

Diego Mauricio Riaño Pachón

List of Publications by Year in descending order

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83
papers

8,069
citations

159585

30
h-index

91884

69
g-index

91
all docs

91
docs citations

91
times ranked

12302
citing authors

#	ARTICLE	IF	CITATIONS
1	The <i>Chlamydomonas</i> Genome Reveals the Evolution of Key Animal and Plant Functions. <i>Science</i> , 2007, 318, 245-250.	12.6	2,354
2	The <i>Selaginella</i> Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. <i>Science</i> , 2011, 332, 960-963.	12.6	794
3	PlnTFDB: updated content and new features of the plant transcription factor database. <i>Nucleic Acids Research</i> , 2010, 38, D822-D827.	14.5	635
4	QuantPrime – a flexible tool for reliable high-throughput primer design for quantitative PCR. <i>BMC Bioinformatics</i> , 2008, 9, 465.	2.6	452
5	Pan genome of the phytoplankton <i>Emiliania</i> underpins its global distribution. <i>Nature</i> , 2013, 499, 209-213.	27.8	448
6	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus <i>Aspergillus</i> . <i>Genome Biology</i> , 2017, 18, 28.	8.8	417
7	PlnTFDB: an integrative plant transcription factor database. <i>BMC Bioinformatics</i> , 2007, 8, 42.	2.6	332
8	Transcription factors regulating leaf senescence in <i>Arabidopsis thaliana</i> . <i>Plant Biology</i> , 2008, 10, 63-75.	3.8	278
9	The Role of bZIP Transcription Factors in Green Plant Evolution: Adaptive Features Emerging from Four Founder Genes. <i>PLoS ONE</i> , 2008, 3, e2944.	2.5	251
10	Genome-Wide Phylogenetic Comparative Analysis of Plant Transcriptional Regulation: A Timeline of Loss, Gain, Expansion, and Correlation with Complexity. <i>Genome Biology and Evolution</i> , 2010, 2, 488-503.	2.5	174
11	Genome-wide analysis of ABA-responsive elements ABRE and CE3 reveals divergent patterns in <i>Arabidopsis</i> and rice. <i>BMC Genomics</i> , 2007, 8, 260.	2.8	159
12	Combined transcription factor profiling, microarray analysis and metabolite profiling reveals the transcriptional control of metabolic shifts occurring during tomato fruit development. <i>Plant Journal</i> , 2011, 68, 999-1013.	5.7	118
13	Insights into immune responses in oral cancer through proteomic analysis of saliva and salivary extracellular vesicles. <i>Scientific Reports</i> , 2015, 5, 16305.	3.3	109
14	Molecular Evolution of Slow and Quick Anion Channels (SLACs and QUACs/ALMTs). <i>Frontiers in Plant Science</i> , 2012, 3, 263.	3.6	104
15	Phylogenetic Analysis of K ⁺ Transporters in Bryophytes, Lycophytes, and Flowering Plants Indicates a Specialization of Vascular Plants. <i>Frontiers in Plant Science</i> , 2012, 3, 167.	3.6	91
16	Draft genome sequencing of the sugarcane hybrid SP80-3280. <i>F1000Research</i> , 2017, 6, 861.	1.6	82
17	Green Transcription Factors: A <i>Chlamydomonas</i> Overview. <i>Genetics</i> , 2008, 179, 31-39.	2.9	81
18	Comparative transcriptome analysis reveals different strategies for degradation of steam-exploded sugarcane bagasse by <i>Aspergillus niger</i> and <i>Trichoderma reesei</i> . <i>BMC Genomics</i> , 2017, 18, 501.	2.8	79

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19	<i>Aspergillus fumigatus</i> protein phosphatase PpzA is involved in iron assimilation, secondary metabolite production, and virulence. <i>Cellular Microbiology</i> , 2017, 19, e12770.	2.1	72
20	Physiological and transcriptional analyses of developmental stages along sugarcane leaf. <i>BMC Plant Biology</i> , 2015, 15, 300.	3.6	64
21	Transcriptome and secretome analysis of <i>Aspergillus fumigatus</i> in the presence of sugarcane bagasse. <i>BMC Genomics</i> , 2018, 19, 232.	2.8	60
22	ploidyNGS: visually exploring ploidy with Next Generation Sequencing data. <i>Bioinformatics</i> , 2017, 33, 2575-2576.	4.1	54
23	Genome-wide transcriptome analysis of <i>Aspergillus fumigatus</i> exposed to osmotic stress reveals regulators of osmotic and cell wall stresses that are SakA ^{HOG1} and MpkC dependent. <i>Cellular Microbiology</i> , 2017, 19, e12681.	2.1	52
24	Analysis of autotrophic, mixotrophic and heterotrophic phenotypes in the microalgae <i>Chlorella vulgaris</i> using time-resolved proteomics and transcriptomics approaches. <i>Algal Research</i> , 2020, 51, 102060.	4.6	44
25	RNAseq reveals hydrophobins that are involved in the adaptation of <i>Aspergillus nidulans</i> to lignocellulose. <i>Biotechnology for Biofuels</i> , 2016, 9, 145.	6.2	43
26	Draft genome sequencing of the sugarcane hybrid SP80-3280. <i>F1000Research</i> , 2017, 6, 861.	1.6	43
27	On and Under the Skin: Emerging Basidiomycetous Yeast Infections Caused by <i>Trichosporon</i> Species. <i>PLoS Pathogens</i> , 2015, 11, e1004982.	4.7	42
28	GabiPD: the GABI primary database—a plant integrative 'omics' database. <i>Nucleic Acids Research</i> , 2009, 37, D954-D959.	14.5	40
29	Gene Co-expression Network Reveals Potential New Genes Related to Sugarcane Bagasse Degradation in <i>Trichoderma reesei</i> RUT-30. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018, 6, 151.	4.1	36
30	Annotation of a hybrid partial genome of the coffee rust (<i>Hemileia vastatrix</i>) contributes to the gene repertoire catalog of the Pucciniales. <i>Frontiers in Plant Science</i> , 2014, 5, 594.	3.6	34
31	A step-by-step protocol for formaldehyde-assisted isolation of regulatory elements from <i>Arabidopsis thaliana</i> . <i>Journal of Integrative Plant Biology</i> , 2014, 56, 527-538.	8.5	34
32	The <i>Aspergillus fumigatus</i> SchA ^{SCH9} kinase modulates SakA ^{HOG1} MAP kinase activity and it is essential for virulence. <i>Molecular Microbiology</i> , 2016, 102, 642-671.	2.5	33
33	Targeted metatranscriptomics of compost-derived consortia reveals a GH11 exerting an unusual exo-1,4- β -xylanase activity. <i>Biotechnology for Biofuels</i> , 2017, 10, 254.	6.2	30
34	Thermal adaptation strategies of the extremophile bacterium <i>Thermus filiformis</i> based on multi-omics analysis. <i>Extremophiles</i> , 2017, 21, 775-788.	2.3	27
35	Draft Genome Sequence of <i>Komagataeibacter rhaeticus</i> Strain AF1, a High Producer of Cellulose, Isolated from Kombucha Tea. <i>Genome Announcements</i> , 2014, 2, .	0.8	24
36	Proteome-wide survey of phosphorylation patterns affected by nuclear DNA polymorphisms in <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2010, 11, 411.	2.8	21

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37	Biochemical characterization of an endoxylanase from <i>Pseudozyma brasiliensis</i> sp. nov. strain GHG001 isolated from the intestinal tract of Chrysomelidae larvae associated to sugarcane roots. <i>Process Biochemistry</i> , 2014, 49, 77-83.	3.7	21
38	The low affinity glucose transporter HxtB is also involved in glucose signalling and metabolism in <i>Aspergillus nidulans</i> . <i>Scientific Reports</i> , 2017, 7, 45073.	3.3	20
39	Gene regulatory networks on transfer entropy (GRNTE): a novel approach to reconstruct gene regulatory interactions applied to a case study for the plant pathogen <i>Phytophthora infestans</i> . <i>Theoretical Biology and Medical Modelling</i> , 2019, 16, 7.	2.1	20
40	Orphan transcripts in <i>Arabidopsis thaliana</i> : identification of several hundred previously unrecognized genes. <i>Plant Journal</i> , 2005, 43, 205-212.	5.7	19
41	Structural and functional characterization of a highly secreted β -l-arabinofuranosidase (GH62) from <i>Aspergillus nidulans</i> grown on sugarcane bagasse. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1758-1769.	2.3	19
42	Draft Genome Sequence of <i>Pseudozyma brasiliensis</i> sp. nov. Strain GHG001, a High Producer of Endo-1,4-Xylanase Isolated from an Insect Pest of Sugarcane. <i>Genome Announcements</i> , 2013, 1, .	0.8	17
43	<i>Pseudozyma brasiliensis</i> sp. nov., a xylanolytic, ustilaginomycetous yeast species isolated from an insect pest of sugarcane roots. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 2159-2168.	1.7	17
44	The nuclear proteome of the green alga <i>Chlamydomonas reinhardtii</i> . <i>Proteomics</i> , 2012, 12, 95-100.	2.2	16
45	Analysis of Sensitive CO ₂ Pathways and Genes Related to Carbon Uptake and Accumulation in <i>Chlamydomonas reinhardtii</i> through Genomic Scale Modeling and Experimental Validation. <i>Frontiers in Plant Science</i> , 2016, 7, 43.	3.6	16
46	The sugarcane mitochondrial genome: assembly, phylogenetics and transcriptomics. <i>PeerJ</i> , 2019, 7, e7558.	2.0	15
47	Genome-Wide Identification of Regulatory Elements and Reconstruction of Gene Regulatory Networks of the Green Alga <i>Chlamydomonas reinhardtii</i> under Carbon Deprivation. <i>PLoS ONE</i> , 2013, 8, e79909.	2.5	14
48	Identification, classification and transcriptional profiles of dirigent domain-containing proteins in sugarcane. <i>Molecular Genetics and Genomics</i> , 2017, 292, 1323-1340.	2.1	14
49	Analysis of NAC Domain Transcription Factor Genes of <i>Tectona grandis</i> L.f. Involved in Secondary Cell Wall Deposition. <i>Genes</i> , 2020, 11, 20.	2.4	14
50	Identification of Transcription Factor Genes and Their Correlation with the High Diversity of Stramenopiles. <i>PLoS ONE</i> , 2014, 9, e111841.	2.5	12
51	Draft Genome Sequence of <i>Saccharomyces cerevisiae</i> Barra Grande (BG-1), a Brazilian Industrial Bioethanol-Producing Strain. <i>Genome Announcements</i> , 2017, 5, .	0.8	12
52	Genome sequence of the H ₂ -producing <i>Clostridium beijerinckii</i> strain Br21 isolated from a sugarcane vinasse treatment plant. <i>Genetics and Molecular Biology</i> , 2019, 42, 139-144.	1.3	12
53	A Reductionist Approach Using Primary and Metastatic Cell-Derived Extracellular Vesicles Reveals Hub Proteins Associated with Oral Cancer Prognosis. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100118.	3.8	12
54	Draft Genome Sequence of <i>Komagataeibacter intermedius</i> Strain AF2, a Producer of Cellulose, Isolated from Kombucha Tea. <i>Genome Announcements</i> , 2015, 3, .	0.8	11

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55	Overexpression of a Sugarcane BAHD Acyltransferase Alters Hydroxycinnamate Content in Maize Cell Wall. <i>Frontiers in Plant Science</i> , 2021, 12, 626168.	3.6	11
56	Shedding Light on the Dynamic Role of the “Target of Rapamycin” Kinase in the Fast-Growing C4 Species <i>Setaria viridis</i> , a Suitable Model for Biomass Crops. <i>Frontiers in Plant Science</i> , 2021, 12, 637508.	3.6	10
57	Chromosome 10 in the tomato plant carries clusters of genes responsible for field resistance/defence to <i>Phytophthora infestans</i> . <i>Genomics</i> , 2013, 101, 249-255.	2.9	7
58	Draft genome sequence of <i>Wickerhamomyces anomalus</i> LBCM1105, isolated from cachaça fermentation. <i>Genetics and Molecular Biology</i> , 2020, 43, e20190122.	1.3	7
59	Genome-wide sequencing and metabolic annotation of <i>Pythium irregulare</i> CBS 494.86: understanding Eicosapentaenoic acid production. <i>BMC Biotechnology</i> , 2019, 19, 41.	3.3	6
60	Revealing the high variability on nonconserved core and mobile elements of <i>Austropuccinia psidii</i> and other rust mitochondrial genomes. <i>PLoS ONE</i> , 2021, 16, e0248054.	2.5	5
61	Genomic and transcriptomic resources for candidate gene discovery in the Ranunculids. <i>Applications in Plant Sciences</i> , 2021, 9, e11407.	2.1	4
62	Draft Genome Sequence of the Thermophile <i>Thermus filiformis</i> ATCC 43280, Producer of Carotenoid-(Di)glucoside-Branched Fatty Acid (Di)esters and Source of Hyperthermostable Enzymes of Biotechnological Interest. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
63	Draft Genome Sequences of <i>Clostridium</i> Strains Native to Colombia with the Potential To Produce Solvents. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
64	PlnTFDB: Plant Transcription Factor Database “ Update. <i>Nature Precedings</i> , 0, , .	0.1	2
65	Infection by <i>Moniliophthora perniciosa</i> reprograms tomato Micro-Tom physiology, establishes a sink, and increases secondary cell wall synthesis. <i>Journal of Experimental Botany</i> , 2022, 73, 3651-3670.	4.8	2
66	Bioinformatic analyses to uncover genes involved in trehalose metabolism in the polyploid sugarcane. <i>Scientific Reports</i> , 2022, 12, 7516.	3.3	2
67	Editorial: Advances in Microalgae Biology and Sustainable Applications. <i>Frontiers in Plant Science</i> , 2016, 7, 1385.	3.6	1
68	Evolutionary history of the group formerly known as protists using a phylogenomics approach. <i>Revista De La Academia Colombiana De Ciencias Exactas, Fisicas Y Naturales</i> , 2016, 40, 147.	0.2	1
69	The Hologenome of <i>Haliclona fulva</i> (Porifera, Demospongiae) Reveals an Abundant and Diverse Viral Community. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	1
70	High-quality genome assembly of <i>Pseudocercospora ulei</i> the main threat to natural rubber trees. <i>Genetics and Molecular Biology</i> , 2022, 45, e50510051.	1.3	1
71	PlnTFDB: Plant Transcription Factor Database “ Update. <i>Nature Precedings</i> , 2007, , .	0.1	0
72	Plant Transcription Factors @ uni-potsdam.de. <i>Nature Precedings</i> , 2007, , .	0.1	0

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73	GabiPD: Gabi Primary Database - a plant integrative 'omics' database in GABI-FUTURE. Nature Precedings, 2008, , .	0.1	0
74	GabiPD: The GABI Primary Database - a plant integrative 'omics' database. Nature Precedings, 2008, , .	0.1	0
75	GabiPD: GABI primary database - a plant integrative 'omics' database. Nature Precedings, 2008, , .	0.1	0
76	The GABI Primary Database: GABIPD - Integration of Plant 'Omics'-Data in Gene Context. Nature Precedings, 2009, , .	0.1	0
77	Molecular evolution of RRM-containing proteins and glycine-rich RNA-binding proteins in plants. Nature Precedings, 2011, , .	0.1	0
78	Identification of transcription regulation associated proteins in plants and stramenopiles. Nature Precedings, 2012, , .	0.1	0
79	FAIRE-seq data analysis of Chlamydomonas reinhardtii under carbon deprivation. Nature Precedings, 2012, , .	0.1	0
80	Abstract 5649: Multi-omics data indicate that primary and lymph node oral cancer cells-derived extracellular vesicles carry cargo molecules with a specific aggressive pattern. , 2018, , .		0
81	ContFree-NGS: Removing Reads from Contaminating Organisms in Next Generation Sequencing Data. Lecture Notes in Computer Science, 2021, , 65-68.	1.3	0
82	Modern Approaches for Transcriptome Analyses in Plants. Advances in Experimental Medicine and Biology, 2021, 1346, 11-50.	1.6	0
83	The GABI Primary Database: GABIPD ' Integration of Plant 'Omics'-Data in Gene Context. Nature Precedings, 0, , .	0.1	0