## Wei Liu

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1238346/publications.pdf

Version: 2024-02-01

687363 713466 22 531 13 21 citations h-index g-index papers 22 22 22 410 docs citations citing authors all docs times ranked

#	Article	IF	CITATIONS
1	Label-free based comparative proteomic analysis of Morchella importuna development from the vegetative to the sexual reproductive stages. Journal of Agriculture and Food Research, 2022, 7, 100247.	2.5	2
2	Genetic polymorphism of Mel-21 Morchella tissue isolates. Journal of Agriculture and Food Research, 2022, 9, 100324.	2.5	0
3	Physiological Characteristics and Comparative Secretome Analysis of Morchella importuna Grown on Glucose, Rice Straw, Sawdust, Wheat Grain, and MIX Substrates. Frontiers in Microbiology, 2021, 12, 636344.	3.5	13
4	Spatial and temporal disequilibrium of nuclear distribution in heterothallic Morchella importuna. Journal of Agriculture and Food Research, 2021, 6, 100240.	2.5	7
5	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.	7.5	63
6	Interspecific hybridization between cultivated morels Morchella importuna and Morchella sextelata by PEG-induced double inactivated protoplast fusion. World Journal of Microbiology and Biotechnology, 2020, 36, 58.	3.6	12
7	Subchromosome-Scale Nuclear and Complete Mitochondrial Genome Characteristics of Morchella crassipes. International Journal of Molecular Sciences, 2020, 21, 483.	4.1	27
8	Comparative transcriptomics reveals potential genes involved in the vegetative growth of Morchella importuna. 3 Biotech, 2019, 9, 81.	2.2	21
9	Effect of Aging on Culture and Cultivation of the Culinary-Medicinal Mushrooms Morchella importuna and M. sextelata (Ascomycetes). International Journal of Medicinal Mushrooms, 2019, 21, 1089-1098.	1.5	13
10	First report of pileus rot disease on cultivated Morchella importuna caused by Diploöspora longispora in China. Journal of General Plant Pathology, 2018, 84, 65-69.	1.0	25
11	Involvement of autophagy and apoptosis and lipid accumulation in sclerotial morphogenesis of Morchella importuna. Micron, 2018, 109, 34-40.	2.2	20
12	Validation of Internal Control Genes for Quantitative Real-Time PCR Gene Expression Analysis in Morchella. Molecules, 2018, 23, 2331.	3.8	24
13	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.	4.1	31
14	Comparative secretomic analysis of lignocellulose degradation by Lentinula edodes grown on microcrystalline cellulose, lignosulfonate and glucose. Journal of Proteomics, 2017, 163, 92-101.	2.4	41
15	Live cell confocal laser imaging studies on the nuclear behavior during meiosis and ascosporogenesis in Morchella importuna under artificial cultivation. Micron, 2017, 101, 108-113.	2.2	23
16	Genome Sequence of the Edible Cultivated Mushroom Lentinula edodes (Shiitake) Reveals Insights into Lignocellulose Degradation. PLoS ONE, 2016, 11, e0160336.	2.5	110
17	Morphological and ultrastructural examination of senescence in Morchella elata. Micron, 2015, 78, 79-84.	2.2	15
18	Constructing a new integrated genetic linkage map and mapping quantitative trait loci for vegetative mycelium growth rate in Lentinula edodes. Fungal Biology, 2014, 118, 295-308.	2.5	37

#	Article	IF	CITATION
19	Development of IRAP-SCAR marker for strain identification in Lentinula edodes. World Journal of Microbiology and Biotechnology, 2011, 27, 1731-1734.	3.6	4
20	Comparative analysis on the diversity of Auricularia auricula-judae by physiological characteristics, somatic incompatibility and TRAP fingerprinting. World Journal of Microbiology and Biotechnology, 2011, 27, 2081-2093.	3.6	6
21	Using SSR markers to evaluate the genetic diversity of Lentinula edodes' natural germplasm in China. World Journal of Microbiology and Biotechnology, 2010, 26, 527-536.	3.6	29
22	Applying target region amplification polymorphism markers for analyzing genetic diversity of <i>Lentinula edodes</i> in China. Journal of Basic Microbiology, 2010, 50, 475-483.	3.3	8