

David S Hibbett

List of Publications by Year in descending order

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131
papers

23,221
citations

13332

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times ranked

16197
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#	ARTICLE	IF	CITATIONS
1	Population genomics provides insights into the genetic basis of adaptive evolution in the mushroom-forming fungus <i>Lentinula edodes</i> . <i>Journal of Advanced Research</i> , 2022, 38, 91-106.	4.4	16
2	Evolutionary Morphogenesis of Sexual Fruiting Bodies in Basidiomycota: Toward a New Evo-Devo Synthesis. <i>Microbiology and Molecular Biology Reviews</i> , 2022, 86, e0001921.	2.9	13
3	Evolutionary transition to the ectomycorrhizal habit in the genomes of a hyperdiverse lineage of mushroom-forming fungi. <i>New Phytologist</i> , 2022, 233, 2294-2309.	3.5	21
4	Global phylogeny of the Shiitake mushroom and related <i>Lentinula</i> species uncovers novel diversity and suggests an origin in the Neotropics. <i>Molecular Phylogenetics and Evolution</i> , 2022, 173, 107494.	1.2	8
5	Genomic Analysis Enlightens Agaricales Lifestyle Evolution and Increasing Peroxidase Diversity. <i>Molecular Biology and Evolution</i> , 2021, 38, 1428-1446.	3.5	72
6	RNA-editing in Basidiomycota, revisited. <i>ISME Communications</i> , 2021, 1, .	1.7	2
7	Fungal functional ecology: bringing a trait-based approach to plant-associated fungi. <i>Biological Reviews</i> , 2020, 95, 409-433.	4.7	171
8	Large-scale genome sequencing of mycorrhizal fungi provides insights into the early evolution of symbiotic traits. <i>Nature Communications</i> , 2020, 11, 5125.	5.8	258
9	Fruiting body form, not nutritional mode, is the major driver of diversification in mushroom-forming fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 32528-32534.	3.3	65
10	Transcriptomic atlas of mushroom development reveals conserved genes behind complex multicellularity in fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7409-7418.	3.3	115
11	Megaphylogeny resolves global patterns of mushroom evolution. <i>Nature Ecology and Evolution</i> , 2019, 3, 668-678.	3.4	187
12	Proposals for consideration at IMC11 to modify provisions related solely to fungi in the International Code of Nomenclature for algae, fungi, and plants. <i>IMA Fungus</i> , 2018, 9, i-vii.	1.7	10
13	Phylogenetic taxon definitions for Fungi, Dikarya, Ascomycota and Basidiomycota. <i>IMA Fungus</i> , 2018, 9, 291-298.	1.7	26
14	Genomics and Development of <i>Lentinus tigrinus</i> : A White-Rot Wood-Decaying Mushroom with Dimorphic Fruiting Bodies. <i>Genome Biology and Evolution</i> , 2018, 10, 3250-3261.	1.1	53
15	Contemporaneous radiations of fungi and plants linked to symbiosis. <i>Nature Communications</i> , 2018, 9, 5451.	5.8	189
16	Evolutionary dynamics of host specialization in wood-decay fungi. <i>BMC Evolutionary Biology</i> , 2018, 18, 119.	3.2	104
17	Substrate-Specific Differential Gene Expression and RNA Editing in the Brown Rot Fungus <i>Fomitopsis pinicola</i> . <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	22
18	A revised family-level classification of the Polyporales (Basidiomycota). <i>Fungal Biology</i> , 2017, 121, 798-824.	1.1	190

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19	Mycophagous rove beetles highlight diverse mushrooms in the Cretaceous. <i>Nature Communications</i> , 2017, 8, 14894.	5.8	38
20	Draft genome sequence of a monokaryotic model brown-rot fungus <i>Postia (Rhodonia) placenta</i> SB12. <i>Genomics Data</i> , 2017, 14, 21-23.	1.3	19
21	Genetic Bases of Fungal White Rot Wood Decay Predicted by Phylogenomic Analysis of Correlated Gene-Phenotype Evolution. <i>Molecular Biology and Evolution</i> , 2017, 34, 35-44.	3.5	65
22	(308–310) Proposals to permit DNA sequence data to serve as types of names of fungi. <i>Taxon</i> , 2016, 65, 899-900.	0.4	42
23	Ectomycorrhizal fungi decompose soil organic matter using oxidative mechanisms adapted from saprotrophic ancestors. <i>New Phytologist</i> , 2016, 209, 1705-1719.	3.5	264
24	Draft Genome Sequence of the White-Rot Fungus <i>Obba rivulosa</i> 3A-2. <i>Genome Announcements</i> , 2016, 4, .	0.8	15
25	Climate, decay, and the death of the coal forests. <i>Current Biology</i> , 2016, 26, R563-R567.	1.8	25
26	Unearthing the roots of ectomycorrhizal symbioses. <i>Nature Reviews Microbiology</i> , 2016, 14, 760-773.	13.6	317
27	Digital identifiers for fungal species—Response. <i>Science</i> , 2016, 352, 1183-1183.	6.0	1
28	Comparative Genomics of Early-Diverging Mushroom-Forming Fungi Provides Insights into the Origins of Lignocellulose Decay Capabilities. <i>Molecular Biology and Evolution</i> , 2016, 33, 959-970.	3.5	213
29	The invisible dimension of fungal diversity. <i>Science</i> , 2016, 351, 1150-1151.	6.0	59
30	The genome of <i>Xylona heveae</i> provides a window into fungal endophytism. <i>Fungal Biology</i> , 2016, 120, 26-42.	1.1	72
31	Sequence-based classification and identification of Fungi. <i>Mycologia</i> , 2016, 108, 1049-1068.	0.8	154
32	Degradation of Bunker C Fuel Oil by White-Rot Fungi in Sawdust Cultures Suggests Potential Applications in Bioremediation. <i>PLoS ONE</i> , 2015, 10, e0130381.	1.1	43
33	Unexpected diversity of basidiomycetous endophytes in sapwood and leaves of <i>Hevea</i> . <i>Mycologia</i> , 2015, 107, 284-297.	0.8	73
34	Evolution of novel wood decay mechanisms in Agaricales revealed by the genome sequences of <i>Fistulina hepatica</i> and <i>Cylindrobasidium torrendii</i> . <i>Fungal Genetics and Biology</i> , 2015, 76, 78-92.	0.9	141
35	Phylogenetic relationships and morphological evolution in <i>Lentinus</i> , <i>Polyporellus</i> and <i>Neofavolus</i> , emphasizing southeastern Asian taxa. <i>Mycologia</i> , 2015, 107, 460-474.	0.8	31
36	Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 2015, 47, 410-415.	9.4	870

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37	Revisiting the taxonomy of Phanerochaete (Polyporales, Basidiomycota) using a four gene dataset and extensive ITS sampling. Fungal Biology, 2015, 119, 679-719.	1.1	86
38	Towards the unification of sequence-based classification and sequence-based identification of host-associated microorganisms. New Phytologist, 2015, 205, 27-31.	3.5	21
39	Synthesis of phylogeny and taxonomy into a comprehensive tree of life. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 12764-12769.	3.3	584
40	Latent homology and convergent regulatory evolution underlies the repeated emergence of yeasts. Nature Communications, 2014, 5, 4471.	5.8	133
41	Extensive sampling of basidiomycete genomes demonstrates inadequacy of the white-rot/brown-rot paradigm for wood decay fungi. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9923-9928.	3.3	595
42	Species delimitation in <i>Trametes</i> : a comparison of ITS, RPB1, RPB2 and TEF1 gene phylogenies. Mycologia, 2014, 106, 735-745.	0.8	33
43	Molecular phylogeny and phylogeography of Holarctic species of <i>Pluteus</i> section <i>Pluteus</i> (Agaricales: Tj ETQq1 1 0,784314 rgBT /Overlock 0,1 83	0.1	33
44	Toward genome-enabled mycology. Mycologia, 2013, 105, 1339-1349.	0.8	38
45	Lignin-degrading peroxidases in Polyporales: an evolutionary survey based on 10 sequenced genomes. Mycologia, 2013, 105, 1428-1444.	0.8	134
46	A phylogenetic overview of the antrodia clade (Basidiomycota, Polyporales). Mycologia, 2013, 105, 1391-1411.	0.8	86
47	Genomewide analysis of polysaccharides degrading enzymes in 11 white- and brown-rot Polyporales provides insight into mechanisms of wood decay. Mycologia, 2013, 105, 1412-1427.	0.8	110
48	Phylogenetic and phylogenomic overview of the Polyporales. Mycologia, 2013, 105, 1350-1373.	0.8	259
49	Fungal systematics: is a new age of enlightenment at hand?. Nature Reviews Microbiology, 2013, 11, 129-133.	13.6	153
50	Phylogenetic overview of the Boletineae. Fungal Biology, 2013, 117, 479-511.	1.1	143
51	Toward Sequence-Based Classification of Fungal Species. IMA Fungus, 2013, 4, A33-A34.	1.7	7
52	ll.14. Major Events in the Evolution of Fungi. , 2013, , 152-158.		0
53	Genome sequence of the button mushroom <i>Agaricus bisporus</i> reveals mechanisms governing adaptation to a humic-rich ecological niche. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17501-17506.	3.3	359
54	Diversity and evolution of ectomycorrhizal host associations in the Sclerodermatineae (Boletales,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 00 3,5 73	3.5	73

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55	The genome of the xerotolerant mold <i>Wallemia sebi</i> reveals adaptations to osmotic stress and suggests cryptic sexual reproduction. <i>Fungal Genetics and Biology</i> , 2012, 49, 217-226.	0.9	103
56	Comparative genomics of <i>Ceriporiopsis subvermispora</i> and <i>Phanerochaete chrysosporium</i> provide insight into selective ligninolysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5458-5463.	3.3	259
57	The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 2012, 336, 1715-1719.	6.0	1,424
58	The phylogeny of selected <i>Phylloporus</i> species, inferred from NUC-LSU and ITS sequences, and descriptions of new species from the Old World. <i>Fungal Diversity</i> , 2012, 55, 109-123.	4.7	37
59	Molecular phylogenetics of the Gloeophyllales and relative ages of clades of Agaricomycotina producing a brown rot. <i>Mycologia</i> , 2011, 103, 510-524.	0.8	69
60	Phylogeny of the Pluteaceae (Agaricales, Basidiomycota): taxonomy and character evolution. <i>Fungal Biology</i> , 2011, 115, 1-20.	1.1	86
61	Phylogenetic classification of <i>Trametes</i> (Basidiomycota, Polyporales) based on a fiveâ€‘marker dataset. <i>Taxon</i> , 2011, 60, 1567-1583.	0.4	111
62	Where are all the undocumented fungal species? A study of <i>Mortierella</i> demonstrates the need for sequenceâ€‘based classification. <i>New Phytologist</i> , 2011, 191, 592-596.	3.5	24
63	EFFECTS OF GASTEROID FRUITING BODY MORPHOLOGY ON DIVERSIFICATION RATES IN THREE INDEPENDENT CLADES OF FUNGI ESTIMATED USING BINARY STATE SPECIATION AND EXTINCTION ANALYSIS. <i>Evolution; International Journal of Organic Evolution</i> , 2011, 65, 1305-1322.	1.1	63
64	Progress in molecular and morphological taxon discovery in Fungi and options for formal classification of environmental sequences. <i>Fungal Biology Reviews</i> , 2011, 25, 38-47.	1.9	296
65	The Plant Cell Wallâ€‘Decomposing Machinery Underlies the Functional Diversity of Forest Fungi. <i>Science</i> , 2011, 333, 762-765.	6.0	512
66	The Amsterdam Declaration on Fungal Nomenclature. <i>IMA Fungus</i> , 2011, 2, 105-111.	1.7	320
67	Amylocorticiales ord. nov. and Jaapiales ord. nov.: Early diverging clades of Agaricomycetidae dominated by corticioid forms. <i>Mycologia</i> , 2010, 102, 865-880.	0.8	165
68	Convergent evolution of sequestrate forms in <i>Amanita</i> under Mediterranean climate conditions. <i>Mycologia</i> , 2010, 102, 675-688.	0.8	59
69	Characterization of Three <i>mnp</i> Genes of <i>Fomitiporia mediterranea</i> and Report of Additional Class II Peroxidases in the Order Hymenochaetales. <i>Applied and Environmental Microbiology</i> , 2010, 76, 6431-6440.	1.4	32
70	<i>Neocampanella</i> , a new corticioid fungal genus, and a note on <i>Dendrothele bispora</i> . <i>Botany</i> , 2009, 87, 875-882.	0.5	13
71	The Fungi. <i>Current Biology</i> , 2009, 19, R840-R845.	1.8	279
72	The relative ages of ectomycorrhizal mushrooms and their plant hosts estimated using Bayesian relaxed molecular clock analyses. <i>BMC Biology</i> , 2009, 7, 13.	1.7	152

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73	Out of the Palaeotropics? Historical biogeography and diversification of the cosmopolitan ectomycorrhizal mushroom family <i>Inocybaceae</i> . <i>Journal of Biogeography</i> , 2009, 36, 577-592.	1.4	184
74	Fungal ecology catches fire. <i>New Phytologist</i> , 2009, 184, 279-282.	3.5	104
75	Genome, transcriptome, and secretome analysis of wood decay fungus <i>Postia placenta</i> supports unique mechanisms of lignocellulose conversion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1954-1959.	3.3	530
76	The search for the fungal tree of life. <i>Trends in Microbiology</i> , 2009, 17, 488-497.	3.5	139
77	Molecular Evolution and Diversity of Lignin Degrading Heme Peroxidases in the Agaricomycetes. <i>Journal of Molecular Evolution</i> , 2008, 66, 243-257.	0.8	120
78	Contributions of <i>rpb2</i> and <i>tef1</i> to the phylogeny of mushrooms and allies (Basidiomycota, Fungi). <i>Molecular Phylogenetics and Evolution</i> , 2007, 43, 430-451.	1.2	341
79	After the gold rush, or before the flood? Evolutionary morphology of mushroom-forming fungi (Agaricomycetes) in the early 21st century. <i>Mycological Research</i> , 2007, 111, 1001-1018.	2.5	116
80	A higher-level phylogenetic classification of the Fungi. <i>Mycological Research</i> , 2007, 111, 509-547.	2.5	1,994
81	Molecular systematics and biological diversification of Boletales. <i>Mycologia</i> , 2006, 98, 971-981.	0.8	167
82	Resolving the phylogenetic position of the Wallemiomycetes: an enigmatic major lineage of Basidiomycota. <i>Canadian Journal of Botany</i> , 2006, 84, 1794-1805.	1.2	91
83	Research Coordination Networks: a phylogeny for kingdom Fungi (Deep Hypha). <i>Mycologia</i> , 2006, 98, 829-837.	0.8	97
84	Toward a phylogenetic classification of the Leotiomycetes based on rDNA data. <i>Mycologia</i> , 2006, 98, 1065-1075.	0.8	64
85	Major clades of Agaricales: a multilocus phylogenetic overview. <i>Mycologia</i> , 2006, 98, 982-995.	0.8	268
86	An overview of the higher level classification of Pucciniomycotina based on combined analyses of nuclear large and small subunit rDNA sequences. <i>Mycologia</i> , 2006, 98, 896-905.	0.8	80
87	Phylogeny and a new species of <i>Sparassis</i> (Polyporales, Basidiomycota): evidence from mitochondrial <i>atp6</i> , nuclear rDNA and <i>rpb2</i> genes. <i>Mycologia</i> , 2006, 98, 584-592.	0.8	25
88	Molecular systematics and biological diversification of Boletales. <i>Mycologia</i> , 2006, 98, 971-981.	0.8	215
89	A phylogenetic overview of the Agaricomycotina. <i>Mycologia</i> , 2006, 98, 917-925.	0.8	87
90	Research Coordination Networks: a phylogeny for kingdom Fungi (Deep Hypha). <i>Mycologia</i> , 2006, 98, 829-837.	0.8	114

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91	Reconstructing the early evolution of Fungi using a six-gene phylogeny. <i>Nature</i> , 2006, 443, 818-822.	13.7	1,625
92	Evolution of helotialean fungi (Leotiomycetes, Pezizomycotina): A nuclear rDNA phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 2006, 41, 295-312.	1.2	165
93	Evolutionary relationships of <i>Mycaureola dilseae</i> (Agaricales), a basidiomycete pathogen of a subtidal rhodophyte. <i>American Journal of Botany</i> , 2006, 93, 547-556.	0.8	58
94	An overview of the higher level classification of Pucciniomycotina based on combined analyses of nuclear large and small subunit rDNA sequences. <i>Mycologia</i> , 2006, 98, 896-905.	0.8	143
95	Major clades of Agaricales: a multilocus phylogenetic overview. <i>Mycologia</i> , 2006, 98, 982-995.	0.8	449
96	A phylogenetic overview of the Agaricomycotina. <i>Mycologia</i> , 2006, 98, 917-925.	0.8	172
97	Automated Phylogenetic Taxonomy: An Example in the Homobasidiomycetes (Mushroom-Forming) Tj ETQq1 1 0.784314 rgBT /Overlock 2.7 63	2.7	63
98	The phylogenetic distribution of resupinate forms across the major clades of mushroom-forming fungi (Homobasidiomycetes). <i>Systematics and Biodiversity</i> , 2005, 3, 113-157.	0.5	340
99	Phylogenetic Relationships of <i>Sparassis</i> Inferred from Nuclear and Mitochondrial Ribosomal DNA and RNA Polymerase Sequences. <i>Mycologia</i> , 2004, 96, 1015.	0.8	35
100	Trends in Morphological Evolution in Homobasidiomycetes Inferred Using Maximum Likelihood: A Comparison of Binary and Multistate Approaches. <i>Systematic Biology</i> , 2004, 53, 889-903.	2.7	92
101	Phylogenetic relationships of cyphelloid homobasidiomycetes. <i>Molecular Phylogenetics and Evolution</i> , 2004, 33, 501-515.	1.2	92
102	Assembling the fungal tree of life: progress, classification, and evolution of subcellular traits. <i>American Journal of Botany</i> , 2004, 91, 1446-1480.	0.8	718
103	Phylogenetic relationships of <i>Sparassis</i> inferred from nuclear and mitochondrial ribosomal DNA and RNA polymerase sequences. <i>Mycologia</i> , 2004, 96, 1015-1029.	0.8	48
104	<i>Sparassis cystidiosa</i> sp. nov. from Thailand is described using morphological and molecular data. <i>Mycologia</i> , 2004, 96, 1010-1014.	0.8	16
105	Another fossil agaric from Dominican amber. <i>Mycologia</i> , 2003, 95, 685-687.	0.8	27
106	Phylogeny and genetic diversity of <i>Bridgeoporus nobilissimus</i> inferred using mitochondrial and nuclear rDNA sequences. <i>Mycologia</i> , 2003, 95, 836-845.	0.8	12
107	Higher-Level Phylogenetic Relationships of Homobasidiomycetes (Mushroom-Forming Fungi) Inferred from Four rDNA Regions. <i>Molecular Phylogenetics and Evolution</i> , 2002, 22, 76-90.	1.2	140
108	Evolution of complex fruiting body morphologies in homobasidiomycetes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2002, 269, 1963-1969.	1.2	179

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109	Evolution of Marine Mushrooms. <i>Biological Bulletin</i> , 2001, 201, 319-322.	0.7	42
110	Phylogenetic relationships of the marine gasteromycete <i>Nia vibrissa</i> . <i>Mycologia</i> , 2001, 93, 679-688.	0.8	29
111	Phylogenetic analyses of <i>Aleurodiscus</i> s.l. and allied genera. <i>Mycologia</i> , 2001, 93, 720-731.	0.8	28
112	Phylogenetic Relationships of the Marine Gasteromycete <i>Nia vibrissa</i> . <i>Mycologia</i> , 2001, 93, 679.	0.8	19
113	Analysis of Character Correlations Among Wood Decay Mechanisms, Mating Systems, and Substrate Ranges in Homobasidiomycetes. <i>Systematic Biology</i> , 2001, 50, 215-242.	2.7	161
114	Analysis of Character Correlations Among Wood Decay Mechanisms, Mating Systems, and Substrate Ranges in Homobasidiomycetes. <i>Systematic Biology</i> , 2001, 50, 215-242.	2.7	170
115	Evolutionary instability of ectomycorrhizal symbioses in basidiomycetes. <i>Nature</i> , 2000, 407, 506-508.	13.7	426
116	Phylogenetic Species Recognition and Species Concepts in Fungi. <i>Fungal Genetics and Biology</i> , 2000, 31, 21-32.	0.9	1,585
117	Phylogenetic relationships of cantharelloid and clavarioid Homobasidiomycetes based on mitochondrial and nuclear rDNA sequences. <i>Mycologia</i> , 1999, 91, 944-963.	0.8	85
118	Phylogenetic Relationships of Cantharelloid and Clavarioid Homobasidiomycetes Based on Mitochondrial and Nuclear rDNA Sequences. <i>Mycologia</i> , 1999, 91, 944.	0.8	64
119	Integrating Phylogenetic Analysis and Classification in Fungi. <i>Mycologia</i> , 1998, 90, 347.	0.8	33
120	Integrating phylogenetic analysis and classification in fungi. <i>Mycologia</i> , 1998, 90, 347-356.	0.8	62
121	Fossil mushrooms from Miocene and Cretaceous ambers and the evolution of Homobasidiomycetes. <i>American Journal of Botany</i> , 1997, 84, 981-991.	0.8	125
122	Progress toward a phylogenetic classification of the Polyporaceae through parsimony analysis of mitochondrial ribosomal DNA sequences. <i>Canadian Journal of Botany</i> , 1995, 73, 853-861.	1.2	132
123	The Secotioid From of <i>Lentinus tigrinus</i> : Genetics and Development of a Fungal Morphological Innovation. <i>American Journal of Botany</i> , 1994, 81, 466.	0.8	18
124	Phylogenetic Relationships of <i>Lentinus</i> (Basidiomycotina) Inferred from Molecular and Morphological Characters. <i>Systematic Botany</i> , 1993, 18, 409.	0.2	101
125	Hymenophore Development and Evolution in <i>Lentinus</i> . <i>Mycologia</i> , 1993, 85, 428.	0.8	12
126	Sporocarp ontogeny in <i>Panus</i> (Basidiomycotina): evolution and classification. <i>American Journal of Botany</i> , 1993, 80, 1336-1348.	0.8	9

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127	Hymenophore Development and Evolution in <i>Lentinus</i> . <i>Mycologia</i> , 1993, 85, 428-443.	0.8	17
128	Sporocarp ontogeny in <i>Panus</i> (Basidiomycotina): evolution and classification. , 1993, 80, 1336.		6
129	Evolutionary Relationships of <i>Lentinus</i> to the Polyporaceae: Evidence from Restriction Analysis of Enzymatically Amplified Ribosomal Dna. <i>Mycologia</i> , 1991, 83, 425-439.	0.8	52
130	Evolutionary Relationships of <i>Lentinus</i> to the Polyporaceae: Evidence from Restriction Analysis of Enzymatically Amplified Ribosomal DNA. <i>Mycologia</i> , 1991, 83, 425.	0.8	36
131	Polypores and genus concepts in Phanerochaetaceae (Polyporales, Basidiomycota). <i>MycKeys</i> , 0, 17, 1-46.	0.8	54