

# Togawa Rc

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1042947/publications.pdf>

Version: 2024-02-01

24  
papers

523  
citations

759233

12  
h-index

713466

21  
g-index

26  
all docs

26  
docs citations

26  
times ranked

943  
citing authors

#	ARTICLE	IF	CITATIONS
1	Metabarcoding versus mapping unassembled shotgun reads for identification of prey consumed by arthropod epigeal predators. <i>GigaScience</i> , 2022, 11, .	6.4	7
2	Molecular characterization of the Rpv3 locus towards the development of KASP markers for downy mildew resistance in grapevine ( <i>Vitis</i> spp.). <i>Euphytica</i> , 2022, 218, 1.	1.2	0
3	Dissecting protein domain variability in the core RNA interference machinery of five insect orders. <i>RNA Biology</i> , 2021, 18, 1653-1681.	3.1	16
4	Transcriptome profile of drought responsive candidate genes in varieties of citrus rootstocks with different tolerance strategies. <i>Scientia Horticulturae</i> , 2021, 277, 109838.	3.6	5
5	The Mi-EFF1/Minc17998 effector interacts with the soybean GmHub6 protein to promote host plant parasitism by <i>Meloidogyne incognita</i> . <i>Physiological and Molecular Plant Pathology</i> , 2021, 114, 101630.	2.5	8
6	Comparative Genomics Reveals Novel Target Genes towards Specific Control of Plant-Parasitic Nematodes. <i>Genes</i> , 2020, 11, 1347.	2.4	29
7	Transcriptome Profiling-Based Analysis of Carbohydrate-Active Enzymes in <i>Aspergillus terreus</i> Involved in Plant Biomass Degradation. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 564527.	4.1	12
8	MiDaf16-like and MiSkn1-like gene families are reliable targets to develop biotechnological tools for the control and management of <i>Meloidogyne incognita</i> . <i>Scientific Reports</i> , 2020, 10, 6991.	3.3	18
9	Spring Is Coming: Genetic Analyses of the Bud Break Date Locus Reveal Candidate Genes From the Cold Perception Pathway to Dormancy Release in Apple ( <i>Malus domestica</i> Borkh.). <i>Frontiers in Plant Science</i> , 2019, 10, 33.	3.6	28
10	Systemic and sex-biased regulation of OBP expression under semiochemical stimuli. <i>Scientific Reports</i> , 2018, 8, 6035.	3.3	12
11	Analysis of the Transcriptome in <i>Aspergillus tamaris</i> During Enzymatic Degradation of Sugarcane Bagasse. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018, 6, 123.	4.1	26
12	Comparative root transcriptome of wild <i>Arachis</i> reveals NBS-LRR genes related to nematode resistance. <i>BMC Plant Biology</i> , 2018, 18, 159.	3.6	27
13	Gene expression analysis in <i>Musa acuminata</i> during compatible interactions with <i>Meloidogyne incognita</i> . <i>Annals of Botany</i> , 2017, 119, mcw272.	2.9	22
14	Mitogenome sequence accuracy using different elucidation methods. <i>PLoS ONE</i> , 2017, 12, e0179971.	2.5	15
15	GPCRs from <i>Fusarium graminearum</i> detection, modeling and virtual screening - the search for new routes to control head blight disease. <i>BMC Bioinformatics</i> , 2016, 17, 463.	2.6	7
16	First Microsatellite Markers Developed from Cupuassu ESTs: Application in Diversity Analysis and Cross-Species Transferability to Cacao. <i>PLoS ONE</i> , 2016, 11, e0151074.	2.5	10
17	Knock-Down of Heat-Shock Protein 90 and Isocitrate Lyase Gene Expression Reduced Root-Knot Nematode Reproduction. <i>Phytopathology</i> , 2015, 105, 628-637.	2.2	29
18	A Storage Policy for a Hybrid Federated Cloud platform: A Case Study for Bioinformatics. , 2014, , .		3

#	ARTICLE	IF	CITATIONS
19	Transcription profile of soybean-root-knot nematode interaction reveals a key role of phytohormones in the resistance reaction. <i>BMC Genomics</i> , 2013, 14, 322.	2.8	56
20	Transcriptome Analysis in Cotton Boll Weevil ( <i>Anthonomus grandis</i> ) and RNA Interference in Insect Pests. <i>PLoS ONE</i> , 2013, 8, e85079.	2.5	52
21	Worker Honeybee Brain Proteome. <i>Journal of Proteome Research</i> , 2012, 11, 1485-1493.	3.7	48
22	Global transcriptome analysis of two wild relatives of peanut under drought and fungi infection. <i>BMC Genomics</i> , 2012, 13, 387.	2.8	83
23	Differentially expressed genes in cotton plant genotypes infected with <i>Meloidogyne incognita</i> . <i>Plant Science</i> , 2009, 177, 492-497.	3.6	9
24	A new field-tested electronic system for data gathering, recording, transfer and dissemination via the World Wide Web. <i>Taxon</i> , 1998, 47, 381-386.	0.7	0