Dominik Begerow

List of Publications by Year
in descending order

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40	5,881	361296	330025
papers	citations	20 h-index	37 g-index

42	42	42	7791
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6241-6246.	3.3	4,012
2	One fungus, which genes? Development and assessment of universal primers for potential secondary fungal DNA barcodes. Persoonia: Molecular Phylogeny and Evolution of Fungi, 2015, 35, 242-263.	1.6	416
3	Multigene phylogeny and taxonomic revision of yeasts and related fungi in the Ustilaginomycotina. Studies in Mycology, 2015, 81, 55-83.	4.5	174
4	Phylogenetic placements of ustilaginomycetous anamorphs as deduced from nuclear LSU rDNA sequences. Mycological Research, 2000, 104, 53-60.	2.5	142
5	Molecular phylogeny of Ustilago, Sporisorium, and related taxa based on combined analyses of rDNA sequences. Mycological Research, 2005, 109, 342-356.	2.5	102
6	Fungal diversity notes 1387â€“1511: taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity, 2021, 111, 1-335.	4.7	88
7	Multiple convergent supergene evolution events in mating-type chromosomes. Nature Communications, 2018, 9, 2000.	5.8	81
8	Anther smuts of Caryophyllaceae: Molecular characters indicate host-dependent species delimitation. Mycological Progress, 2005, 4, 225-238.	0.5	71
9	Interspecific Sex in Grass Smuts and the Genetic Diversity of Their Pheromone-Receptor System. PLoS Genetics, 2011, 7, e1002436.	1.5	70
10	Implications of molecular characters for the phylogeny of the Microbotryaceae (Basidiomycota:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 38	3.2	68
11	Transient leaf endophytes are the most active fungi in 1-year-old beech leaf litter. Fungal Diversity, 2018, 89, 237-251.	4.7	62
12	The illustrated life cycle ofMicrobotryumon the host plantSilene latifolia. Botany, 2010, 88, 875-885.	0.5	55
13	The Exobasidiales: An evolutionary hypothesis. Mycological Progress, 2002, 1, 187-199.	0.5	48
14	11 Ustilaginomycotina. , 2014, , 295-329.		43
15	Pyricularia graminisâ€tritici is not the correct species name for the wheat blast fungus: response to Ceresini etÂal. (MPP 20:2). Molecular Plant Pathology, 2019, 20, 173-179.	2.0	42
16	The evolving species concepts used for yeasts: from phenotypes and genomes to speciation networks. Fungal Diversity, 2021, 109, 27-55.	4.7	37
17	Hidden diversity in the nonâ€caryophyllaceous plantâ€parasitic members ofMicrobotryum(Pucciniomycotina: Microbotryales). Systematics and Biodiversity, 2009, 7, 297-306.	0.5	35
18	Aboveground Deadwood Deposition Supports Development of Soil Yeasts. Diversity, 2012, 4, 453-474.	0.7	34

#	Article	IF	Citations
19	Yeast diversity and species recovery rates from beech forest soils. Mycological Progress, 2016, 15, 845-859.	0.5	28
20	Parasitism in Yeasts. , 2017, , 179-210.		26
21	Distinct sensitivity of fungal freshwater guilds to water quality. Mycological Progress, 2017, 16, 155-169.	0.5	24
22	Fungal guilds are evenly distributed along a vertical spruce forest soil profile while individual fungi show pronounced niche partitioning. Mycological Progress, 2018, 17, 925-939.	0.5	23
23	Contrasting phylogenetic patterns of anther smuts (Pucciniomycotina: Microbotryum) reflect phylogenetic patterns of their caryophyllaceous hosts. Organisms Diversity and Evolution, 2013, 13, 111-126.	0.7	22
24	Rare and undersampled dimorphic basidiomycetes. Mycological Progress, 2019, 18, 945-971.	0.5	20
25	Delimiting species in Basidiomycota: a review. Fungal Diversity, 2021, 109, 181-237.	4.7	18
26	New isolation method for endophytes based on enzyme digestion. Mycological Progress, 2014, 13, 849-856.	0.5	16
27	Host preference and sorus location correlate with parasite phylogeny in the smut fungal genus Microbotryum (Basidiomycota, Microbotryales). Mycological Progress, 2020, 19, 481-493.	0.5	16
28	Experimental hybridization and backcrossing reveal forces of reproductive isolation in Microbotryum. BMC Evolutionary Biology, 2013, 13, 224.	3.2	14
29	Insect herbivory facilitates the establishment of an invasive plant pathogen. ISME Communications, 2021, 1, .	1.7	14
30	Flooding Duration Affects the Structure of Terrestrial and Aquatic Microbial Eukaryotic Communities. Microbial Ecology, 2018, 75, 875-887.	1.4	13
31	Effects of short-term flooding on aquatic and terrestrial microeukaryotic communities: a mesocosm approach. Aquatic Microbial Ecology, 2017, 80, 257-272.	0.9	13
32	Knowing your neighbourhoodâ€”the effects of EpichloÃ« endophytes on foliar fungal assemblages in perennial ryegrass in dependence of season and land-use intensity. PeerJ, 2018, 6, e4660.	0.9	13
33	Onset and stepwise extensions of recombination suppression are common in matingâ€type chromosomes of Microbotryum antherâ€smut fungi. Journal of Evolutionary Biology, 2022, 35, 1619-1634.	0.8	11
34	Molecular and morphological evidence reveals a new smut fungus, Microbotryum arcticum (Microbotryaceae), on Silene uralensis (Caryophyllaceae) from Greenland and Canada. Willdenowia, 2019, 49, 241.	0.5	8
35	Comparison of Denitrification Induced by Various Organic Substancesâ€”Reaction Rates, Microbiology, and Temperature Effect. Water Resources Research, 2021, 57, e2021WR029793.	1.7	7
36	Improved strategies to efficiently isolate thermophilic, thermotolerant, and heat-resistant fungi from compost and soil. Mycological Progress, 2021, 20, 325-339.	0.5	4

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37	Proposal of Two New Combinations, Twenty New Species, Four New Genera, One New Family, and One New Order for the Anamorphic Basidiomycetous Yeast Species in Ustilaginomycotina. Frontiers in Microbiology, 2021, 12, 777338.	1.5	4
38	Meiotic recombination in the offspring of Microbotryum hybrids and its impact on pathogenicity. BMC Evolutionary Biology, 2020, 20, 123.	3.2	2
39	Interaction between growth environment and host progeny shape fungal endophytic assemblages in transplanted Fagus sylvatica. Fungal Ecology, 2022, 60, 101175.	0.7	2
40	Kalmanago gen. nov. (Microbotryaceae) on Commelina and Tinantia (Commelinaceae). Mycobiota, 0, 10, 21-37.	1.3	1