

Michiel Van Bel

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3292495/publications.pdf>

Version: 2024-02-01

33
papers

3,629
citations

304743

22
h-index

434195

31
g-index

37
all docs

37
docs citations

37
times ranked

6070
citing authors

#	ARTICLE	IF	CITATIONS
1	PLAZA 4.0: an integrative resource for functional, evolutionary and comparative plant genomics. <i>Nucleic Acids Research</i> , 2018, 46, D1190-D1196.	14.5	460
2	The <i>Physcomitrella patens</i> chromosome-scale assembly reveals moss genome structure and evolution. <i>Plant Journal</i> , 2018, 93, 515-533.	5.7	406
3	PLAZA 3.0: an access point for plant comparative genomics. <i>Nucleic Acids Research</i> , 2015, 43, D974-D981.	14.5	329
4	PLAZA: A Comparative Genomics Resource to Study Gene and Genome Evolution in Plants. <i>Plant Cell</i> , 2010, 21, 3718-3731.	6.6	243
5	Dissecting Plant Genomes with the PLAZA Comparative Genomics Platform. <i>Plant Physiology</i> , 2012, 158, 590-600.	4.8	238
6	Capturing the phosphorylation and protein interaction landscape of the plant TOR kinase. <i>Nature Plants</i> , 2019, 5, 316-327.	9.3	205
7	Drought Tolerance Conferred to Sugarcane by Association with <i>Gluconacetobacter diazotrophicus</i> : A Transcriptomic View of Hormone Pathways. <i>PLoS ONE</i> , 2014, 9, e114744.	2.5	187
8	Dynamic Changes in ANGUSTIFOLIA3 Complex Composition Reveal a Growth Regulatory Mechanism in the Maize Leaf. <i>Plant Cell</i> , 2015, 27, 1605-1619.	6.6	154
9	Gene functionalities and genome structure in <i>Bathycoccus prasinus</i> reflect cellular specializations at the base of the green lineage. <i>Genome Biology</i> , 2012, 13, R74.	9.6	143
10	PhyD3: a phylogenetic tree viewer with extended phyloXML support for functional genomics data visualization. <i>Bioinformatics</i> , 2017, 33, 2946-2947.	4.1	142
11	A conserved core of PCD indicator genes discriminates developmentally and environmentally induced programmed cell death in plants. <i>Plant Physiology</i> , 2015, 169, pp.00769.2015.	4.8	141
12	Insights into the Evolution of Multicellularity from the Sea Lettuce Genome. <i>Current Biology</i> , 2018, 28, 2921-2933.e5.	3.9	134
13	TRAPID: an efficient online tool for the functional and comparative analysis of de novo RNA-Seq transcriptomes. <i>Genome Biology</i> , 2013, 14, R134.	9.6	108
14	PLAZA 5.0: extending the scope and power of comparative and functional genomics in plants. <i>Nucleic Acids Research</i> , 2022, 50, D1468-D1474.	14.5	95
15	picoPLAZA, a genome database of microbial photosynthetic eukaryotes. <i>Environmental Microbiology</i> , 2013, 15, 2147-2153.	3.8	87
16	Neoproterozoic origin and multiple transitions to macroscopic growth in green seaweeds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 2551-2559.	7.1	85
17	It's Time for Some Seeing: Novel Tools to Monitor the Ubiquitin Landscape in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2016, 28, 6-16.	6.6	84
18	Reciprocally Retained Genes in the Angiosperm Lineage Show the Hallmarks of Dosage Balance Sensitivity. <i>Plant Cell</i> , 2017, 29, 2766-2785.	6.6	81

#	ARTICLE	IF	CITATIONS
19	Up-to-Date Workflow for Plant (Phospho)proteomics Identifies Differential Drought-Responsive Phosphorylation Events in Maize Leaves. <i>Journal of Proteome Research</i> , 2016, 15, 4304-4317.	3.7	50
20	PP2A-3 interacts with ACR4 and regulates formative cell division in the <i>Arabidopsis</i> root. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 1447-1452.	7.1	43
21	Integrative inference of transcriptional networks in <i>Arabidopsis</i> yields novel ROS signalling regulators. <i>Nature Plants</i> , 2021, 7, 500-513.	9.3	43
22	A Collection of Conserved Noncoding Sequences to Study Gene Regulation in Flowering Plants. <i>Plant Physiology</i> , 2016, 171, 2586-2598.	4.8	39
23	Comparative transcriptomics enables the identification of functional orthologous genes involved in early leaf growth. <i>Plant Biotechnology Journal</i> , 2020, 18, 553-567.	8.3	24
24	TRAPID 2.0: a web application for taxonomic and functional analysis of <i>de novo</i> transcriptomes. <i>Nucleic Acids Research</i> , 2021, 49, e101-e101.	14.5	21
25	Chromosome-scale assembly and annotation of the perennial ryegrass genome. <i>BMC Genomics</i> , 2022, 23, .	2.8	17
26	Gene space completeness in complex plant genomes. <i>Current Opinion in Plant Biology</i> , 2019, 48, 9-17.	7.1	16
27	BLSSpeller: exhaustive comparative discovery of conserved <i>cis</i> -regulatory elements. <i>Bioinformatics</i> , 2015, 31, 3758-3766.	4.1	14
28	Plant-RRBS, a bisulfite and next-generation sequencing-based methylome profiling method enriching for coverage of cytosine positions. <i>BMC Plant Biology</i> , 2017, 17, 115.	3.6	13
29	Exploring Plant Co-Expression and Gene-Gene Interactions with CORNET 3.0. <i>Methods in Molecular Biology</i> , 2017, 1533, 201-212.	0.9	11
30	The <i>Arabidopsis</i> condensin CAP ϵ subunits arrange interphase chromatin. <i>New Phytologist</i> , 2021, 230, 972-987.	7.3	9
31	Comment on "Hayai-Annotation Plants: an ultrafast and comprehensive functional gene annotation system in plants": the importance of taking the GO graph structure into account. <i>Bioinformatics</i> , 2021, 36, 5558-5560.	4.1	2
32	FunSiP: a modular and extensible classifier for the prediction of functional sites in DNA. <i>Bioinformatics</i> , 2008, 24, 1532-1533.	4.1	0
33	Plant-RRBS: DNA Methylome Profiling Adjusted to Plant Genomes, Utilizing Efficient Endonuclease Combinations, for Multi-Sample Studies. <i>Methods in Molecular Biology</i> , 2020, 2093, 65-80.	0.9	0