

Barbara Montanini

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4990530/publications.pdf>

Version: 2024-02-01

43
papers

8,074
citations

236612

25
h-index

243296

44
g-index

45
all docs

45
docs citations

45
times ranked

10773
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genome of Black Cottonwood, <i>Populus trichocarpa</i> (Torr. & Gray). <i>Science</i> , 2006, 313, 1596-1604.	6.0	3,945
2	The genome of <i>Laccaria bicolor</i> provides insights into mycorrhizal symbiosis. <i>Nature</i> , 2008, 452, 88-92.	13.7	1,003
3	PA ^o rigord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. <i>Nature</i> , 2010, 464, 1033-1038.	13.7	641
4	Phylogenetic and functional analysis of the Cation Diffusion Facilitator (CDF) family: improved signature and prediction of substrate specificity. <i>BMC Genomics</i> , 2007, 8, 107.	1.2	353
5	Eukaryotic snoRNAs: A paradigm for gene expression flexibility. <i>Genomics</i> , 2009, 94, 83-88.	1.3	278
6	Targeting mitochondrial dysfunction can restore antiviral activity of exhausted HBV-specific CD8 T cells in chronic hepatitis B. <i>Nature Medicine</i> , 2017, 23, 327-336.	15.2	251
7	A secretory pathway-localized cation diffusion facilitator confers plant manganese tolerance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 8532-8537.	3.3	250
8	The expanded family of ammonium transporters in the perennial poplar plant. <i>New Phytologist</i> , 2007, 174, 137-150.	3.5	182
9	In vivo targeting of de novo DNA methylation by histone modifications in yeast and mouse. <i>ELife</i> , 2015, 4, e06205.	2.8	146
10	Genome-wide analysis of plant metal transporters, with an emphasis on poplar. <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 3763-3784.	2.4	111
11	Peizomyces genomes reveal the molecular basis of ectomycorrhizal truffle lifestyle. <i>Nature Ecology and Evolution</i> , 2018, 2, 1956-1965.	3.4	95
12	Transcriptomic Analysis of Human Polarized Macrophages: More than One Role of Alternative Activation?. <i>PLoS ONE</i> , 2015, 10, e0119751.	1.1	70
13	Non-exhaustive DNA methylation-mediated transposon silencing in the black truffle genome, a complex fungal genome with massive repeat element content. <i>Genome Biology</i> , 2014, 15, 411.	3.8	67
14	The anti-HIV cyanovirin-N domain is evolutionarily conserved and occurs as a protein module in eukaryotes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 670-678.	1.5	62
15	A high-affinity ammonium transporter from the mycorrhizal ascomycete <i>Tuber borchii</i> . <i>Fungal Genetics and Biology</i> , 2002, 36, 22-34.	0.9	61
16	Functional properties and differential mode of regulation of the nitrate transporter from a plant symbiotic ascomycete. <i>Biochemical Journal</i> , 2006, 394, 125-134.	1.7	48
17	Structure-Function Analysis of a CVNH-LysM Lectin Expressed during Plant Infection by the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>Structure</i> , 2011, 19, 662-674.	1.6	47
18	A metaproteomic approach dissecting major bacterial functions in the rhizosphere of plants living in serpentine soil. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 2327-2339.	1.9	46

#	ARTICLE	IF	CITATIONS
19	Distinctive properties and expression profiles of glutamine synthetase from a plant symbiotic fungus. <i>Biochemical Journal</i> , 2003, 373, 357-368.	1.7	44
20	Targeting p53 and histone methyltransferases restores exhausted CD8+ T cells in HCV infection. <i>Nature Communications</i> , 2020, 11, 604.	5.8	44
21	Ability of <i>Bifidobacterium breve</i> To Grow on Different Types of Milk: Exploring the Metabolism of Milk through Genome Analysis. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7408-7417.	1.4	42
22	Genome-wide search and functional identification of transcription factors in the mycorrhizal fungus <i>Tuber melanosporum</i> . <i>New Phytologist</i> , 2011, 189, 736-750.	3.5	35
23	Transcript Profiling Reveals Novel Marker Genes Involved in Fruiting Body Formation in <i>Tuber borchii</i> . <i>Eukaryotic Cell</i> , 2005, 4, 1599-1602.	3.4	30
24	Gene expression profiling of the nitrogen starvation stress response in the mycorrhizal ascomycete <i>Tuber borchii</i> . <i>Fungal Genetics and Biology</i> , 2006, 43, 630-641.	0.9	28
25	Global Genome Transcription Profiling of <i>Bifidobacterium bifidum</i> PRL2010 under <i>In Vitro</i> Conditions and Identification of Reference Genes for Quantitative Real-Time PCR. <i>Applied and Environmental Microbiology</i> , 2011, 77, 8578-8587.	1.4	27
26	Biostimulants applied to maize seeds modulate the enzymatic activity and metaproteome of the rhizosphere. <i>Applied Soil Ecology</i> , 2020, 148, 103480.	2.1	25
27	A threonine synthase homolog from a mammalian genome. <i>Biochemical and Biophysical Research Communications</i> , 2006, 350, 922-928.	1.0	15
28	Screening for Protein-Protein Interaction Inhibitors Using a Bioluminescence Resonance Energy Transfer (BRET)-Based Assay in Yeast. <i>SLAS Discovery</i> , 2017, 22, 751-759.	1.4	14
29	Tapping Genomics to Unravel Ectomycorrhizal Symbiosis. <i>Methods in Molecular Biology</i> , 2011, 722, 249-281.	0.4	11
30	Identification of an early transcriptomic signature of insulin resistance and related diseases in lymphomonocytes of healthy subjects. <i>PLoS ONE</i> , 2017, 12, e0182559.	1.1	11
31	A comprehensive resource of genomic, epigenomic and transcriptomic sequencing data for the black truffle <i>Tuber melanosporum</i> . <i>GigaScience</i> , 2014, 3, 25.	3.3	10
32	New Antimicrobials Targeting Bacterial RNA Polymerase Holoenzyme Assembly Identified with an <i>In Vivo</i> BRET-Based Discovery Platform. <i>ACS Chemical Biology</i> , 2019, 14, 1727-1736.	1.6	10
33	Alu RNA Modulates the Expression of Cell Cycle Genes in Human Fibroblasts. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3315.	1.8	10
34	Expression of DinJ-YafQ System of <i>Lactobacillus casei</i> Group Strains in Response to Food Processing Stresses. <i>Microorganisms</i> , 2019, 7, 438.	1.6	9
35	Integrative gene transfer in the truffle <i>Tuber borchii</i> by <i>Agrobacterium tumefaciens</i> -mediated transformation. <i>AMB Express</i> , 2014, 4, 43.	1.4	8
36	Moonlighting transcriptional activation function of a fungal sulfur metabolism enzyme. <i>Scientific Reports</i> , 2016, 6, 25165.	1.6	7

#	ARTICLE	IF	CITATIONS
37	A family of archaea-like carboxylesterases preferentially expressed in the symbiotic phase of the mycorrhizal fungus <i>Tuber melanosporum</i> . <i>Scientific Reports</i> , 2017, 7, 7628.	1.6	7
38	Identification and first characterization of DinJ-YafQ toxin-antitoxin systems in <i>Lactobacillus</i> species of biotechnological interest. <i>Scientific Reports</i> , 2019, 9, 7645.	1.6	7
39	Dry and wet approaches for genome-wide functional annotation of conventional and unconventional transcriptional activators. <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 262-270.	1.9	6
40	Virus-Mediated Metalloproteinase 1 Induction Revealed by Transcriptome Profiling of Bovine Herpesvirus 4-Infected Bovine Endometrial Stromal Cells. <i>Biology of Reproduction</i> , 2016, 95, 12-12.	1.2	6
41	Photoreceptors in the dark: A functional white collar-like complex and other putative light-sensing components encoded by the genome of the subterranean fungus <i>Tuber melanosporum</i> . <i>Fungal Biology</i> , 2017, 121, 253-263.	1.1	5
42	An RNA Polymerase III General Transcription Factor Engages in Cell Type-Specific Chromatin Looping. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2260.	1.8	4
43	Interpreting and integrating big data in non-coding RNA research. <i>Emerging Topics in Life Sciences</i> , 2019, 3, 343-355.	1.1	2