

Maria Victoria Aguilar-Pontes

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

866
citations

623699

14
h-index

580810

25
g-index

26
all docs

26
docs citations

26
times ranked

912
citing authors

#	ARTICLE	IF	CITATIONS
1	Regulators of plant biomass degradation in ascomycetous fungi. <i>Biotechnology for Biofuels</i> , 2017, 10, 152.	6.2	202
2	Diversity of fungal feruloyl esterases: updated phylogenetic classification, properties, and industrial applications. <i>Biotechnology for Biofuels</i> , 2016, 9, 231.	6.2	133
3	The transcriptional activator GaaR of <i>Aspergillus niger</i> is required for release and utilization of galacturonic acid from pectin. <i>FEBS Letters</i> , 2016, 590, 1804-1815.	2.8	64
4	The gold-standard genome of <i>Aspergillus niger</i> NRRL 3 enables a detailed view of the diversity of sugar catabolism in fungi. <i>Studies in Mycology</i> , 2018, 91, 61-78.	7.2	62
5	The molecular response of the white-rot fungus <i>Dichomitus squalens</i> to wood and non-woody biomass as examined by transcriptome and exoproteome analyses. <i>Environmental Microbiology</i> , 2017, 19, 1237-1250.	3.8	55
6	In Silico Analysis of Putative Sugar Transporter Genes in <i>Aspergillus niger</i> Using Phylogeny and Comparative Transcriptomics. <i>Frontiers in Microbiology</i> , 2018, 9, 1045.	3.5	47
7	Comparative analysis of basidiomycete transcriptomes reveals a core set of expressed genes encoding plant biomass degrading enzymes. <i>Fungal Genetics and Biology</i> , 2018, 112, 40-46.	2.1	42
8	ARA1 regulates not only arabinose but also galactose catabolism in <i>Trichoderma reesei</i> . <i>FEBS Letters</i> , 2018, 592, 60-70.	2.8	37
9	The pathway intermediate 2-keto-3-deoxy-L-galactonate mediates the induction of genes involved in galacturonic acid utilization in <i>Aspergillus niger</i> . <i>FEBS Letters</i> , 2017, 591, 1408-1418.	2.8	25
10	The fungus <i>Aspergillus niger</i> consumes sugars in a sequential manner that is not mediated by the carbon catabolite repressor CreA. <i>Scientific Reports</i> , 2018, 8, 6655.	3.3	24
11	Temporal transcriptome analysis of the white-rot fungus <i>Obba rivulosa</i> shows expression of a constitutive set of plant cell wall degradation targeted genes during growth on solid spruce wood. <i>Fungal Genetics and Biology</i> , 2018, 112, 47-54.	2.1	21
12	A community-driven reconstruction of the <i>Aspergillus niger</i> metabolic network. <i>Fungal Biology and Biotechnology</i> , 2018, 5, 16.	5.1	20
13	In vivo functional analysis of L-rhamnose metabolic pathway in <i>Aspergillus niger</i> : a tool to identify the potential inducer of RhaR. <i>BMC Microbiology</i> , 2017, 17, 214.	3.3	18
14	(Post-)Genomics approaches in fungal research. <i>Briefings in Functional Genomics</i> , 2014, 13, 424-439.	2.7	16
15	CreA-mediated repression of gene expression occurs at low monosaccharide levels during fungal plant biomass conversion in a time and substrate dependent manner. <i>Cell Surface</i> , 2021, 7, 100050.	3.0	16
16	Blocking hexose entry into glycolysis activates alternative metabolic conversion of these sugars and upregulates pentose metabolism in <i>Aspergillus nidulans</i> . <i>BMC Genomics</i> , 2018, 19, 214.	2.8	11
17	Enzymatic Adaptation of <i>Podospora anserina</i> to Different Plant Biomass Provides Leads to Optimized Commercial Enzyme Cocktails. <i>Biotechnology Journal</i> , 2019, 14, 1800185.	3.5	11
18	Identification of a gene encoding the last step of the L-rhamnose catabolic pathway in <i>Aspergillus niger</i> revealed the inducer of the pathway regulator. <i>Microbiological Research</i> , 2020, 234, 126426.	5.3	11

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19	Deletion of either the regulatory gene <i>ara1</i> or metabolic gene <i>xki1</i> in <i>Trichoderma reesei</i> leads to increased CAZyme gene expression on crude plant biomass. <i>Biotechnology for Biofuels</i> , 2019, 12, 81.	6.2	10
20	Revisiting a "simple" fungal metabolic pathway reveals redundancy, complexity and diversity. <i>Microbial Biotechnology</i> , 2021, 14, 2525-2537.	4.2	10
21	The physiology of <i>Agaricus bisporus</i> in semi-commercial compost cultivation appears to be highly conserved among unrelated isolates. <i>Fungal Genetics and Biology</i> , 2018, 112, 12-20.	2.1	9
22	Sexual crossing of thermophilic fungus <i>Myceliophthora heterothallica</i> improved enzymatic degradation of sugar beet pulp. <i>Biotechnology for Biofuels</i> , 2016, 9, 41.	6.2	6
23	l-Arabinose induces d-galactose catabolism via the Leloir pathway in <i>Aspergillus nidulans</i> . <i>Fungal Genetics and Biology</i> , 2019, 123, 53-59.	2.1	6
24	Transcriptome analysis of <i>Aspergillus niger</i> <i>xlnR</i> and <i>xkiA</i> mutants grown on corn Stover and soybean hulls reveals a highly complex regulatory network. <i>BMC Genomics</i> , 2019, 20, 853.	2.8	5
25	Characterization of d-xylose reductase, <i>XyrB</i> , from <i>Aspergillus niger</i> . <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2021, 30, e00610.	4.4	5
26	Metabolic Modeling of Fungi. , 2021, , 394-405.		0