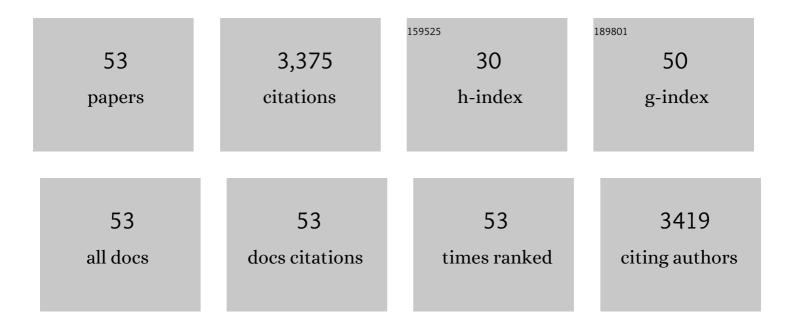
Mohammed Bendahmane

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7976175/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Cantaloupe melon genome reveals 3D chromatin features and structural relationship with the ancestral cucurbitaceae karyotype. IScience, 2022, 25, 103696.	1.9	12
2	Integrated multiâ€omic data and analyses reveal the pathways underlying key ornamental traits in carnation flowers. Plant Biotechnology Journal, 2022, 20, 1182-1196.	4.1	21
3	Tissue-Specific Expression of the Terpene Synthase Family Genes in Rosa chinensis and Effect of Abiotic Stress Conditions. Genes, 2022, 13, 547.	1.0	11
4	Comprehensive Genome-Wide Analysis of Histone Acetylation Genes in Roses and Expression Analyses in Response to Heat Stress. Genes, 2022, 13, 980.	1.0	1
5	Regeneration and Agrobacterium-mediated genetic transformation in Dianthus chinensis. Scientia Horticulturae, 2021, 287, 110279.	1.7	6
6	Rosa spp Trends in Genetics, 2020, 36, 146-147.	2.9	2
7	Integrative genome-wide analysis reveals the role of WIP proteins in inhibition of growth and development. Communications Biology, 2020, 3, 239.	2.0	16
8	Mapping a double flower phenotype-associated gene DcAP2L in Dianthus chinensis. Journal of Experimental Botany, 2020, 71, 1915-1927.	2.4	19
9	TCTP and CSN4 control cell cycle progression and development by regulating CULLIN1 neddylation in plants and animals. PLoS Genetics, 2019, 15, e1007899.	1.5	20
10	The development of a high-density genetic map significantly improves the quality of reference genome assemblies for rose. Scientific Reports, 2019, 9, 5985.	1.6	14
11	Rose floral scent. Acta Horticulturae, 2019, , 69-80.	0.1	3
12	Biosynthesis of 2-Phenylethanol in Rose Petals Is Linked to the Expression of One Allele of <i>RhPAAS</i> . Plant Physiology, 2019, 179, 1064-1079.	2.3	23
13	The Rosa genome provides new insights into the domestication of modern roses. Nature Genetics, 2018, 50, 772-777.	9.4	344
14	Genome-Wide Identification and Characterization of Aquaporins and Their Role in the Flower Opening Processes in Carnation (Dianthus caryophyllus). Molecules, 2018, 23, 1895.	1.7	42
15	A miR172 target-deficient AP2-like gene correlates with the double flower phenotype in roses. Scientific Reports, 2018, 8, 12912.	1.6	51
16	Identification and Characterization of the MADS-Box Genes and Their Contribution to Flower Organ in Carnation (Dianthus caryophyllus L.). Genes, 2018, 9, 193.	1.0	24
17	Roles of the Translationally Controlled Tumor Protein (TCTP) in Plant Development. Results and Problems in Cell Differentiation, 2017, 64, 149-172.	0.2	14
18	HAWAIIAN SKIRT controls size and floral organ number by modulating CUC1 and CUC2 expression. PLoS ONE, 2017, 12, e0185106.	1.1	31

2

#	Article	IF	CITATIONS
19	The Arabidopsis thaliana F-box gene HAWAIIAN SKIRT is a new player in the microRNA pathway. PLoS ONE, 2017, 12, e0189788.	1.1	27
20	Genome-wide identification and characterization of aquaporin gene family in <i>Beta vulgaris</i> . PeerJ, 2017, 5, e3747.	0.9	48
21	The Rosa chinensis cv. Viridiflora Phyllody Phenotype Is Associated with Misexpression of Flower Organ Identity Genes. Frontiers in Plant Science, 2016, 7, 996.	1.7	17
22	ROSE GENOMICS: CHALLENGES AND PERSPECTIVES. Acta Horticulturae, 2015, , 35-40.	0.1	1
23	Biosynthesis of monoterpene scent compounds in roses. Science, 2015, 349, 81-83.	6.0	177
24	Single Cell Wall Nonlinear Mechanics Revealed by a Multiscale Analysis of AFM Force-Indentation Curves. Biophysical Journal, 2015, 108, 2235-2248.	0.2	32
25	Genetic and Phenotypic Analyses of Petal Development in Arabidopsis. Methods in Molecular Biology, 2014, 1110, 191-202.	0.4	7
26	A Comparative Mechanical Analysis of Plant and Animal Cells Reveals Convergence across Kingdoms. Biophysical Journal, 2014, 107, 2237-2244.	0.2	32
27	The Contribution of the Structural Elements of a Single Plant Cell to its Mechanics: How the Plant Cell becomes Animal-Like. Biophysical Journal, 2014, 106, 356a.	0.2	Ο
28	Transcriptome and gene expression analysis during flower blooming in Rosa chinensis â€~Pallida'. Gene, 2014, 540, 96-103.	1.0	31
29	Genetics and genomics of flower initiation and development in roses. Journal of Experimental Botany, 2013, 64, 847-857.	2.4	129
30	Transcriptome database resource and gene expression atlas for the rose. BMC Genomics, 2012, 13, 638.	1.2	76
31	Genomic Approach to Study Floral Development Genes in Rosa sp PLoS ONE, 2011, 6, e28455.	1.1	44
32	AUXIN RESPONSE FACTOR8 Regulates <i>Arabidopsis</i> Petal Growth by Interacting with the bHLH Transcription Factor BIGPETALp Â. Plant Cell, 2011, 23, 973-983.	3.1	206
33	Somatic embryogenesis and transformation of the diploid Rosa chinensis cv Old Blush. Plant Cell, Tissue and Organ Culture, 2010, 100, 73-81.	1.2	60
34	Tinkering with the C-Function: A Molecular Frame for the Selection of Double Flowers in Cultivated Roses. PLoS ONE, 2010, 5, e9288.	1.1	94
35	Translationally controlled tumor protein is a conserved mitotic growth integrator in animals and plants. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 16384-16389.	3.3	137
36	Jasmonate controls late development stages of petal growth in <i>Arabidopsis thaliana</i> . Plant Journal, 2009, 60, 1070-1080.	2.8	90

#	Article	IF	CITATIONS
37	Scent evolution in Chinese roses. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 5927-5932.	3.3	86
38	Coat protein-mediated resistance to TMV infection of Nicotiana tabacum involves multiple modes of interference by coat protein. Virology, 2007, 366, 107-116.	1.1	52
39	BIGPETALp, a bHLH transcription factor is involved in the control of Arabidopsis petal size. EMBO Journal, 2006, 25, 3912-3920.	3.5	188
40	Characterization of mutant tobacco mosaic virus coat protein that interferes with virus cell-to-cell movement. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 3645-3650.	3.3	62
41	Analysis of gene expression in rose petals using expressed sequence tags. FEBS Letters, 2002, 515, 35-38.	1.3	78
42	Biosynthesis of the major scent components 3,5-dimethoxytoluene and 1,3,5-trimethoxybenzene by novel roseO-methyltransferases. FEBS Letters, 2002, 523, 113-118.	1.3	76
43	Chimeric animal and plant viruses expressing epitopes of outer membrane protein F as a combined vaccine againstPseudomonas aeruginosalung infection. FEMS Immunology and Medical Microbiology, 2000, 27, 291-297.	2.7	52
44	Immunization with a chimeric tobacco mosaic virus containing an epitope of outer membrane protein F of Pseudomonas aeruginosa provides protection against challenge with P. aeruginosa. Vaccine, 2000, 18, 2266-2274.	1.7	73
45	Protective immunity against murine hepatitis virus (MHV) induced by intranasal or subcutaneous administration of hybrids of tobacco mosaic virus that carries an MHV epitope. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 7774-7779.	3.3	134
46	Control of Tobamovirus Infections Via Pathogen-Derived Resistance. Advances in Virus Research, 1999, 53, 369-386.	0.9	39
47	Display of epitopes on the surface of tobacco mosaic virus: impact of charge and isoelectric point of the epitope on virus-host interactions 1 1Edited by N-H Chua. Journal of Molecular Biology, 1999, 290, 9-20.	2.0	120
48	Development of Tobacco Mosaic Virus Infection Sites in Nicotiana benthamiana. Molecular Plant-Microbe Interactions, 1999, 12, 143-152.	1.4	80
49	Identification of viral mutants by mass spectrometry. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 8596-8601.	3.3	34
50	Engineering resistance against tomato yellow leaf curl virus (TYLCV) using antisense RNA. , 1997, 33, 351-357.		96
51	Studies of coat protein-mediated resistance to tobacco mosaic tobamovirus: correlation between assembly of mutant coat proteins and resistance. Journal of Virology, 1997, 71, 7942-7950.	1.5	72
52	Tomato yellow leaf curl virus from sardinia is a whitefly- transmitted monoparatite geminivirus. Nucleic Acids Research, 1991, 19, 6763-6769.	6.5	271
53	Production of homozygous rose line derived from heterozygous genotype. Protocol Exchange, 0, , .	0.3	0