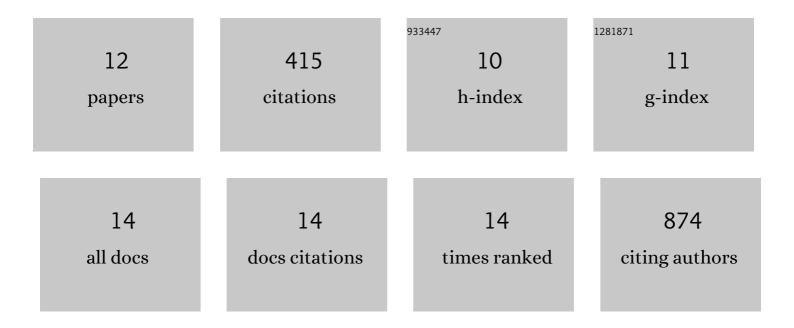
Sahra Uygun

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7594319/publications.pdf Version: 2024-02-01



SAHDA LIVCUM

#	Article	IF	CITATIONS
1	Diversity, expansion, and evolutionary novelty of plant DNA-binding transcription factor families. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2017, 1860, 3-20.	1.9	75
2	The Impact of the Branched-Chain Ketoacid Dehydrogenase Complex on Amino Acid Homeostasis in Arabidopsis. Plant Physiology, 2015, 169, pp.00461.2015.	4.8	74
3	Utility and Limitations of Using Gene Expression Data to Identify Functional Associations. PLoS Computational Biology, 2016, 12, e1005244.	3.2	63
4	Measuring semantic similarities by combining gene ontology annotations and gene co-function networks. BMC Bioinformatics, 2015, 16, 44.	2.6	39
5	Recovery from N Deprivation Is a Transcriptionally and Functionally Distinct State in Chlamydomonas. Plant Physiology, 2018, 176, 2007-2023.	4.8	30
6	Cis-Regulatory Code for Predicting Plant Cell-Type Transcriptional Response to High Salinity. Plant Physiology, 2019, 181, 1739-1751.	4.8	29
7	Molecular Evidence for Functional Divergence and Decay of a Transcription Factor Derived from Whole-Genome Duplication in <i>Arabidopsis thaliana</i> . Plant Physiology, 2015, 168, 1717-1734.	4.8	28
8	Phase II Trial of Neoadjuvant Carboplatin and Nab-Paclitaxel in Patients with Triple-Negative Breast Cancer. Oncologist, 2021, 26, e382-e393.	3.7	27
9	Predictive Models of Spatial Transcriptional Response to High Salinity. Plant Physiology, 2017, 174, 450-464.	4.8	24
10	Regulatory Divergence in Wound-Responsive Gene Expression between Domesticated and Wild Tomato. Plant Cell, 2018, 30, 1445-1460.	6.6	23
11	Optimising the use of gene expression data to predict plant metabolic pathway memberships. New Phytologist, 2021, 231, 475-489.	7.3	3
12	Evaluating the effects of clustering methods in co-expression-based functional inference in Arabidopsis thaliana. New Biotechnology, 2012, 29, S149.	4.4	0