Yinbing Bian

List of Publications by Year
in descending order

53 papers	926 citations	535685 17 h-index	591227 27 g-index
53 all docs	53 docs citations	53 times ranked	817 citing authors

#	Article	IF	Citations
1	Population genomics provides insights into the genetic basis of adaptive evolution in the mushroom-forming fungus Lentinula edodes. Journal of Advanced Research, 2022, 38, 91-106.	4.4	16
2	Curing two predominant viruses occurring in Lentinula edodes by chemotherapy and mycelial fragmentation methods. Journal of Virological Methods, 2022, 300, 114370.	1.0	5
3	RNA-Seq-based high-resolution linkage map reveals the genetic architecture of fruiting body development in shiitake mushroom, Lentinula edodes. Computational and Structural Biotechnology Journal, 2021, 19, 1641-1653.	1.9	12
4	Identification of microRNA-like RNAs in Cordyceps guangdongensis and their expression profile under differential developmental stages. Fungal Genetics and Biology, 2021, 147, 103505.	0.9	4
5	Mycoviral diversity and characteristics of a negative-stranded RNA virus LeNSRV1 in the edible mushroom Lentinula edodes. Virology, 2021, 555, 89-101.	1.1	16
6	Enhanced Expression of Thaumatin-like Protein Gene (LeTLP1) Endows Resistance to Trichoderma atroviride in Lentinula edodes. Life, 2021, 11, 863.	1.1	10
7	Biological Characterization and Antagonist Screening of Cladosporium anthropophilum, a Novel Pathogen Causing Stipe Black Rot on Commercial Medicinal Mushroom, Flammulina filiformis (Agaricomycetes). International Journal of Medicinal Mushrooms, 2021, 23, 65-73.	0.9	0
8	Biosynthetic Pathway and the Potential Role of Melatonin at Different Abiotic Stressors and Developmental Stages in Tolypocladium guangdongense. Frontiers in Microbiology, 2021, 12, 746141.	1.5	1
9	Chromosome-Wide Characterization of Intragenic Crossover in Shiitake Mushroom, Lentinula edodes. Journal of Fungi (Basel, Switzerland), 2021, 7, 1076.	1.5	0
10	The mitochondrial genome of Morchella importuna (272.2Âkb) is the largest among fungi and contains numerous introns, mitochondrial non-conserved open reading frames and repetitive sequences. International Journal of Biological Macromolecules, 2020, 143, 373-381.	3.6	63
11	Characterization of Two Mitochondrial Genomes and Gene Expression Analysis Reveal Clues for Variations, Evolution, and Large-Sclerotium Formation in Medical Fungus Wolfiporia cocos. Frontiers in Microbiology, 2020, 11, 1804.	1.5	2
12	Transcriptome and proteome analyses reveal the regulatory networks and metabolite biosynthesis pathways during the development of Tolypocladium guangdongense. Computational and Structural Biotechnology Journal, 2020, 18, 2081-2094.	1.9	14
13	The development of an efficient RNAi system based on Agrobacterium-mediated transformation approach for studying functional genomics in medical fungus Wolfiporia cocos. World Journal of Microbiology and Biotechnology, 2020, 36, 140.	1.7	4
14	Mitogenome of Tolypocladium guangdongense. Applied Microbiology and Biotechnology, 2020, 104, 9295-9308.	1.7	6
15	Expression profiling of Cordyceps DnaJ protein family in Tolypocladium guangdongense during developmental and temperature stress processes. Gene, 2020, 743, 144563.	1.0	4
16	Bioconversion of rice straw agro-residues by Lentinula edodes and evaluation of non-volatile taste compounds in mushrooms. Scientific Reports, 2020, 10, 1814.	1.6	23
17	Subchromosome-Scale Nuclear and Complete Mitochondrial Genome Characteristics of Morchella crassipes. International Journal of Molecular Sciences, 2020, 21, 483.	1.8	27
18	Selection and validation of reliable reference genes for Tolypocladium guangdongense gene expression analysis under differentially developmental stages and temperature stresses. Gene, 2020, 734, 144380.	1.0	12

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19	Hsp40 Protein LeDnaJ07 Enhances the Thermotolerance of Lentinula edodes and Regulates IAA Biosynthesis by Interacting LetrpE. Frontiers in Microbiology, 2020, 11, 707.	1.5	14
20	Distribution, evolution and expression ofGATA-TFsprovide new insights into their functions in light response and fruiting body development ofTolypocladium guangdongense. PeerJ, 2020, 8, e9784.	0.9	2
21	Effects of Medium Composition and Genetic Background on Agrobacterium-Mediated Transformation Efficiency of Lentinula edodes. Genes, 2019, 10, 467.	1.0	12
22	Selection and Validation of Reference Genes for qRT-PCR in Lentinula edodes under Different Experimental Conditions. Genes, 2019, 10, 647.	1.0	10
23	Selection of Reference Genes for qRT-PCR Analysis in Lentinula edodes after Hot-Air Drying. Molecules, 2019, 24, 136.	1.7	16
24	Identification of a Heat-Inducible Element of Cysteine Desulfurase Gene Promoter in Lentinula edodes. Molecules, 2019, 24, 2223.	1.7	6
25	Comparative transcriptomics reveals potential genes involved in the vegetative growth of Morchella importuna. 3 Biotech, 2019, 9, 81.	1.1	21
26	Transcriptional Changes on Blight Fruiting Body of Flammulina velutipes Caused by Two New Bacterial Pathogens. Frontiers in Microbiology, 2019, 10, 2845.	1.5	12
27	Expression Profile of Laccase Gene Family in White-Rot Basidiomycete Lentinula edodes under Different Environmental Stresses. Genes, 2019, 10, 1045.	1.0	16
28	Effects of GGT and C-S Lyase on the Generation of Endogenous Formaldehyde in Lentinula edodes at Different Growth Stages. Molecules, 2019, 24, 4203.	1.7	12
29	The DnaJ Gene Family in Shiitake Culinary-Medicinal Mushroom, Lentinus edodes (Agaricomycetes): Comprehensive Identification, Characterization, and Expression Profiles under Different Conditions. International Journal of Medicinal Mushrooms, 2019, 21, 909-919.	0.9	4
30	Comprehensive Evaluation of Shiitake Strains (Lentinus edodes, Agaricomycetes) Based on Polysaccharide Content and Agronomic Traits. International Journal of Medicinal Mushrooms, 2019, 21, 851-864.	0.9	2
31	First report of a cross-kingdom pathogenic bacterium, Achromobacter xylosoxidans isolated from stipe-rot Coprinus comatus. Microbiological Research, 2018, 207, 249-255.	2.5	11
32	First report of pileus rot disease on cultivated Morchella importuna caused by DiploÃ¶spora longispora in China. Journal of General Plant Pathology, 2018, 84, 65-69.	0.6	25
33	Agrobacterium-mediated transformation of the ascomycete mushroom Morchella importuna using polyubiquitin and glyceraldehyde-3-phosphate dehydrogenase promoter-based binary vectors. World Journal of Microbiology and Biotechnology, 2018, 34, 148.	1.7	10
34	Validation of Internal Control Genes for Quantitative Real-Time PCR Gene Expression Analysis in Morchella. Molecules, 2018, 23, 2331.	1.7	24
35	Opposite Polarity Monospore Genome De Novo Sequencing and Comparative Analysis Reveal the Possible Heterothallic Life Cycle of Morchella importuna. International Journal of Molecular Sciences, 2018, 19, 2525.	1.8	31
36	The heat shock protein 40 LeDnaJ regulates stress resistance and indole-3-acetic acid biosynthesis in Lentinula edodes. Fungal Genetics and Biology, 2018, 118, 37-44.	0.9	38

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37	Genetic variation and phylogenetic analyses reveal transmission clues of Lentinula edodes partitivirus 1 (LePV1) from the Chinese L. edodes core collection. Virus Research, 2018, 255, 127-132.	1.1	8
38	Detection of Quantitative Trait Loci Underlying Yield-Related Traits in Shiitake Culinary-Medicinal Mushroom, Lentinus edodes (Agaricomycetes). International Journal of Medicinal Mushrooms, 2018, 20, 451-458.	0.9	9
39	Phenotypic and Genetic Diversity of the Culinary-Medicinal Winter Mushroom Flammulina velutipes (Agaricomycetes) in China. International Journal of Medicinal Mushrooms, 2018, 20, 517-536.	0.9	5
40	Biological and Molecular Characteristics of a Novel Partitivirus Infecting the Edible Fungus Lentinula edodes. Plant Disease, 2017, 101, 726-733.	0.7	24
41	Comparative secretomic analysis of lignocellulose degradation by Lentinula edodes grown on microcrystalline cellulose, lignosulfonate and glucose. Journal of Proteomics, 2017, 163, 92-101.	1.2	41
42	Association Mapping Reveals Genetic Loci Associated with Important Agronomic Traits in Lentinula edodes, Shiitake Mushroom. Frontiers in Microbiology, 2017, 8, 237.	1.5	13
43	Diversity and effect of Trichoderma spp. associated with green mold disease on Lentinula edodes in China. MicrobiologyOpen, 2016, 5, 709-718.	1.2	42
44	Population genomic analysis uncovers environmental stress-driven selection and adaptation of Lentinula edodes population in China. Scientific Reports, 2016, 6, 36789.	1.6	23
45	Identification of and antimicrobial activity of plant extracts against Pseudomonas putida from rot fruiting bodies of Pleurotus eryngii. Scientia Horticulturae, 2016, 212, 235-239.	1.7	7
46	Development of crossbreeding high-yield-potential strains for commercial cultivation in the medicinal mushroom Wolfiporia cocos (Higher Basidiomycetes). Journal of Natural Medicines, 2016, 70, 645-652.	1.1	28
47	Genome Sequence of the Edible Cultivated Mushroom Lentinula edodes (Shiitake) Reveals Insights into Lignocellulose Degradation. PLoS ONE, 2016, 11, e0160336.	1.1	110
48	De Novo Assembly of Auricularia polytricha Transcriptome Using Illumina Sequencing for Gene Discovery and SSR Marker Identification. PLoS ONE, 2014, 9, e91740.	1.1	45
49	Effective Removal of Cadmium Ions from a Simulated Gastrointestinal Fluid by Lentinus edodes. International Journal of Environmental Research and Public Health, 2014, 11, 12486-12498.	1.2	9
50	Cloning, expression and phylogenetic analysis of a divergent laccase multigene family in Auricularia auricula-judae. Microbiological Research, 2014, 169, 453-462.	2.5	34
51	Biological Characteristics of Teleomorph and Optimized In Vitro Fruiting Conditions of the Hoelen Medicinal Mushroom, Wolfiporia extensa (Higher Basidiomycetes). International Journal of Medicinal Mushrooms, 2014, 16, 421-429.	0.9	10
52	Development of IRAP-SCAR marker for strain identification in Lentinula edodes. World Journal of Microbiology and Biotechnology, 2011, 27, 1731-1734.	1.7	4
53	Using SSR markers to evaluate the genetic diversity of Lentinula edodesâ€™ natural germplasm in China. World Journal of Microbiology and Biotechnology, 2010, 26, 527-536.	1.7	29