

Conrad L Schoch

List of Publications by Year in descending order

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34493

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54771

88
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93
all docs

93
docs citations

93
times ranked

33866
citing authors

#	ARTICLE	IF	CITATIONS
1	GenBank. Nucleic Acids Research, 2022, 50, D161-D164.	6.5	119
2	Publicly Available and Validated DNA Reference Sequences Are Critical to Fungal Identification and Global Plant Protection Efforts: A Use-Case in <i>Colletotrichum</i> . Plant Disease, 2022, , PDIS09212083SR.	0.7	5
3	GenBank. Nucleic Acids Research, 2021, 49, D92-D96.	6.5	199
4	Fungal taxonomy and sequence-based nomenclature. Nature Microbiology, 2021, 6, 540-548.	5.9	101
5	How to publish a new fungal species, or name, version 3.0. IMA Fungus, 2021, 12, 11.	1.7	76
6	Ribovore: ribosomal RNA sequence analysis for GenBank submissions and database curation. BMC Bioinformatics, 2021, 22, 400.	1.2	3
7	Unambiguous identification of fungi: where do we stand and how accurate and precise is fungal DNA barcoding?. IMA Fungus, 2020, 11, 14.	1.7	232
8	NCBI Taxonomy: a comprehensive update on curation, resources and tools. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	925
9	Species Identification in Plant-Associated Prokaryotes and Fungi Using DNA. Phytobiomes Journal, 2020, 4, 103-114.	1.4	7
10	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2019, 47, D23-D28.	6.5	502
11	Revisions to the Classification, Nomenclature, and Diversity of Eukaryotes. Journal of Eukaryotic Microbiology, 2019, 66, 4-119.	0.8	904
12	The NCBI BioCollections Database. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	43
13	Using average nucleotide identity to improve taxonomic assignments in prokaryotic genomes at the NCBI. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2386-2392.	0.8	337
14	Using standard keywords in publications to facilitate updates of new fungal taxonomic names. IMA Fungus, 2017, 8, A70-A73.	1.7	11
15	Improving taxonomic accuracy for fungi in public sequence databases: applying "one name one species"™ in well-defined genera with <i>Trichoderma</i> / <i>Hypocrea</i> as a test case. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	28
16	Scaling up discovery of hidden diversity in fungi: impacts of barcoding approaches. Philosophical Transactions of the Royal Society B: Biological Sciences, 2016, 371, 20150336.	1.8	84
17	Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Research, 2016, 44, D733-D745.	6.5	4,739
18	Sequence-based classification and identification of Fungi. Mycologia, 2016, 108, 1049-1068.	0.8	154

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19	6 Pezizomycotina: Dothideomycetes and Arthoniomycetes. , 2015, , 143-176.		7
20	An overview of the genus <i>Glyphium</i> and its phylogenetic placement in Patellariales. Mycologia, 2015, 107, 607-618.	0.8	14
21	International Society of Human and Animal Mycology (ISHAM)-ITS reference DNA barcoding database – the quality controlled standard tool for routine identification of human and animal pathogenic fungi. Medical Mycology, 2015, 53, 313-337.	0.3	252
22	Transposable element-assisted evolution and adaptation to host plant within the Leptosphaeria maculans-Leptosphaeria biglobosa species complex of fungal pathogens. BMC Genomics, 2014, 15, 891.	1.2	189
23	A multigene phylogenetic synthesis for the class Lecanoromycetes (Ascomycota): 1307 fungi representing 1139 infrageneric taxa, 317 genera and 66 families. Molecular Phylogenetics and Evolution, 2014, 79, 132-168.	1.2	248
24	The Genera of Fungi: fixing the application of type species of generic names. IMA Fungus, 2014, 5, 141-160.	1.7	54
25	Finding needles in haystacks: linking scientific names, reference specimens and molecular data for Fungi. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau061-bau061.	1.4	272
26	Mycobank gearing up for new horizons. IMA Fungus, 2013, 4, 371-379.	1.7	170
27	Meeting Report: Fungal ITS Workshop (October 2012). Standards in Genomic Sciences, 2013, 8, 118-123.	1.5	34
28	Filling Gaps in Biodiversity Knowledge for Macrofungi: Contributions and Assessment of an Herbarium Collection DNA Barcode Sequencing Project. PLoS ONE, 2013, 8, e62419.	1.1	164
29	Diverse Lifestyles and Strategies of Plant Pathogenesis Encoded in the Genomes of Eighteen Dothideomycetes Fungi. PLoS Pathogens, 2012, 8, e1003037.	2.1	595
30	The Revised Classification of Eukaryotes. Journal of Eukaryotic Microbiology, 2012, 59, 429-514.	0.8	1,340
31	Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for <i>Fungi</i> . Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6241-6246.	3.3	4,012
32	Phylogenetic placement of the ectomycorrhizal genus <i>Cenococcum</i> in Gloniaceae (Dothideomycetes). Mycologia, 2012, 104, 758-765.	0.8	61
33	Pleosporales. Fungal Diversity, 2012, 53, 1-221.	4.7	282
34	Geographic, climatic, and chemical differentiation in the <i>Hypogymnia imshaugii</i> species complex (Lecanoromycetes, Parmeliaceae) in North America. Bryologist, 2011, 114, 526.	0.1	8
35	Hypogymnia phylogeny, including <i>Cavernularia</i> , reveals biogeographic structure. Bryologist, 2011, 114, 392.	0.1	27
36	A molecular, morphological and ecological re-appraisal of Venturiales – a new order of Dothideomycetes. Fungal Diversity, 2011, 51, 249-277.	4.7	96

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37	A reappraisal of Microthyriaceae. <i>Fungal Diversity</i> , 2011, 51, 189-248.	4.7	95
38	Capnodiaceae. <i>Fungal Diversity</i> , 2011, 51, 103-134.	4.7	108
39	Effector diversification within compartments of the <i>Leptosphaeria maculans</i> genome affected by Repeat-Induced Point mutations. <i>Nature Communications</i> , 2011, 2, 202.	5.8	481
40	Testing the phylogenetic utility of MCM7 in the Ascomycota. <i>MycologyKeys</i> , 2011, 1, 63-94.	0.8	58
41	<i>Dolabra nepheliae</i> on rambutan and lychee represents a novel lineage of phytopathogenic Eurotiomycetes. <i>Mycoscience</i> , 2010, 51, 300-309.	0.3	16
42	On the evolution of the Hysteriaceae and Mytiliniaceae (Pleosporomycetidae, Dothideomycetes). <i>Trends in Microbiology</i> , 2010, 18, 10-15.	2.5	68
43	The Ascomycota Tree of Life: A Phylum-wide Phylogeny Clarifies the Origin and Evolution of Fundamental Reproductive and Ecological Traits. <i>Systematic Biology</i> , 2009, 58, 224-239.	2.7	581
44	<i>Hypogymnia minilobata</i> (Parmeliaceae), a new lichen from coastal California. <i>Bryologist</i> , 2009, 112, 94-100.	0.1	10
45	Phylogeny of rock-inhabiting fungi related to Dothideomycetes. <i>Studies in Mycology</i> , 2009, 64, 123-133.	4.5	202
46	A class-wide phylogenetic assessment of Dothideomycetes. <i>Studies in Mycology</i> , 2009, 64, 1-15.	4.5	540
47	Multi-locus phylogeny of Pleosporales: a taxonomic, ecological and evolutionary re-evaluation. <i>Studies in Mycology</i> , 2009, 64, 85-102.	4.5	258
48	Phylogenetic lineages in the Capnodiales. <i>Studies in Mycology</i> , 2009, 64, 17-47.	4.5	305
49	A molecular phylogenetic reappraisal of the Hysteriaceae, Mytiliniaceae and Gloniaceae (Pleosporomycetidae, Dothideomycetes) with keys to world species. <i>Studies in Mycology</i> , 2009, 64, 49-83.	4.5	93
50	<i>Geoglossomycetes</i> cl. nov., <i>Geoglossales</i> ord. nov. and taxa above class rank in the Ascomycota Tree of Life. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2009, 22, 129-138.	1.6	55
51	Genome sequencing and analysis of the biomass-degrading fungus <i>Trichoderma reesei</i> (syn. <i>Hypocrea</i>). <i>Genome Research</i> , 2009, 19, 1516-1524.	9.4	1516
52	Homologs of ToxB, a host-selective toxin gene from <i>Pyrenophora tritici-repentis</i> , are present in the genome of sister-species <i>Pyrenophora bromi</i> and other members of the Ascomycota. <i>Fungal Genetics and Biology</i> , 2008, 45, 363-377.	0.9	66
53	Detection and Identification of Fungi Intimately Associated with the Brown Seaweed <i>Fucus serratus</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 931-941.	1.4	161
54	Dothideomycete "Plant Interactions Illuminated by Genome Sequencing and EST Analysis of the Wheat Pathogen <i>Stagonospora nodorum</i> ". <i>Plant Cell</i> , 2007, 19, 3347-3368.	3.1	235

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55	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
56	Marine fungal lineages in the Hypocreomycetidae. <i>Mycological Research</i> , 2007, 111, 154-162.	2.5	29
57	A higher-level phylogenetic classification of the Fungi. <i>Mycological Research</i> , 2007, 111, 509-547.	2.5	1,994
58	A multigene phylogeny of the Dothideomycetes using four nuclear loci. <i>Mycologia</i> , 2006, 98, 1041-1052.	0.8	269
59	An overview of the systematics of the Sordariomycetes based on a four-gene phylogeny. <i>Mycologia</i> , 2006, 98, 1076-1087.	0.8	212
60	A phylogenomic analysis of the Ascomycota. <i>Fungal Genetics and Biology</i> , 2006, 43, 715-725.	0.9	128
61	A five-gene phylogeny of Pezizomycotina. <i>Mycologia</i> , 2006, 98, 1018-1028.	0.8	280
62	A multigene phylogeny of the Dothideomycetes using four nuclear loci. <i>Mycologia</i> , 2006, 98, 1041-1052.	0.8	388
63	Eurotiomycetes: Eurotiomycetidae and Chaetothyriomycetidae. <i>Mycologia</i> , 2006, 98, 1053-1064.	0.8	91
64	A five-gene phylogeny of Pezizomycotina. <i>Mycologia</i> , 2006, 98, 1018-1028.	0.8	283
65	An overview of the systematics of the Sordariomycetes based on a four-gene phylogeny. <i>Mycologia</i> , 2006, 98, 1076-1087.	0.8	275
66	New insights into classification and evolution of the Lecanoromycetes (Pezizomycotina, Ascomycota) from phylogenetic analyses of three ribosomal RNA- and two protein-coding genes. <i>Mycologia</i> , 2006, 98, 1088-1103.	0.8	140
67	Reconstructing the early evolution of Fungi using a six-gene phylogeny. <i>Nature</i> , 2006, 443, 818-822.	13.7	1,625
68	Evolution of helotialean fungi (Leotiomycetes, Pezizomycotina): A nuclear rDNA phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 2006, 41, 295-312.	1.2	165
69	The halotolerant fungus <i>Glomerobolus gelineus</i> is a member of the Ostropales. <i>Mycological Research</i> , 2006, 110, 257-263.	2.5	35
70	Eurotiomycetes: Eurotiomycetidae and Chaetothyriomycetidae. <i>Mycologia</i> , 2006, 98, 1053-1064.	0.8	158
71	New insights into classification and evolution of the Lecanoromycetes (Pezizomycotina, Ascomycota) from phylogenetic analyses of three ribosomal RNA- and two protein-coding genes. <i>Mycologia</i> , 2006, 98, 1088-1103.	0.8	227
72	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

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73	Deletion of all <i>Cochliobolus heterostrophus</i> Monofunctional Catalase-Encoding Genes Reveals a Role for One in Sensitivity to Oxidative Stress but None with a Role in Virulence. <i>Molecular Plant-Microbe Interactions</i> , 2003, 16, 1013-1021.	1.4	28
74	A complete inventory of fungal kinesins in representative filamentous ascomycetes. <i>Fungal Genetics and Biology</i> , 2003, 39, 1-15.	0.9	54
75	Female Fertility and Single Nucleotide Polymorphism Comparisons in <i>Cylindrocladium pauciramosum</i> . <i>Plant Disease</i> , 2001, 85, 941-946.	0.7	20
76	Species Concepts in the <i>Cylindrocladium floridanum</i> and <i>Cy. spathiphylli</i> Complexes (Hypocreaceae) Based on Multi-allelic Sequence Data, Sexual Compatibility and Morphology. <i>Systematic and Applied Microbiology</i> , 2001, 24, 206-217.	1.2	44
77	Phylogeny of <i>Calonectria</i> based on comparisons of β -tubulin DNA sequences. <i>Mycological Research</i> , 2001, 105, 1045-1052.	2.5	30
78	Recombination in <i>Calonectria morganii</i> and Phylogeny with Other Heterothallic Small-Spored <i>Calonectria</i> Species. <i>Mycologia</i> , 2000, 92, 665.	0.8	16
79	<i>Cylindrocladium angustatum</i> sp. nov., a new leaf spot pathogen of <i>Tillandsia capitata</i> from Florida, U.S.A. <i>Mycoscience</i> , 2000, 41, 521-526.	0.3	6
80	Recombination in <i>Calonectria morganii</i> and phylogeny with other heterothallic small-spored <i>Calonectria</i> species. <i>Mycologia</i> , 2000, 92, 665-673.	0.8	14
81	Phylogenetic relationships of <i>Cylindrocladium pseudogracile</i> and <i>Cylindrocladium rumohrae</i> with morphologically similar taxa, based on morphology and DNA sequences of internal transcribed spacers and beta-tubulin. <i>Canadian Journal of Botany</i> , 2000, 77, 1813-1820.	1.2	9
82	The <i>Cylindrocladium candelabrum</i> species complex includes four distinct mating populations. <i>Mycologia</i> , 1999, 91, 286-298.	0.8	54
83	First report of <i>Cylindrocladium</i> root and petiole rot of <i>Spathiphyllum</i> in South Africa. <i>South African Journal of Botany</i> , 1999, 65, 208-211.	1.2	8
84	The <i>Cylindrocladium candelabrum</i> Species Complex Includes Four Distinct Mating Populations. <i>Mycologia</i> , 1999, 91, 286.	0.8	42
85	Phylogenetic relationships of <i>Cylindrocladium pseudogracile</i> and <i>Cylindrocladium rumohrae</i> with morphologically similar taxa, based on morphology and DNA sequences of internal transcribed spacers and beta-tubulin. <i>Canadian Journal of Botany</i> , 1999, 77, 1813-1820.	1.2	32
86	A <i>Saccharomyces cerevisiae</i> mutant defective in the kinesin-like protein Kar3 is sensitive to NaCl-stress. <i>Current Genetics</i> , 1997, 32, 315-322.	0.8	7
87	Five simple guidelines for establishing basic authenticity and reliability of newly generated fungal ITS sequences. <i>MycoKeys</i> , 0, 4, 37-63.	0.8	157