	Knock-Down of Heat-Shock Protein 90 and Isocitrate Lyase Gene Expression Reduced Root-Knot Nematode Reproduction. Phytopathology, 2015, 105, 628-637.	2.2	29
6	Comparative Genomics Reveals Novel Target Genes towards Specific Control of Plant-Parasitic Nematodes. Genes, 2020, 11, 1347.	2.4	29
7	Spring Is Coming: Genetic Analyses of the Bud Break Date Locus Reveal Candidate Genes From the Cold Perception Pathway to Dormancy Release in Apple (Malus × domestica Borkh.). Frontiers in Plant Science, 2019, 10, 33.	3.6	28
8	Comparative root transcriptome of wild Arachis reveals NBS-LRR genes related to nematode resistance. BMC Plant Biology, 2018, 18, 159.	3.6	27
9	Analysis of the Transcriptome in Aspergillus tamarii During Enzymatic Degradation of Sugarcane Bagasse. Frontiers in Bioengineering and Biotechnology, 2018, 6, 123.	4.1	26
10	Gene expression analysis in <i>Musa acuminata</i> during compatible interactions with <i>Meloidogyne incognita</i> . Annals of Botany, 2017, 119, mcw272.	2.9	22
11	MiDaf16-like and MiSkn1-like gene families are reliable targets to develop biotechnological tools for the control and management of Meloidogyne incognita. Scientific Reports, 2020, 10, 6991.	3.3	18
12	Dissecting protein domain variability in the core RNA interference machinery of five insect orders. RNA Biology, 2021, 18, 1653-1681.	3.1	16
13	Mitogenome sequence accuracy using different elucidation methods. PLoS ONE, 2017, 12, e0179971.	2.5	15
14	Systemic and sex-biased regulation of OBP expression under semiochemical stimuli. Scientific Reports, 2018, 8, 6035.	3.3	12
15	Transcriptome Profiling-Based Analysis of Carbohydrate-Active Enzymes in Aspergillus terreus Involved in Plant Biomass Degradation. Frontiers in Bioengineering and Biotechnology, 2020, 8, 564527.	4.1	12
16	First Microsatellite Markers Developed from Cupuassu ESTs: Application in Diversity Analysis and Cross-Species Transferability to Cacao. PLoS ONE, 2016, 11, e0151074.	2.5	10
17	Differentially expressed genes in cotton plant genotypes infected with Meloidogyne incognita. Plant Science, 2009, 177, 492-497.	3.6	9
18	The Mi-EFF1/Minc17998 effector interacts with the soybean GmHub6 protein to promote host plant parasitism by Meloidogyne incognita. Physiological and Molecular Plant Pathology, 2021, 114, 101630.	2.5	8

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19	GPCRs from fusarium graminearum detection, modeling and virtual screening - the search for new routes to control head blight disease. BMC Bioinformatics, 2016, 17, 463.	2.6	7
20	Metabarcoding versus mapping unassembled shotgun reads for identification of prey consumed by arthropod epigeal predators. GigaScience, 2022, 11, .	6.4	7
21	Transcriptome profile of drought responsive candidate genes in varieties of citrus rootstocks with different tolerance strategies. Scientia Horticulturae, 2021, 277, 109838.	3.6	5
22	A Storage Policy for a Hybrid Federated Cloud platform: A Case Study for Bioinformatics. , 2014, , .		3
23	A new fieldâ€ŧested electronic system for data gathering, recording, transfer and dissemination via the World Wide Web. Taxon, 1998, 47, 381-386.	0.7	Ο
24	Molecular characterization of the Rpv3 locus towards the development of KASP markers for downy mildew resistance in grapevine (Vitis spp.). Euphytica, 2022, 218, 1.	1.2	0