

CALabate

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1105200/publications.pdf>

Version: 2024-02-01

67
papers

2,169
citations

185998

28
h-index

243296

44
g-index

71
all docs

71
docs citations

71
times ranked

3045
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	1.1	5
2	Targeted Metabolic Profiles of the Leaves and Xylem Sap of Two Sugarcane Genotypes Infected with the Vascular Bacterial Pathogen <i>Leifsonia xyli</i> subsp. <i>xyli</i> . <i>Metabolites</i> , 2021, 11, 234.	1.3	6
3	Light-stimulated <i>T. thermophilus</i> two-domain LPMO9H: Low-resolution SAXS model and synergy with cellulases. <i>Carbohydrate Polymers</i> , 2021, 260, 117814.	5.1	14
4	The pentose phosphate pathway constitutes a major metabolic hub in pathogenic <i>Francisella</i> . <i>PLoS Pathogens</i> , 2021, 17, e1009326.	2.1	16
5	Proteomics Reveals an Increase in the Abundance of Glycolytic and Ethanolic Fermentation Enzymes in Developing Sugarcane Culms During Sucrose Accumulation. <i>Frontiers in Plant Science</i> , 2021, 12, 716964.	1.7	4
6	A simple enzymatic assay for the quantification of C1-specific cellulose oxidation by lytic polysaccharide monooxygenases. <i>Biotechnology Letters</i> , 2020, 42, 93-102.	1.1	18
7	Network Analysis Combining Proteomics and Metabolomics Reveals New Insights Into Early Responses of <i>Eucalyptus grandis</i> During Rust Infection. <i>Frontiers in Plant Science</i> , 2020, 11, 604849.	1.7	12
8	Plant Cell Wall Proteomics: A Focus on Monocot Species, <i>Brachypodium distachyon</i> , <i>Saccharum</i> spp. and <i>Oryza sativa</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 1975.	1.8	53
9	A systems biology view of wood formation in <i>Eucalyptus grandis</i> trees submitted to different potassium and water regimes. <i>New Phytologist</i> , 2019, 223, 766-782.	3.5	48
10	Sugarcane must fed-batch fermentation by <i>Saccharomyces cerevisiae</i> : impact of sterilized and non-sterilized sugarcane must. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 1177-1187.	0.7	2
11	Network Analyses and Data Integration of Proteomics and Metabolomics From Leaves of Two Contrasting Varieties of Sugarcane in Response to Drought. <i>Frontiers in Plant Science</i> , 2019, 10, 1524.	1.7	41
12	<i>Spiroplasma</i> affects host aphid proteomics feeding on two nutritional resources. <i>Scientific Reports</i> , 2018, 8, 2466.	1.6	9
13	Cell Wall Proteome of Sugarcane Young and Mature Leaves and Stems. <i>Proteomics</i> , 2018, 18, 1700129.	1.3	14
14	Hyper response to ovarian stimulation affects the follicular fluid metabolomic profile of women undergoing IVF similarly to polycystic ovary syndrome. <i>Metabolomics</i> , 2018, 14, 51.	1.4	17
15	Development of a quantitative real-time PCR assay using SYBR Green for early detection and quantification of <i>Austropuccinia psidii</i> in <i>Eucalyptus grandis</i> . <i>European Journal of Plant Pathology</i> , 2018, 150, 735-746.	0.8	32
16	Glycoside Hydrolases in Plant Cell Wall Proteomes: Predicting Functions That Could Be Relevant for Improving Biomass Transformation Processes. , 2018, , .		6
17	The <i>Eucalyptus</i> Cuticular Waxes Contribute in Preformed Defense Against <i>Austropuccinia psidii</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1978.	1.7	47
18	Metabolomic profiling in follicular fluid of patients with infertility-related deep endometriosis. <i>Metabolomics</i> , 2017, 13, 1.	1.4	6

#	ARTICLE	IF	CITATIONS
19	Characterization of the contaminant bacterial communities in sugarcane first-generation industrial ethanol production. <i>FEMS Microbiology Letters</i> , 2017, 364, .	0.7	20
20	Metabolome Dynamics of Smutted Sugarcane Reveals Mechanisms Involved in Disease Progression and Whip Emission. <i>Frontiers in Plant Science</i> , 2017, 8, 882.	1.7	40
21	Seasonal Variation of Carbon Metabolism in the Cambial Zone of <i>Eucalyptus grandis</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 932.	1.7	8
22	Proteomic profiling identifies <i>N</i> -acetylmuramoyl-alanine amidase as a novel biomarker of sepsis. <i>Biomarkers in Medicine</i> , 2016, 10, 1225-1229.	0.6	5
23	Integrated analysis of gene expression from carbon metabolism, proteome and metabolome, reveals altered primary metabolism in <i>Eucalyptus grandis</i> bark, in response to seasonal variation. <i>BMC Plant Biology</i> , 2016, 16, 149.	1.6	28
24	Metabolic profiles of planktonic and biofilm cells of <i>Candida orthopsilosis</i> . <i>Future Microbiology</i> , 2016, 11, 1299-1313.	1.0	7
25	Differentially Accumulated Proteins in <i>Coffea arabica</i> Seeds during Perisperm Tissue Development and Their Relationship to Coffee Grain Size. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 1635-1647.	2.4	9
26	Proteomic response of the phytopathogen <i>Phyllosticta citricarpa</i> to antimicrobial volatile organic compounds from <i>Saccharomyces cerevisiae</i> . <i>Microbiological Research</i> , 2016, 183, 1-7.	2.5	22
27	Comparative Proteome Analysis of the Tuberous Roots of Six Cassava (<i>Manihot esculenta</i>) Varieties Reveals Proteins Related to Phenotypic Traits. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 3293-3301.	2.4	11
28	Cell wall proteome of sugarcane stems: comparison of a destructive and a non-destructive extraction method showed differences in glycoside hydrolases and peroxidases. <i>BMC Plant Biology</i> , 2016, 16, 14.	1.6	29
29	Label-Free Quantitative Proteomic Analysis of <i>Puccinia psidii</i> Uredospores Reveals Differences of Fungal Populations Infecting <i>Eucalyptus</i> and <i>Guava</i> . <i>PLoS ONE</i> , 2016, 11, e0145343.	1.1	18
30	Physiological and transcriptional analyses of developmental stages along sugarcane leaf. <i>BMC Plant Biology</i> , 2015, 15, 300.	1.6	64
31	Prospection and Evaluation of (Hemi) Cellulolytic Enzymes Using Untreated and Pretreated Biomasses in Two Argentinean Native Termites. <i>PLoS ONE</i> , 2015, 10, e0136573.	1.1	24
32	Proteomics and Metabolomics as Large-Scale Phenotyping Tools. , 2015, , 125-139.		1
33	Alterations of protein expression in conditions of copper-deprivation for <i>Paracoccidioides lutzii</i> in the presence of extracellular matrix components. <i>BMC Microbiology</i> , 2014, 14, 302.	1.3	23
34	ProbMetab: an <i>R</i> package for Bayesian probabilistic annotation of LC-MS-based metabolomics. <i>Bioinformatics</i> , 2014, 30, 1336-1337.	1.8	51
35	Cell wall proteomics of sugarcane cell suspension cultures. <i>Proteomics</i> , 2014, 14, 738-749.	1.3	55
36	Genetic Variability in <i>Puccinia psidii</i> Populations as Revealed by PCR-DGGE and T-RFLP Markers. <i>Plant Disease</i> , 2014, 98, 16-23.	0.7	9

#	ARTICLE	IF	CITATIONS
37	Heat shock and structural proteins associated with meat tenderness in Nellore beef cattle, a <i>Bos indicus</i> breed. <i>Meat Science</i> , 2014, 96, 1318-1324.	2.7	79
38	Evaluating the composition and processing potential of novel sources of Brazilian biomass for sustainable biorenewables production. <i>Biotechnology for Biofuels</i> , 2014, 7, 10.	6.2	87
39	Effects of pretreatment on morphology, chemical composition and enzymatic digestibility of eucalyptus bark: a potentially valuable source of fermentable sugars for biofuel production – part 1. <i>Biotechnology for Biofuels</i> , 2013, 6, 75.	6.2	108
40	Relationship between N, P, and K and the quality and stem structural characteristics of <i>Caesalpinia echinata</i> Lam. plants. <i>Trees - Structure and Function</i> , 2013, 27, 1477-1484.	0.9	9
41	A simple protocol for whole leaf preparation to investigate the interaction between <i>Puccinia psidii</i> and <i>Eucalyptus grandis</i> . <i>Australasian Plant Pathology</i> , 2013, 42, 79-84.	0.5	26
42	Renal Proteome in Mice with Different Susceptibilities to Fluorosis. <i>PLoS ONE</i> , 2013, 8, e53261.	1.1	21
43	Characterization of a <i>Toxoneuron nigriceps</i> (Viereck) (Hymenoptera: Braconidae) – derived chitinase and its potential for pest control. <i>Pesticide Biochemistry and Physiology</i> , 2012, 104, 96-102.	1.6	9
44	Proteomic analysis of <i>Porphyromonas gingivalis</i> exposed to nicotine and cotinine. <i>Journal of Periodontal Research</i> , 2012, 47, 766-775.	1.4	14
45	Proteomic analysis of papaya fruit ripening using 2DE-DIGE. <i>Journal of Proteomics</i> , 2012, 75, 1428-1439.	1.2	78
46	Germination, carbohydrate composition and vigor of cryopreserved <i>Caesalpinia echinata</i> seeds. <i>Brazilian Archives of Biology and Technology</i> , 2012, 55, 661-669.	0.5	6
47	Analysis of the biofilm proteome of <i>Xylella fastidiosa</i> . <i>Proteome Science</i> , 2011, 9, 58.	0.7	25
48	Cloning and endogenous expression of a <i>Eucalyptus grandis</i> UDP-glucose dehydrogenase cDNA. <i>Genetics and Molecular Biology</i> , 2010, 33, 686-695.	0.6	7
49	Expression of <i>Xylella fastidiosa</i> Fimbrial and Afimbrial Proteins during Biofilm Formation. <i>Applied and Environmental Microbiology</i> , 2010, 76, 4250-4259.	1.4	62
50	Phosphoproteomics Profiling Suggests a Role for Nuclear β -TMK in Transcription Processes of Undifferentiated Murine Embryonic Stem Cells. <i>Journal of Proteome Research</i> , 2010, 9, 6191-6206.	1.8	12
51	Bacterial community in the rhizosphere and rhizoplane of wild type and transgenic eucalyptus. <i>World Journal of Microbiology and Biotechnology</i> , 2009, 25, 1065-1073.	1.7	20
52	Culture-Independent Assessment of Rhizobiales-Related Alphaproteobacteria and the Diversity of <i>Methylobacterium</i> in the Rhizosphere and Rhizoplane of Transgenic Eucalyptus. <i>Microbial Ecology</i> , 2009, 57, 82-93.	1.4	44
53	Transgenic tobacco revealing altered bacterial diversity in the rhizosphere during early plant development. <i>Antonie Van Leeuwenhoek</i> , 2008, 93, 415-424.	0.7	53
54	SAGE transcript profiling of the juvenile cambial region of <i>Eucalyptus grandis</i> . <i>Tree Physiology</i> , 2008, 28, 905-919.	1.4	31

#	ARTICLE	IF	CITATIONS
55	Comparison of the expression profiles of susceptible and resistant <i>Eucalyptus grandis</i> exposed to <i>Puccinia psidii</i> Winter using SAGE. <i>Functional Plant Biology</i> , 2007, 34, 1010.	1.1	36
56	Proteomic analysis of the cambial region in juvenile <i>Eucalyptus grandis</i> at three ages. <i>Proteomics</i> , 2007, 7, 2258-2274.	1.3	51
57	Brazilian coffee genome project: an EST-based genomic resource. <i>Brazilian Journal of Plant Physiology</i> , 2006, 18, 95-108.	0.5	112
58	Constitutive expression of pea Lhcb 1?2 in tobacco affects plant development, morphology and photosynthetic capacity. <i>Plant Molecular Biology</i> , 2004, 55, 701-714.	2.0	34
59	Production of transgenic <i>Eucalyptus grandis</i> x <i>E. urophylla</i> using the sonication-assisted <i>Agrobacterium</i> transformation (SAAT) system. <i>Functional Plant Biology</i> , 2002, 29, 97.	1.1	32
60	Symptomless infection of banana and maize by endophytic fungi impairs photosynthetic efficiency. <i>New Phytologist</i> , 2000, 147, 609-615.	3.5	117
61	Targeting of the soybean leghemoglobin to tobacco chloroplasts: effects on aerobic metabolism in transgenic plants. <i>Plant Science</i> , 2000, 155, 193-202.	1.7	27
62	Factors influencing the capacity for photosynthetic carbon assimilation in barley leaves at low temperatures. <i>Planta</i> , 1990, 182, 492-500.	1.6	8
63	Effects of temperature on the regulation of photosynthetic carbon assimilation in leaves of maize and barley. <i>Planta</i> , 1990, 181, 547-54.	1.6	81
64	Influence of Low Temperature on Respiration and Contents of Phosphorylated Intermediates in Darkened Barley Leaves. <i>Plant Physiology</i> , 1989, 91, 905-910.	2.3	32
65	Limitation of photosynthesis by changes in temperature. <i>Planta</i> , 1988, 173, 519-527.	1.6	114
66	Phosphate sequestration by glycerol and its effects on photosynthetic carbon assimilation by leaves. <i>Planta</i> , 1988, 176, 117-126.	1.6	44
67	Proline Exogenously Supplied or Endogenously Overproduced Induces Different Nutritional, Metabolic, and Antioxidative Responses in Transgenic Tobacco Exposed to Cadmium. <i>Journal of Plant Growth Regulation</i> , 0, , 1.	2.8	8