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	An RNA Polymerase III General Transcription Factor Engages in Cell Type-Specific Chromatin Looping. International Journal of Molecular Sciences, 2022, 23, 2260.	1.8	4
2	Biostimulants applied to maize seeds modulate the enzymatic activity and metaproteome of the rhizosphere. Applied Soil Ecology, 2020, 148, 103480.	2.1	25
3	Targeting p53 and histone methyltransferases restores exhausted CD8+ T cells in HCV infection. Nature Communications, 2020, 11, 604.	5.8	44
4	New Antimicrobials Targeting Bacterial RNA Polymerase Holoenzyme Assembly Identified with an in Vivo BRET-Based Discovery Platform. ACS Chemical Biology, 2019, 14, 1727-1736.	1.6	10
5	Alu RNA Modulates the Expression of Cell Cycle Genes in Human Fibroblasts. International Journal of Molecular Sciences, 2019, 20, 3315.	1.8	10
6	Expression of DinJ-YafQ System of Lactobacillus casei Group Strains in Response to Food Processing Stresses. Microorganisms, 2019, 7, 438.	1.6	9
7	Identification and first characterization of DinJ-YafQ toxin-antitoxin systems in Lactobacillus species of biotechnological interest. Scientific Reports, 2019, 9, 7645.	1.6	7
8	Interpreting and integrating big data in non-coding RNA research. Emerging Topics in Life Sciences, 2019, 3, 343-355.	1.1	2
9	Pezizomycetes genomes reveal the molecular basis of ectomycorrhizal truffle lifestyle. Nature Ecology and Evolution, 2018, 2, 1956-1965.	3.4	95
10	Photoreceptors in the dark: A functional white collar-like complex and other putative light-sensing components encoded by the genome of the subterranean fungus Tuber melanosporum. Fungal Biology, 2017, 121, 253-263.	1.1	5
11	A metaproteomic approach dissecting major bacterial functions in the rhizosphere of plants living in serpentine soil. Analytical and Bioanalytical Chemistry, 2017, 409, 2327-2339.	1.9	46
12	Targeting mitochondrial dysfunction can restore antiviral activity of exhausted HBV-specific CD8 T cells in chronic hepatitis B. Nature Medicine, 2017, 23, 327-336.	15.2	251
13	Screening for Protein-Protein Interaction Inhibitors Using a Bioluminescence Resonance Energy Transfer (BRET)â€"Based Assay in Yeast. SLAS Discovery, 2017, 22, 751-759.	1.4	14
14	A family of archaea-like carboxylesterases preferentially expressed in the symbiotic phase of the mycorrhizal fungus Tuber melanosporum. Scientific Reports, 2017, 7, 7628.	1.6	7
15	Identification of an early transcriptomic signature of insulin resistance and related diseases in lymphomonocytes of healthy subjects. PLoS ONE, 2017, 12, e0182559.	1.1	11
16	Dry and wet approaches for genome-wide functional annotation of conventional and unconventional transcriptional activators. Computational and Structural Biotechnology Journal, 2016, 14, 262-270.	1.9	6
17	Moonlighting transcriptional activation function of a fungal sulfur metabolism enzyme. Scientific Reports, 2016, 6, 25165.	1.6	7
18	Virus-Mediated Metalloproteinase 1 Induction Revealed by Transcriptome Profiling of Bovine Herpesvirus 4-Infected Bovine Endometrial Stromal Cells. Biology of Reproduction, 2016, 95, 12-12.	1.2	6

#	Article	IF	Citations
19	Transcriptomic Analysis of Human Polarized Macrophages: More than One Role of Alternative Activation?. PLoS ONE, 2015, 10, e0119751.	1.1	70
20	In vivo targeting of de novo DNA methylation by histone modifications in yeast and mouse. ELife, 2015, 4, e06205.	2.8	146
21	A comprehensive resource of genomic, epigenomic and transcriptomic sequencing data for the black truffle Tuber melanosporum. GigaScience, 2014, 3, 25.	3.3	10
22	Non-exhaustive DNA methylation-mediated transposon silencing in the black truffle genome, a complex fungal genome with massive repeat element content. Genome Biology, 2014, 15, 411.	3.8	67
23	Integrative gene transfer in the truffle Tuber borchii by Agrobacterium tumefaciens-mediated transformation. AMB Express, 2014, 4, 43.	1.4	8
24	Tapping Genomics to Unravel Ectomycorrhizal Symbiosis. Methods in Molecular Biology, 2011, 722, 249-281.	0.4	11
25	Genomeâ€wide search and functional identification of transcription factors in the mycorrhizal fungus Tuber melanosporum. New Phytologist, 2011, 189, 736-750.	3.5	35
26	Structure-Function Analysis of a CVNH-LysM Lectin Expressed during Plant Infection by the Rice Blast Fungus Magnaporthe oryzae. Structure, 2011, 19, 662-674.	1.6	47
27	Global Genome Transcription Profiling of Bifidobacterium bifidum PRL2010 under In Vitro Conditions and Identification of Reference Genes for Quantitative Real-Time PCR. Applied and Environmental Microbiology, 2011, 77, 8578-8587.	1.4	27
28	Ability of Bifidobacterium breve To Grow on Different Types of Milk: Exploring the Metabolism of Milk through Genome Analysis. Applied and Environmental Microbiology, 2011, 77, 7408-7417.	1.4	42
29	Genome-wide analysis of plant metal transporters, with an emphasis on poplar. Cellular and Molecular Life Sciences, 2010, 67, 3763-3784.	2.4	111
30	PÃ©rigord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. Nature, 2010, 464, 1033-1038.	13.7	641
31	Eukaryotic snoRNAs: A paradigm for gene expression flexibility. Genomics, 2009, 94, 83-88.	1.3	278
32	The genome of Laccaria bicolor provides insights into mycorrhizal symbiosis. Nature, 2008, 452, 88-92.	13.7	1,003
33	A secretory pathway-localized cation diffusion facilitator confers plant manganese tolerance. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 8532-8537.	3.3	250
34	The expanded family of ammonium transporters in the perennial poplar plant. New Phytologist, 2007, 174, 137-150.	3.5	182
35	Phylogenetic and functional analysis of the Cation Diffusion Facilitator (CDF) family: improved signature and prediction of substrate specificity. BMC Genomics, 2007, 8, 107.	1.2	353
36	Gene expression profiling of the nitrogen starvation stress response in the mycorrhizal ascomycete Tuber borchii. Fungal Genetics and Biology, 2006, 43, 630-641.	0.9	28

#	Article	IF	Citations
37	A threonine synthase homolog from a mammalian genome. Biochemical and Biophysical Research Communications, 2006, 350, 922-928.	1.0	15
38	Functional properties and differential mode of regulation of the nitrate transporter from a plant symbiotic ascomycete. Biochemical Journal, 2006, 394, 125-134.	1.7	48
39	The Genome of Black Cottonwood, Populus trichocarpa (Torr. & Gray). Science, 2006, 313, 1596-1604.	6.0	3,945
40	The anti-HIV cyanovirin-N domain is evolutionarily conserved and occurs as a protein module in eukaryotes. Proteins: Structure, Function and Bioinformatics, 2005, 60, 670-678.	1.5	62
41	Transcript Profiling Reveals Novel Marker Genes Involved in Fruiting Body Formation in Tuber borchii. Eukaryotic Cell, 2005, 4, 1599-1602.	3.4	30
42	Distinctive properties and expression profiles of glutamine synthetase from a plant symbiotic fungus. Biochemical Journal, 2003, 373, 357-368.	1.7	44
43	A high-affinity ammonium transporter from the mycorrhizal ascomycete Tuber borchii. Fungal Genetics and Biology, 2002, 36, 22-34.	0.9	61