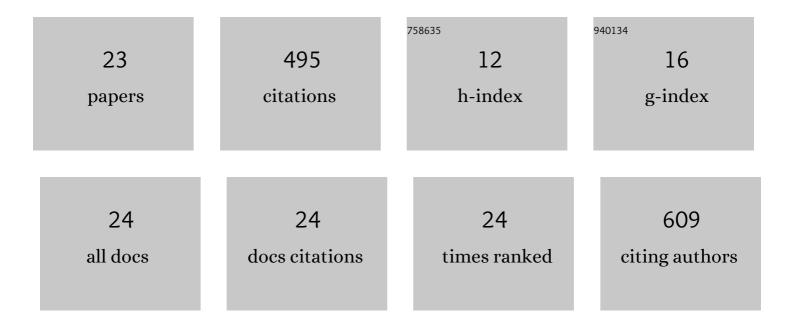
Savio Siqueira Ferreira

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2359455/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	A matter of time: regulatory events behind the synchronization of C4 and crassulacean acid metabolism in <i>Portulaca oleracea</i> . Journal of Experimental Botany, 2022, 73, 4867-4885.	2.4	7
2	Isolation of Promoters and Transcription Factors Involved in the Regulation of Lignin Biosynthesis in Saccharum Species. Methods in Molecular Biology, 2022, 2469, 103-118.	0.4	1
3	Genome-wide characterization of the laccase gene family in Setaria viridis reveals members potentially involved in lignification. Planta, 2020, 251, 46.	1.6	46
4	The sugarcane ShMYB78 transcription factor activates suberin biosynthesis in Nicotiana benthamiana. Plant Molecular Biology, 2020, 104, 411-427.	2.0	15
5	Differentiation of Tracheary Elements in Sugarcane Suspension Cells Involves Changes in Secondary Wall Deposition and Extensive Transcriptional Reprogramming. Frontiers in Plant Science, 2020, 11, 617020.	1.7	10
6	In silico guided structural and functional analysis of genes with potential involvement in resistance to coffee leaf rust: A functional marker based approach. PLoS ONE, 2020, 15, e0222747.	1.1	13
7	Title is missing!. , 2020, 15, e0222747.		0
8	Title is missing!. , 2020, 15, e0222747.		0
9	Title is missing!. , 2020, 15, e0222747.		0
10	Title is missing!. , 2020, 15, e0222747.		0
11	Title is missing!. , 2020, 15, e0222747.		0
12	Title is missing!. , 2020, 15, e0222747.		0
13	The lignin toolbox of the model grass Setaria viridis. Plant Molecular Biology, 2019, 101, 235-255.	2.0	28
14	Genomic resources for energy cane breeding in the post genomics era. Computational and Structural Biotechnology Journal, 2019, 17, 1404-1414.	1.9	38
15	Assembly of the 373k gene space of the polyploid sugarcane genome reveals reservoirs of functional diversity in the world's leading biomass crop. GigaScience, 2019, 8, .	3.3	106
16	High throughput transcriptome analysis of coffee reveals prehaustorial resistance in response to Hemileia vastatrix infection. Plant Molecular Biology, 2017, 95, 607-623.	2.0	25
17	Co-expression network analysis reveals transcription factors associated to cell wall biosynthesis in sugarcane. Plant Molecular Biology, 2016, 91, 15-35.	2.0	99
18	Full-Length Enriched cDNA Libraries and ORFeome Analysis of Sugarcane Hybrid and Ancestor Genotypes. PLoS ONE, 2014, 9, e107351.	1.1	26

#	Article	IF	CITATIONS
19	Transcriptome Analysis in the Saccharinae. , 2013, , 121-139.		2
20	Biofuel and energy crops: high-yield Saccharinae take center stage in the post-genomics era. Genome Biology, 2013, 14, 210.	3.8	27
21	Characterization of Passionfruit severe leaf distortion virus, a novel begomovirus infecting passionfruit in Brazil, reveals a close relationship with tomatoâ€infecting begomoviruses. Plant Pathology, 2010, 59, 221-230.	1.2	17
22	Characterization of Tomato yellow spot virus, a novel tomato-infecting begomovirus in Brazil. Pesquisa Agropecuaria Brasileira, 2007, 42, 1335-1343.	0.9	21
23	Traditional and novel strategies for geminivirus management in Brazil. Australasian Plant Pathology, 2005, 34, 475.	0.5	14