

Michiel Van Bel

List of Publications by Year in descending order

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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 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 |
| 2 | Chromosome-scale assembly and annotation of the perennial ryegrass genome. <i>BMC Genomics</i> , 2022, 23, . | 2.8 | 17 |
| 3 | The <i>Arabidopsis</i> condensin CAP ϵ subunits arrange interphase chromatin. <i>New Phytologist</i> , 2021, 230, 972-987. | 7.3 | 9 |
| 4 | 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 |
| 5 | 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 |
| 6 | 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 |
| 7 | 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 |
| 8 | 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 |
| 9 | 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 |
| 10 | Capturing the phosphorylation and protein interaction landscape of the plant TOR kinase. <i>Nature Plants</i> , 2019, 5, 316-327. | 9.3 | 205 |
| 11 | Gene space completeness in complex plant genomes. <i>Current Opinion in Plant Biology</i> , 2019, 48, 9-17. | 7.1 | 16 |
| 12 | 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 |
| 13 | 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 |
| 14 | Insights into the Evolution of Multicellularity from the Sea Lettuce Genome. <i>Current Biology</i> , 2018, 28, 2921-2933.e5. | 3.9 | 134 |
| 15 | 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 |
| 16 | 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 |
| 17 | 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 |
| 18 | PhyD3: a phylogenetic tree viewer with extended phyloXML support for functional genomics data visualization. <i>Bioinformatics</i> , 2017, 33, 2946-2947. | 4.1 | 142 |

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|----|---|------|-----------|
| 19 | A Collection of Conserved Noncoding Sequences to Study Gene Regulation in Flowering Plants. <i>Plant Physiology</i> , 2016, 171, 2586-2598. | 4.8 | 39 |
| 20 | 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 |
| 21 | 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 |
| 22 | It's Time for Some Site-Seeing: Novel Tools to Monitor the Ubiquitin Landscape in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2016, 28, 6-16. | 6.6 | 84 |
| 23 | BLSSpeller: exhaustive comparative discovery of conserved cis-regulatory elements. <i>Bioinformatics</i> , 2015, 31, 3758-3766. | 4.1 | 14 |
| 24 | PLAZA 3.0: an access point for plant comparative genomics. <i>Nucleic Acids Research</i> , 2015, 43, D974-D981. | 14.5 | 329 |
| 25 | 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 |
| 26 | 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 |
| 27 | 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 |
| 28 | 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 |
| 29 | picoPLAZA, a genome database of microbial photosynthetic eukaryotes. <i>Environmental Microbiology</i> , 2013, 15, 2147-2153. | 3.8 | 87 |
| 30 | Dissecting Plant Genomes with the PLAZA Comparative Genomics Platform. <i>Plant Physiology</i> , 2012, 158, 590-600. | 4.8 | 238 |
| 31 | Gene functionalities and genome structure in <i>Bathycoccus prasinos</i> reflect cellular specializations at the base of the green lineage. <i>Genome Biology</i> , 2012, 13, R74. | 9.6 | 143 |
| 32 | PLAZA: A Comparative Genomics Resource to Study Gene and Genome Evolution in Plants. <i>Plant Cell</i> , 2010, 21, 3718-3731. | 6.6 | 243 |
| 33 | FunSiP: a modular and extensible classifier for the prediction of functional sites in DNA. <i>Bioinformatics</i> , 2008, 24, 1532-1533. | 4.1 | 0 |