Jerome Verdier

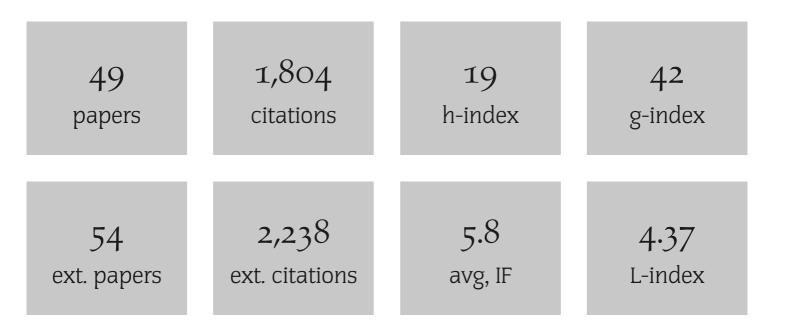
List of Publications by Year in Descending Order

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Version: 2024-04-17

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.



#	Paper	IF	Citations
49	Chromatin Immunoprecipitation dataset of H3ac and H3K27me3 histone marks followed by DNA sequencing of embryos during control and heat stress conditions to decipher epigenetic regulation of desiccation tolerance acquisition <i>Data in Brief</i> , 2022 , 40, 107793	1.2	1
48	Seed Maturation Events in Medicago truncatula: Focus on Desiccation Tolerance. <i>Compendium of Plant Genomes</i> , 2022 , 139-152	0.8	0
47	Early Stages of Seed Development in Medicago truncatula: Lessons from Genomic Studies. <i>Compendium of Plant Genomes</i> , 2022 , 131-138	0.8	
46	Gene co-expression analysis of tomato seed maturation reveals tissue-specific regulatory networks and hubs associated with the acquisition of desiccation tolerance and seed vigour. <i>BMC Plant Biology</i> , 2021 , 21, 124	5.3	4
45	RNA sequencing data for heat stress response in isolated seed tissues. <i>Data in Brief</i> , 2021 , 35, 106726	1.2	1
44	Prediction of moisture transfer in cement-based materials: Use of a porous network model to access transfer parameters. <i>Cement and Concrete Research</i> , 2021 , 142, 106310	10.3	2
43	Genome-Wide Association Studies of Seed Performance Traits in Response to Heat Stress in Uncover as a Regulator of Seed Germination Plasticity. <i>Frontiers in Plant Science</i> , 2021 , 12, 673072	6.2	2
42	Multichannel imaging for monitoring chemical composition and germination capacity of cowpea (Vigna unguiculata) seeds during development and maturation. <i>Crop Journal</i> , 2021 ,	4.6	3
41	Dataset for transcriptome and physiological response of mature tomato seed tissues to light and heat during fruit ripening. <i>Data in Brief</i> , 2021 , 34, 106671	1.2	
40	Genome-wide association study identified candidate genes for seed size and seed composition improvement in M. truncatula. <i>Scientific Reports</i> , 2021 , 11, 4224	4.9	4
39	MtExpress, a Comprehensive and Curated RNAseq-based Gene Expression Atlas for the Model Legume Medicago truncatula. <i>Plant and Cell Physiology</i> , 2021 , 62, 1494-1500	4.9	3
38	Permeability and damage of partially saturated concrete exposed to elevated temperature. <i>Cement and Concrete Composites</i> , 2020 , 109, 103563	8.6	10
37	Physical Dormancy Release in Seeds Is Related to Environmental Variations. <i>Plants</i> , 2020 , 9,	4.5	8
36	A snapshot of functional genetic studies in Medicago truncatula 2020 , 7-30		1
35	Snapshot of epigenetic regulation in legumes 2020 , 3, e60		1
34	New approach for the measurement of gas permeability and porosity accessible to gas in vacuum and under pressure. <i>Cement and Concrete Composites</i> , 2019 , 103, 59-70	8.6	6
33	The genome of cowpea (Vigna unguiculata [L.] Walp.). Plant Journal, 2019 , 98, 767-782	6.9	128

32	Utilization of computer vision and multispectral imaging techniques for classification of cowpea () seeds. <i>Plant Methods</i> , 2019 , 15, 24	5.8	22
31	The Model Legume Medicago truncatula: Past, Present, and Future 2019 , 109-130		1
30	A physiological perspective of late maturation processes and establishment of seed quality in Medicago truncatula seeds 2019 , 44-54		1
29	Impact of reinforcement-concrete interfaces and cracking on gas transfer in concrete. <i>Construction and Building Materials</i> , 2017 , 157, 521-533	6.7	7
28	Gene expression atlas of pigeonpea and its application to gain insights into genes associated with pollen fertility implicated in seed formation. <i>Journal of Experimental Botany</i> , 2017 , 68, 2037-2054	7	37
27	The Vigna unguiculata Gene Expression Atlas (VuGEA) from de novo assembly and quantification of RNA-seq data provides insights into seed maturation mechanisms. <i>Plant Journal</i> , 2016 , 88, 318-327	6.9	32
26	A Snapshot of Functional Genetic Studies in Medicago truncatula. Frontiers in Plant Science, 2016, 7, 11	75.2	28
25	Analysis of Large Seeds from Three Different Medicago truncatula Ecotypes Reveals a Potential Role of Hormonal Balance in Final Size Determination of Legume Grains. <i>International Journal of Molecular Sciences</i> , 2016 , 17,	6.3	5
24	Metabolic engineering of proanthocyanidin production by repressing the isoflavone pathways and redirecting anthocyanidin precursor flux in legume. <i>Plant Biotechnology Journal</i> , 2016 , 14, 1604-18	11.6	45
23	DASH transcription factor impacts Medicago truncatula seed size by its action on embryo morphogenesis and auxin homeostasis. <i>Plant Journal</i> , 2015 , 81, 453-66	6.9	24
22	ITIS, a bioinformatics tool for accurate identification of transposon insertion sites using next-generation sequencing data. <i>BMC Bioinformatics</i> , 2015 , 16, 72	3.6	47
21	Inference of Longevity-Related Genes from a Robust Coexpression Network of Seed Maturation Identifies Regulators Linking Seed Storability to Biotic Defense-Related Pathways. <i>Plant Cell</i> , 2015 , 27, 2692-708	11.6	80
20	A Tutorial on Lotus japonicus Transcriptomic Tools. Compendium of Plant Genomes, 2014, 183-199	0.8	
19	Legume Seed Genomics: How to Respond to the Challenges and Potential of a Key Plant Family? 2013 , 179-201		
18	Sealing process induced by carbonation of localized cracks in cementitious materials. <i>Cement and Concrete Composites</i> , 2013 , 37, 37-46	8.6	16
17	Prediction of relative permeabilities and water vapor diffusion reduction factor for cement-based materials. <i>Cement and Concrete Research</i> , 2013 , 48, 53-63	10.3	23
16	Establishment of the Lotus japonicus Gene Expression Atlas (LjGEA) and its use to explore legume seed maturation. <i>Plant Journal</i> , 2013 , 74, 351-62	6.9	101
15	Diffusivity evolution under decalcification: influence of aggregate natures and cement type. <i>Materials and Structures/Materiaux Et Constructions</i> , 2013 , 46, 787-801	3.4	6

14	A regulatory network-based approach dissects late maturation processes related to the acquisition of desiccation tolerance and longevity of Medicago truncatula seeds. <i>Plant Physiology</i> , 2013 , 163, 757-3	74 ^{6.6}	119
13	A combined histology and transcriptome analysis unravels novel questions on Medicago truncatula seed coat. <i>Journal of Experimental Botany</i> , 2013 , 64, 459-70	7	41
12	LegumeGRN: a gene regulatory network prediction server for functional and comparative studies. <i>PLoS ONE</i> , 2013 , 8, e67434	3.7	31
11	The Vatom-splitting Vanoment of synthetic biology: nuclear physics and synthetic biology share common features. <i>EMBO Reports</i> , 2012 , 13, 677-9	6.5	1
10	MtPAR MYB transcription factor acts as an on switch for proanthocyanidin biosynthesis in Medicago truncatula. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 1766-71	11.5	111
9	The Medicago truncatula Gene Expression Atlas (MtGEA): A Tool for Legume Seed Biology and Biotechnology 2012 , 111-127		2
8	Networks of Seed Storage Protein Regulation in Cereals and Legumes at the Dawn of the Omics Era 2012 , 187-210		1
7	Optimizing TILLING populations for reverse genetics in Medicago truncatula. <i>Plant Biotechnology Journal</i> , 2009 , 7, 430-41	11.6	92
6	A gene expression atlas of the model legume Medicago truncatula. <i>Plant Journal</i> , 2008 , 55, 504-13	6.9	569
5	Transcriptional regulation of storage protein synthesis during dicotyledon seed filling. <i>Plant and Cell Physiology</i> , 2008 , 49, 1263-71	4.9	105
4	Gene expression profiling of M. truncatula transcription factors identifies putative regulators of grain legume seed filling. <i>Plant Molecular Biology</i> , 2008 , 67, 567-80	4.6	77
3	Plasticity of Medicago truncatula seed dormancy relates to large-scale environment variation		1
2	The genome of cowpea (Vigna unguiculata [L.] Walp.)		2
1	MtExpress, a Comprehensive and Curated RNAseq-based Gene Expression Atlas for the Model		1