Towards a unified paradigm for sequenceâ€based ident

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Citation Report

#	Article	IF	CITATIONS
1	Lineages of ectomycorrhizal fungi revisited: Foraging strategies and novel lineages revealed by sequences from belowground. Fungal Biology Reviews, 2013, 27, 83-99.	1.9	431
2	MycoBank gearing up for new horizons. IMA Fungus, 2013, 4, 371-379.	1.7	170
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16	Ectomycorrhizal fungus diversity and community structure with natural and cultivated truffle hosts: applying lessons learned to future truffle culture. Mycorrhiza, 2014, 24, 5-18.	1.3	52
17	Multiple ITS Haplotypes in the Genome of the Lichenized Basidiomycete Cora inversa (Hygrophoraceae): Fact or Artifact?. Journal of Molecular Evolution, 2014, 78, 148-162.	0.8	31
18	Epitypification of Hebeloma crustuliniforme. Mycological Progress, 2014, 13, 553-562.	0.5	12
	Largeâ€scale fungal diversity assessment in the Andean Yungas forests reveals strong community	2.0	151

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20	Ectomycorrhizal <i><scp>C</scp>ortinarius</i> species participate in enzymatic oxidation of humus in northern forest ecosystems. New Phytologist, 2014, 203, 245-256.	3.5	256
21	Improving ITS sequence data for identification of plant pathogenic fungi. Fungal Diversity, 2014, 67, 11-19.	4.7	123
22	Species richness of arbuscular mycorrhizal fungi: associations with grassland plant richness and biomass. New Phytologist, 2014, 203, 233-244.	3.5	256
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28	Integration of Clustering and Multidimensional Scaling to Determine Phylogenetic Trees as Spherical Phylograms Visualized in 3 Dimensions. , 2014, , .		7
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57	Temporal dynamics of plant–soil feedback and rootâ€associated fungal communities over 100Âyears of invasion by a nonâ€native plant. Journal of Ecology, 2015, 103, 1557-1569.	1.9	25
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