Marco Thines

List of Publications by Year
in descending order

179 papers	9,647 citations	71102 41 h-index	45317 90 g-index
192 all docs	192 docs citations	192 times ranked	7099 citing authors

#	Article	IF	Citations
1	Genome sequence and analysis of the Irish potato famine pathogen Phytophthora infestans. Nature, 2009, 461, 393-398.	27.8	1,405
2	Signatures of Adaptation to Obligate Biotrophy in the <i>Hyaloperonospora arabidopsidis</i> Genome. Science, 2010, 330, 1549-1551.	12.6	492
3	Genome Evolution Following Host Jumps in the Irish Potato Famine Pathogen Lineage. Science, 2010, 330, 1540-1543.	12.6	440
4	Genome sequence of the necrotrophic plant pathogen Pythium ultimum reveals original pathogenicity mechanisms and effector repertoire. Genome Biology, 2010, 11, R73.	9.6	391
5	The rise and fall of the Phytophthora infestans lineage that triggered the Irish potato famine. ELife, 2013, 2, e00731.	6.0	339
6	Ancient class of translocated oomycete effectors targets the host nucleus. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 17421-17426.	7.1	326
7	The Amsterdam Declaration on Fungal Nomenclature. IMA Fungus, 2011, 2, 105-111.	3.8	320
8	Genome Sequencing and Mapping Reveal Loss of Heterozygosity as a Mechanism for Rapid Adaptation in the Vegetable Pathogen <i>Phytophthora capsici</i>. Molecular Plant-Microbe Interactions, 2012, 25, 1350-1360.	2.6	264
9	Unambiguous identification of fungi: where do we stand and how accurate and precise is fungal DNA barcoding?. IMA Fungus, 2020, 11, 14.	3.8	232
10	Oomyceteâ€"plant coevolution: recent advances and future prospects. Current Opinion in Plant Biology, 2010, 13, 427-433.	7.1	204
11	Phylogeny and evolution of plant pathogenic oomycetesâ€"a global overview. European Journal of Plant Pathology, 2014, 138, 431-447.	1.7	187
12	Ten things to know about oomycete effectors. Molecular Plant Pathology, 2009, 10, 795-803.	4.2	185
13	Gene Loss Rather Than Gene Gain Is Associated with a Host Jump from Monocots to Dicots in the Smut Fungus Melanopsichium pennsylvanicum. Genome Biology and Evolution, 2014, 6, 2034-2049.	2.5	146
14	Towards a universal barcode of oomycetes â€" a comparison of the <i>cox</i>1 and <i>cox</i>2 loci. Molecular Ecology Resources, 2015, 15, 1275-1288.	4.8	141
15	Genome analyses of the sunflower pathogen Plasmopara halstedii provide insights into effector evolution in downy mildews and Phytophthora. BMC Genomics, 2015, 16, 741.	2.8	135
16	Evolution, Diversity, and Taxonomy of the Peronosporaceae, with Focus on the Genus <i>Peronospora</i>. Phytopathology, 2016, 106, 6-18.	2.2	124
17	The local environment determines the assembly of root endophytic fungi at a continental scale. Environmental Microbiology, 2016, 18, 2418-2434.	3.8	123
18	An evolutionary framework for host shifts â€" jumping ships for survival. New Phytologist, 2019, 224, 605-617.	7.3	122

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19	Identity of the downy mildew pathogens of basil, coleus, and sage with implications for quarantine measures. Mycological Research, 2009, 113, 532-540.	2.5	111
20	Recent developments in effector biology of filamentous plant pathogens. Cellular Microbiology, 2010, 12, 705-715.	2.1	108
21	An Illumina metabarcoding pipeline for fungi. Ecology and Evolution, 2014, 4, 2642-2653.	1.9	107
22	Fungal taxonomy and sequence-based nomenclature. Nature Microbiology, 2021, 6, 540-548.	13.3	101
23	The fungal core effector <scp>P</scp>ep1 is conserved across smuts of dicots and monocots. New Phytologist, 2015, 206, 1116-1126.	7.3	100
24	Phylogenetic investigations in the genus Pseudoperonospora reveal overlooked species and cryptic diversity in the P. cubensis species cluster. European Journal of Plant Pathology, 2011, 129, 135-146.	1.7	91
25	Amplification of cox2 (~620 bp) from 2 mg of Up to 129 Years Old Herbarium Specimens, Comparing 19 Extraction Methods and 15 Polymerases. PLoS ONE, 2008, 3, e3584.	2.5	90
26	How to publish a new fungal species, or name, version 3.0. IMA Fungus, 2021, 12, 11.	3.8	76
27	Mining Herbaria for Plant Pathogen Genomes: Back to the Future. PLoS Pathogens, 2014, 10, e1004028.	4.7	72
28	Facultative rootâ€colonizing fungi dominate endophytic assemblages in roots of nonmycorrhizal <i>Microthlaspi</i> species. New Phytologist, 2018, 217, 1190-1202.	7.3	70
29	Host Jumps and Radiation, Not Coâ€Divergence Drives Diversification of Obligate Pathogens. A Case Study in Downy Mildews and Asteraceae. PLoS ONE, 2015, 10, e0133655.	2.5	69
30	Influence of phylogenetic conservatism and trait convergence on the interactions between fungal root endophytes and plants. ISME Journal, 2017, 11, 777-790.	9.8	63
31	Multi-locus tree and species tree approaches toward resolving a complex clade of downy mildews (Straminipila, Oomycota), including pathogens of beet and spinach. Molecular Phylogenetics and Evolution, 2015, 86, 24-34.	2.7	58
32	A reference genome of the European beech (Fagus sylvatica L.). GigaScience, 2018, 7, .	6.4	58
33	Evidence for uncharted biodiversity in the Albugo candida complex, with the description of a new species. Mycological Research, 2008, 112, 1327-1334.	2.5	56
34	3 Systematics of the Straminipila: Labyrinthulomycota, Hyphochytriomycota, and Oomycota. , 2014, , 39-97.		56
35	Two novel Peronospora species are associated with recent reports of downy mildew on sages. Mycological Research, 2009, 113, 1340-1350.	2.5	55
36	Coupling Spore Traps and Quantitative PCR Assays for Detection of the Downy Mildew Pathogens of Spinach (<i>Peronospora effusa</i>) and Beet (<i>P. schachtii</i>). Phytopathology, 2014, 104, 1349-1359.	2.2	55

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37	Reevaluation of Host Specificity of the Closely Related Species <i>Pseudoperonospora humuli</i> and <i>P. cubensis</i>. Plant Disease, 2012, 96, 55-61.	1.4	54
38	Phylogenetic relationships of graminicolous downy mildews based on cox2 sequence data. Mycological Research, 2008, 112, 345-351.	2.5	53
39	Evolution of diversity in Albugo is driven by high host specificity and multiple speciation events on closely related Brassicaceae. Molecular Phylogenetics and Evolution, 2010, 57, 812-820.	2.7	51
40	Intraspecific Relationship of Plasmopara halstedii Isolates Differing in Pathogenicity and Geographic Origin Based on ITS Sequence Data. European Journal of Plant Pathology, 2006, 114, 309-315.	1.7	50
41	The genome of the basal agaricomycete Xanthophyllomyces dendrorhous provides insights into the organization of its acetyl-CoA derived pathways and the evolution of Agaricomycotina. BMC Genomics, 2015, 16, 233.	2.8	47
42	Biological Characteristics and Assessment of Virulence Diversity in Pathosystems of Economically Important Biotrophic Oomycetes. Critical Reviews in Plant Sciences, 2018, 37, 439-495.	5.7	46
43	Characterisation and phylogeny of repeated elements giving rise to exceptional length of ITS2 in several downy mildew genera (Peronosporaceae). Fungal Genetics and Biology, 2007, 44, 199-207.	2.1	45
44	Fungal root endophytes of tomato from Kenya and their nematode biocontrol potential. Mycological Progress, 2016, 15, 1.	1.4	43
45	Neofunctionalization of the secreted Tin2 effector in the fungal pathogen Ustilago maydis. Nature Microbiology, 2019, 4, 251-257.	13.3	43
46	What is a species in fungal plant pathogens?. Fungal Diversity, 2021, 109, 239-266.	12.3	42
47	The inclusion of downy mildews in a multi-locus-dataset and its reanalysis reveals a high degree of paraphyly in Phytophthora. IMA Fungus, 2011, 2, 163-171.	3.8	41
48	Root-associated fungi of Arabidopsis thaliana and Microthlaspi perfoliatum. Fungal Diversity, 2014, 66, 99-111.	12.3	41
49	Oomycetes. Current Biology, 2018, 28, R812-R813.	3.9	41
50	Phylogeny of Miracula helgolandica gen. et sp. nov. and Olpidiopsis drebesii sp. nov., two basal oomycete parasitoids of marine diatoms, with notes on the taxonomy of Ectrogella-like species. Mycological Progress, 2017, 16, 1041-1050.	1.4	40
51	Ten reasons why a sequence-based nomenclature is not useful for fungi anytime soon. IMA Fungus, 2018, 9, 177-183.	3.8	40
52	Promoter Activation in Î”<i>hfq</i> Mutants as an Efficient Tool for Specialized Metabolite Production Enabling Direct Bioactivity Testing. Angewandte Chemie - International Edition, 2019, 58, 18957-18963.	13.8	40
53	Detection and Quantification of <i>Bremia lactucae</i> by Spore Trapping and Quantitative PCR. Phytopathology, 2016, 106, 1426-1437.	2.2	39
54	Adaptive differentiation coincides with local bioclimatic conditions along an elevational cline in populations of a lichen-forming fungus. BMC Evolutionary Biology, 2017, 17, 93.	3.2	39

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55	The genome sequence of the commercially cultivated mushroom Agrocybe aegerita reveals a conserved repertoire of fruiting-related genes and a versatile suite of biopolymer-degrading enzymes. BMC Genomics, 2018, 19, 48.	2.8	39
56	Hyphochytriomycota and Oomycota. , 2017, , 435-505.		38
57	A revision of Bremia graminicola. Mycological Research, 2006, 110, 646-656.	2.5	36
58	Phylogenetics, ancestral state reconstruction, and a new infrafamilial classification of the pantropical Ochnaceae (Medusagynaceae, Ochnaceae s.str., Quiinaceae) based on five DNA regions. Molecular Phylogenetics and Evolution, 2014, 78, 199-214.	2.7	36
59	The diatom parasite Lagenisma coscinodisci (Lagenismatales, Oomycota) is an early diverging lineage of the Saprolegniomycetes. Mycological Progress, 2015, 14, 1.	1.4	36
60	Asexual and sexual morphs of Moesziomyces revisited. IMA Fungus, 2017, 8, 117-129.	3.8	36
61	A potential perennial host for Pseudoperonospora cubensis in temperate regions. European Journal of Plant Pathology, 2009, 123, 483-486.	1.7	35
62	Obligate biotrophic pathogens of the genus Albugo are widespread as asymptomatic endophytes in natural populations of Brassicaceae. Molecular Ecology, 2011, 20, no-no.	3.9	34
63	The host range of Albugo candida extends from Brassicaceae through Cleomaceae to Capparaceae. Mycological Progress, 2009, 8, 329-335.	1.4	33
64	Genomic basis for drought resistance in European beech forests threatened by climate change. ELife, 2021, 10, .	6.0	33
65	Evidence for high degrees of specialisation, evolutionary diversity, and morphologicalÂdistinctiveness in the genus Bremia. Fungal Biology, 2011, 115, 102-111.	2.5	32
66	Molecular phylogenetic analysis of Peronosclerospora (Oomycetes) reveals cryptic species and genetically distinct species parasitic to maize. European Journal of Plant Pathology, 2011, 130, 521-528.	1.7	32
67	On the necessity of new characters for classification and systematics of biotrophic Peronosporomycetes. Planta, 2004, 219, 910-4.	3.2	31
68	A revision of Plasmopara penniseti, with implications for the host range of the downy mildews with pyriform haustoria. Mycological Research, 2007, 111, 1377-1385.	2.5	31
69	Host matrix has major impact on the morphology of Pseudoperonospora cubensis. European Journal of Plant Pathology, 2011, 129, 147-156.	1.7	31
70	Tropical oomycetes in the German Bight â€“ Climate warming or overlooked diversity?. Fungal Ecology, 2013, 6, 152-160.	1.6	31
71	Seed Transmission of Pseudoperonospora cubensis. PLoS ONE, 2014, 9, e109766.	2.5	31
72	Exceptional length of ITS in Plasmopara halstedii is due to multiple repetitions in the ITS-2 region. European Journal of Plant Pathology, 2005, 112, 395-398.	1.7	30

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73	Cryptic diversity of Plasmopara viticola (Oomycota, Peronosporaceae) in North America. Organisms Diversity and Evolution, 2011, 11, 3-7.	1.6	30
74	Morphology, phylogeny, and taxonomy of <i>Microthlaspi</i> (Brassicaceae: Coluteocarpeae) and related genera. Taxon, 2016, 65, 79-98.	0.7	30
75	Bridging the Gulf: Phytophthora and Downy Mildews Are Connected by Rare Grass Parasites. PLoS ONE, 2009, 4, e4790.	2.5	28
76	Three new phylogenetic lineages are the closest relatives of the widespread species Albugo candida. Fungal Biology, 2011, 115, 598-607.	2.5	28
77	Root filtering, rather than host identity or age, determines the composition of root-associated fungi and oomycetes in three naturally co-occurring Brassicaceae. Soil Biology and Biochemistry, 2020, 146, 107806.	8.8	28
78	The molecular phylogeny of the white blister rust genus Pustula reveals a case of underestimated biodiversity with several undescribed species on ornamentals and crop plants. Fungal Biology, 2011, 115, 214-219.	2.5	27
79	Competing sexual and asexual generic names in Pucciniomycotina and Ustilaginomycotina (Basidiomycota) and recommendations for use. IMA Fungus, 2018, 9, 75-89.	3.8	26
80	siMBaâ€”a simple graphical user interface for the Bayesian phylogenetic inference program MrBayes. Mycological Progress, 2014, 13, 1255.	1.4	25
81	Revision of Plasmopara (Oomycota, Peronosporales) parasitic to Impatiens. Mycological Progress, 2017, 16, 791-799.	1.4	25
82	Plasmoverna gen. nov., and the taxonomy and nomenclature of Plasmopara (Chromista ,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382 Td	0.7	24
83	Evidence for the importance of enzymatic digestion of epidermal walls during subepidermal sporulation and pustule opening in white blister rusts (Albuginaceae). Mycological Research, 2009, 113, 657-667.	2.5	24
84	Recent outbreaks of downy mildew on grape ivy (Parthenocissus tricuspidata, Vitaceae) in Germany are caused by a new species of Plasmopara. Mycological Progress, 2011, 10, 415-422.	1.4	24
85	Ustilago species causing leaf-stripe smut revisited. IMA Fungus, 2018, 9, 49-73.	3.8	24
86	A glimpse into the biogeography, seasonality, and ecological functions of arctic marine Oomycota. IMA Fungus, 2019, 10, 6.	3.8	24
87	Phylogenetic investigations in the downy mildew genus Bremia reveal several distinct lineages and a species with a presumably exceptional wide host range. European Journal of Plant Pathology, 2010, 128, 81-89.	1.7	23
88	Which Morphological Characteristics Are Most Influenced by the Host Matrix in Downy Mildews? A Case Study in Pseudoperonospora cubensis. PLoS ONE, 2012, 7, e44863.	2.5	23
89	Characteristics of a Plasmopara angustiterminalis isolate from Xanthium strumarium. European Journal of Plant Pathology, 2007, 119, 421-428.	1.7	22
90	A new species of Pustula (Oomycetes, Albuginales) is the causal agent of sunflower white rust. Mycological Progress, 2012, 11, 351-359.	1.4	22

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91	Reclassification of an enigmatic downy mildew species on lovegrass (Eragrostis) to the new genus Eraphthora, with a key to the genera of the Peronosporaceae. Mycological Progress, 2012, 11, 121-129.	1.4	20
92	Baobabopsis, a new genus of graminicolous downy mildews from tropical Australia, with an updated key to the genera of downy mildews. IMA Fungus, 2015, 6, 483-491.	3.8	20
93	Setting scientific names at all taxonomic ranks in italics facilitates their quick recognition in scientific papers. IMA Fungus, 2020, 11, 25.	3.8	20
94	Saprotrophic yeasts formerly classified as Pseudozyma have retained a large effector arsenal, including functional Pep1 orthologs. Mycological Progress, 2019, 18, 763-768.	1.4	19
95	An Introduction to the White Blister Rusts (Albuginales). , 0, , 77-92.		18
96	Revision of some central European species of Inocybe (Fr.: Fr.) Fr. subgenus Inocybe, with the description of five new species. Mycological Progress, 2019, 18, 247-294.	1.4	18
97	Delimiting species in Basidiomycota: a review. Fungal Diversity, 2021, 109, 181-237.	12.3	18
98	Diversity and species boundaries in floricolous downy mildews. Mycological Progress, 2013, 12, 321-329.	1.4	17
99	Microthlaspi erraticum (Jord.) T. Ali et Thines has a wide distribution, ranging from the Alps to the Tien Shan. Flora: Morphology, Distribution, Functional Ecology of Plants, 2016, 225, 76-81.	1.2	17
100	Dikaryotic fruiting body development in a single dikaryon of Agrocybe aegerita and the spectrum of monokaryotic fruiting types in its monokaryotic progeny. Mycological Progress, 2016, 15, 947-957.	1.4	17
101	Calycofera gen. nov., an estuarine sister taxon to Phytopythium, Peronosporaceae. Mycological Progress, 2017, 16, 947-954.	1.4	17
102	A Chromosome-Level Genome Assembly of the European Beech (Fagus sylvatica) Reveals Anomalies for Organelle DNA Integration, Repeat Content and Distribution of SNPs. Frontiers in Genetics, 2021, 12, 691058.	2.3	17
103	Comparative Genomics Including the Early-Diverging Smut Fungus<i>Ceraceosorus bombacis</i>Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes. Genome Biology and Evolution, 2015, 7, 2781-2798.	2.5	16
104	Host species identity in annual Brassicaceae has a limited effect on the assembly of root-endophytic fungal communities. Plant Ecology and Diversity, 2018, 11, 569-580.	2.4	16
105	Promoter Activation in Î” hfq Mutants as an Efficient Tool for Specialized Metabolite Production Enabling Direct Bioactivity Testing. Angewandte Chemie, 2019, 131, 19133-19139.	2.0	16
106	A new perspective on the evolution of white blister rusts: Albugo s.str. (Albuginales; Oomycota) is not restricted to Brassicales but also present on Fabales. Organisms Diversity and Evolution, 2011, 11, 193-199.	1.6	15
107	A new presumably widespread species of Albugo parasitic to Strigosella spp. (Brassicaceae). Mycological Progress, 2013, 12, 45-52.	1.4	15
108	The Genome of <i>Peronospora belbahrii</i> Reveals High Heterozygosity, a Low Number of Canonical Effectors, and TC-Rich Promoters. Molecular Plant-Microbe Interactions, 2020, 33, 742-753.	2.6	15

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109	FastQFS â€“ A tool for evaluating and filtering paired-end sequencing data generated from high throughput sequencing. Mycological Progress, 2015, 14, 1.	1.4	14
110	The oomycete Lagenisma coscinodisci hijacks host alkaloid synthesis during infection of a marine diatom. Nature Communications, 2019, 10, 4938.	12.8	14
111	Dual culture of the oomycete Lagenisma coscinodisci Drebes and Coscinodiscus diatoms as a model for plankton/parasite interactions. Helgoland Marine Research, 2019, 73, .	1.3	14
112	Morphological and molecular confirmation of Albugo resedae (Albuginales; Oomycota) as a distinct species from A. candida. Mycological Progress, 2011, 10, 143-148.	1.4	13
113	Diversity of exophillic acid derivatives in strains of an endophytic Exophiala sp.. Phytochemistry, 2015, 118, 83-93.	2.9	13
114	New smut-specific primers for the ITS barcoding of Ustilaginomycotina. Mycological Progress, 2017, 16, 213-221.	1.4	13
115	Labyrinthulomycota. , 2017, , 507-542.		13
116	Multiple evolutionary origins of sequestrate species in the agaricoid genus <i>Chlorophyllum</i>. Mycologia, 2020, 112, 400-422.	1.9	13
117	Crossâ€species analysis between the maize smut fungi <i>Ustilago maydis</i> and <i>Sporisorium reilianum</i> highlights the role of transcriptional change of effector orthologs for virulence and disease. New Phytologist, 2021, 232, 719-733.	7.3	13
118	Genotypic diversity in rootâ€endophytic fungi reflects efficient dispersal and environmental adaptation. Molecular Ecology, 2017, 26, 4618-4630.	3.9	12
119	Rediscovery and phylogenetic placement of Olpidiopsis gillii (deÂWildeman) Friedmann, a holocarpic oomycete parasitoid ofÂfreshwater diatoms. Mycoscience, 2019, 60, 141-146.	0.8	12
120	Comparative transcriptome profiling identifies maize line specificity of fungal effectors in the maizeâ€“<i>Ustilago maydis</i> interaction. Plant Journal, 2021, 106, 733-752.	5.7	12
121	Forecasting the number of species of asexually reproducing fungi (Ascomycota and Basidiomycota). Fungal Diversity, 2022, 114, 463-490.	12.3	12
122	Genetic patterns reflecting Pleistocene range dynamics in the annual calcicole plant Microthlaspi erraticum across its Eurasian range. Flora: Morphology, Distribution, Functional Ecology of Plants, 2017, 236-237, 132-142.	1.2	11
123	Phylogenomics of Bartheletia paradoxa reveals its basal position in Agaricomycotina and that the early evolutionary history of basidiomycetes was rapid and probably not strictly bifurcating. Mycological Progress, 2018, 17, 333-341.	1.4	11
124	Out of Transcaucasia: Origin of Western and Central Palearctic populations of Microthlaspi perfoliatum. Flora: Morphology, Distribution, Functional Ecology of Plants, 2019, 253, 127-141.	1.2	11
125	A molecular phylogeny of Basidiophora reveals several apparently host-specific lineages on Astereae. Mycological Progress, 2014, 13, 1137.	1.4	10
126	(2288) Proposal to reject the name <i>Botrytis farinosa</i> (<i>Peronospora farinosa</i>) (<i>Peronosporaceae: Oomycetes</i>). Taxon, 2014, 63, 675-676.	0.7	10

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127	New smut-specific primers for multilocus genotyping and phylogenetics of Ustilaginaceae. Mycological Progress, 2017, 16, 917-925.	1.4	10
128	Phylogeny and cultivation of the holocarpic oomycete Diatomophthora perforans comb. nov., an endoparasitoid of marine diatoms. Mycological Progress, 2020, 19, 441-454.	1.4	10
129	Community barcoding reveals little effect of ocean acidification on the composition of coastal plankton communities: Evidence from a long-term mesocosm study in the Gullmar Fjord, Skagerrak. PLoS ONE, 2017, 12, e0175808.	2.5	10
130	Peronospora aquilegiicola sp. nov., the downy mildew affecting columbines in the UK is an invasive species from East Asia. European Journal of Plant Pathology, 2019, 155, 515-525.	1.7	9
131	Hyphochytriomycota and Oomycota. , 2016, , 1-71.		9
132	Mitochondrial phylogeny reveals intraspecific variation in Peronospora effusa, the spinach downy mildew pathogen. Journal of Microbiology, 2011, 49, 1039-1043.	2.8	8
133	Perofascia is not monotypic: the description of the second taxon affecting the South American crop maca (Lepidium meyenii). Mycological Progress, 2017, 16, 857-864.	1.4	8
134	Peronosclerospora australiensis is a synonym of P. maydis, which is widespread on Sumatra, and distinct from the most prevalent Java maize downy mildew pathogen. Mycological Progress, 2020, 19, 1309-1315.	1.4	8
135	A Circular Chloroplast Genome of Fagus sylvatica Reveals High Conservation between Two Individuals from Germany and One Individual from Poland and an Alternate Direction of the Small Single-Copy Region. Forests, 2021, 12, 180.	2.1	8
136	<i>Asterotexis cucurbitacearum</i>, a poorly known pathogen of Cucurbitaceae new to Costa Rica, Grenada and Panama. Mycology, 2011, 2, 87-90.	4.4	7
137	Morphological evidence supports the existence of multiple species in Pustula (Albuginaceae,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.4	7
138	Confirmation of Peronospora agrimoniae as a distinct species. European Journal of Plant Pathology, 2017, 147, 887-896.	1.7	7
139	BrRxLR11 â€“ a new phylogenetic marker with high resolution in the downy mildew genus Bremia and related genera. Mycological Progress, 2017, 16, 185-190.	1.4	7
140	A revision of Salispina, its placement in a new family, Salispinaceae (Rhipidiales), and description of a fourth species, S. hoi sp. nov. IMA Fungus, 2018, 9, 259-269.	3.8	7
141	(2467) Proposal to conserve the name <I> Ustilago</I> (<I>Basidiomycota</I>) with a conserved type. Taxon, 2016, 65, 1170-1171.	0.7	6
142	Confirmation that Phytophthora insolita (Peronosporaceae) is present as a marine saprotroph on mangrove leaves and first report of the species for the Philippines. Nova Hedwigia, 2017, 105, 185-196.	0.4	6
143	Hyaloperonospora erucae sp. nov. (Peronosporaceae; Oomycota), the downy mildew pathogen of arugula (Eruca sativa). European Journal of Plant Pathology, 2018, 151, 549-555.	1.7	6
144	Plasmopara elegantissima sp. nov. (Oomycota, Peronosporales), a Downy Mildew Species Specialized to Impatiens textori (Balsaminaceae). Mycobiology, 2020, 48, 304-312.	1.7	6

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145	The first smut fungus, Thecaphora anthemidis sp. nov. (Glomosporiaceae), described from Anthemis (Asteraceae). MycoKeys, 2018, 41, 39-50.	1.9	6
146	Three new hygrophilous species of Inocybe, subgenus Inocybe. Mycological Progress, 2019, 18, 1101-1119.	1.4	5
147	Taxonomy and phylogeny of Aphanomycopsis bacillariacearum, a holocarpic oomycete parasitoid of the freshwater diatom genus Pinnularia. Mycological Progress, 2021, 20, 289-298.	1.4	5
148	Ancestral state reconstruction in Peronospora provides further evidence for host jumping as a key element in the diversification of obligate parasites. Molecular Phylogenetics and Evolution, 2022, 166, 107321.	2.7	5
149	Nutrient Availability Does Not Affect Community Assembly in Root-Associated Fungi but Determines Fungal Effects on Plant Growth. MSystems, 2022, 7, .	3.8	5
150	Characterisation and risk assessment of the emerging Peronospora disease on Aquilegia. Mycological Progress, 2015, 14, 1.	1.4	4
151	Bremia polycephala and Bremia sawadae spp. nov. (Peronosporaceae; Oomycota), parasitic to Northeast Asian Asteraceae. Nova Hedwigia, 2018, 107, 303-314.	0.4	4
152	The Genome of Microthlaspi erraticum (Brassicaceae) Provides Insights Into the Adaptation to Highly Calcareous Soils. Frontiers in Plant Science, 2020, 11, 943.	3.6	4
153	Downy mildew of lavender caused by Peronospora belbahrii in Israel. Mycological Progress, 2020, 19, 1537-1543.	1.4	4
154	A Comparison of Three Circular Mitochondrial Genomes of Fagus sylvatica from Germany and Poland Reveals Low Variation and Complete Identity of the Gene Space. Forests, 2021, 12, 571.	2.1	4
155	Bremia lactucae populations on cultivated lettuce originate from prickly lettuce and are interconnected with the wild pathosystem. European Journal of Plant Pathology, 2021, 161, 411-426.	1.7	4
156	A New Marine Species of <i>Miracula</i> (<i>Oomycota</i>) Parasitic to <i>Minidiscus</i> sp. in Icelandtitle. Mycobiology, 2021, 49, 355-362.	1.7	4
157	Evolution of Hyaloperonospora effectors: ATR1 effector homologs from sister species of the downy mildew pathogen H. arabidopsidis are not recognised by RPP1WsB. Mycological Progress, 2015, 14, 1.	1.4	3
158	Entyloma lagoeciae: a new smut fungus occurring on the annual Apiaceae Lagoecia cuminoides. Nova Hedwigia, 2019, 108, 173-184.	0.4	3
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