

Christian Wurzbacher

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

2,377
citations

394421

19
h-index

302126

39
g-index

59
all docs

59
docs citations

59
times ranked

3457
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 wastewater surveillance in Germany: Long-term RT-digital droplet PCR monitoring, suitability of primer/probe combinations and biomarker stability. <i>Water Research</i> , 2022, 210, 117977.	11.3	40
2	»The curse of the uncultured fungus. <i>Mycology</i> , 2022, 86, 177-194.	1.9	9
3	Large-scale sampling of the freshwater microbiome suggests pollution-driven ecosystem changes. <i>Environmental Pollution</i> , 2022, 308, 119627.	7.5	7
4	Seasonality of parasitic and saprotrophic zoospore-forming fungi: linking sequence data to ecological traits. <i>ISME Journal</i> , 2022, 16, 2242-2254.	9.8	19
5	Single dominant diatom can host diverse parasitic fungi with different degree of host specificity. <i>Limnology and Oceanography</i> , 2021, 66, 667-677.	3.1	16
6	Microbial retention and resistances in stormwater quality improvement devices treating road runoff. <i>FEMS Microbes</i> , 2021, 2, .	2.1	1
7	SARS-CoV-2 Crisis Management With a Wastewater Early-Warning System in the Bavarian District of Berchtesgaden, Germany. <i>Deutsches & International</i> , 2021, 118, 479-480.	0.9	1
8	Declining fungal diversity in Arctic freshwaters along a permafrost thaw gradient. <i>Global Change Biology</i> , 2021, 27, 5889-5906.	9.5	10
9	Community composition of aquatic fungi across the thawing Arctic. <i>Scientific Data</i> , 2021, 8, 221.	5.3	0
10	Early-diverging fungal phyla: taxonomy, species concept, ecology, distribution, anthropogenic impact, and novel phylogenetic proposals. <i>Fungal Diversity</i> , 2021, 109, 59-98.	12.3	35
11	Long rDNA amplicon sequencing of insect-infecting nephridiophagids reveals their affiliation to the Chytridiomycota and a potential to switch between hosts. <i>Scientific Reports</i> , 2021, 11, 396.	3.3	12
12	Evidence for Lignocellulose-Decomposing Enzymes in the Genome and Transcriptome of the Aquatic Hyphomycete <i>Clavariopsis aquatica</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 854.	3.5	6
13	Reducing the Impacts of Biofouling in RO Membrane Systems through In Situ Low Fluence Irradiation Employing UVC-LEDs. <i>Membranes</i> , 2020, 10, 415.	3.0	10
14	Archaea in boreal Swedish lakes are diverse, dominated by Woesearchaeota and follow deterministic community assembly. <i>Environmental Microbiology</i> , 2020, 22, 3158-3171.	3.8	19
15	Fungal communities in groundwater springs along the volcanic zone of Iceland. <i>Inland Waters</i> , 2020, 10, 418-427.	2.2	9
16	Combining the 5.8S and ITS2 to improve classification of fungi. <i>Methods in Ecology and Evolution</i> , 2019, 10, 1702-1711.	5.2	27
17	A Salinity Threshold Separating Fungal Communities in the Baltic Sea. <i>Frontiers in Microbiology</i> , 2019, 10, 680.	3.5	47
18	Fungi in aquatic ecosystems. <i>Nature Reviews Microbiology</i> , 2019, 17, 339-354.	28.6	266

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19	Mycobiome diversity: high-throughput sequencing and identification of fungi. <i>Nature Reviews Microbiology</i> , 2019, 17, 95-109.	28.6	580
20	Introducing ribosomal tandem repeat barcoding for fungi. <i>Molecular Ecology Resources</i> , 2019, 19, 118-127.	4.8	78
21	Mycobiomes of sympatric <i>Amorphophallus albispatus</i> (Araceae) and <i>Camellia sinensis</i> (Theaceae) – a case study reveals clear tissue preferences and differences in diversity and composition. <i>Mycological Progress</i> , 2018, 17, 489-500.	1.4	7
22	Taxonomic annotation of public fungal ITS sequences from the built environment – a report from an April 10–11, 2017 workshop (Aberdeen, UK). <i>MycKeys</i> , 2018, 28, 65-82.	1.9	33
23	Poorly known microbial taxa dominate the microbiome of permafrost thaw ponds. <i>ISME Journal</i> , 2017, 11, 1938-1941.	9.8	32
24	DNA metabarcoding of unfractionated water samples relates phyto-, zoo- and bacterioplankton dynamics and reveals a single-taxon bacterial bloom. <i>Environmental Microbiology Reports</i> , 2017, 9, 383-388.	2.4	13
25	Shifts among Eukaryota, Bacteria, and Archaea define the vertical organization of a lake sediment. <i>Microbiome</i> , 2017, 5, 41.	11.1	60
26	Integrating chytrid fungal parasites into plankton ecology: research gaps and needs. <i>Environmental Microbiology</i> , 2017, 19, 3802-3822.	3.8	171
27	Early diverging lineages within Cryptomycota and Chytridiomycota dominate the fungal communities in ice-covered lakes of the McMurdo Dry Valleys, Antarctica. <i>Scientific Reports</i> , 2017, 7, 15348.	3.3	77
28	Metaxa2 Diversity Tools: Easing microbial community analysis with Metaxa2. <i>Ecological Informatics</i> , 2016, 33, 45-50.	5.2	30
29	Effects of FPOM size and quality on aquatic heterotrophic bacteria. <i>Limnologica</i> , 2016, 59, 109-115.	1.5	7
30	Discovery of dark matter fungi in aquatic ecosystems demands a reappraisal of the phylogeny and ecology of zoosporic fungi. <i>Fungal Ecology</i> , 2016, 19, 28-38.	1.6	183
31	Effects of Light and Autochthonous Carbon Additions on Microbial Turnover of Allochthonous Organic Carbon and Community Composition. <i>Microbial Ecology</i> , 2015, 69, 361-371.	2.8	17
32	Microbial diversity and community respiration in freshwater sediments influenced by artificial light at night. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140130.	4.0	107
33	Metabarcoding-based fungal diversity on coarse and fine particulate organic matter in a first-order stream in Nova Scotia, Canada. <i>F1000Research</i> , 2015, 4, 1378.	1.6	11
34	Metabarcoding-based fungal diversity on coarse and fine particulate organic matter in a first-order stream in Nova Scotia, Canada. <i>F1000Research</i> , 2015, 4, 1378.	1.6	11
35	Importance of Saprotrophic Freshwater Fungi for Pollen Degradation. <i>PLoS ONE</i> , 2014, 9, e94643.	2.5	110
36	Distribution of <i>acrA</i> and <i>acrB</i> cation rhodopsin genes in <i>Baltic Sea</i> salinity gradients indicates adaptation of facultative freshwater photoheterotrophs to brackish waters. <i>Environmental Microbiology</i> , 2014, 16, 586-597.	3.8	19

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37	Preconditioning of leaves by solar radiation and anoxia affects microbial colonisation and rate of leaf mass loss in an intermittent stream. <i>Freshwater Biology</i> , 2013, 58, 1918-1931.	2.4	23
38	Improved detection and identification of aquatic fungi and chitin in aquatic environments. <i>Mycologia</i> , 2012, 104, 1267-1271.	1.9	16
39	Environmental actinorhodopsin expression revealed by a new <i>in situ</i> filtration and fixation sampler. <i>Environmental Microbiology Reports</i> , 2012, 4, 491-497.	2.4	18
40	Effects of pollen leaching and microbial degradation on organic carbon and nutrient availability in lake water. <i>Aquatic Sciences</i> , 2012, 74, 87-99.	1.5	35
41	Top 50 most wanted fungi. <i>MycoKeys</i> , 0, 12, 29-40.	1.9	72
42	Detection of signal recognition particle (SRP) RNAs in the nuclear ribosomal internal transcribed spacer 1 (ITS1) of three lineages of ectomycorrhizal fungi (Agaricomycetes, Basidiomycota). <i>MycoKeys</i> , 0, 13, 21-33.	1.9	8
43	Annotating public fungal ITS sequences from the built environment according to the MixS-Built Environment standard – a report from a May 23-24, 2016 workshop (Gothenburg, Sweden). <i>MycoKeys</i> , 0, 16, 1-15.	1.9	16
44	High habitat-specificity in fungal communities in oligo-mesotrophic, temperate Lake Stechlin (North-East Germany). <i>MycoKeys</i> , 0, 16, 17-44.	1.9	68
45	Morphologic and molecular data help adopting the insect-pathogenic nephridiophagids (Nephridiophagidae) among the early diverging fungal lineages, close to the Chytridiomycota. <i>MycoKeys</i> , 0, 25, 31-50.	1.9	14
46	Read quality-based trimming of the distal ends of public fungal DNA sequences is nowhere near satisfactory. <i>MycoKeys</i> , 0, 26, 13-24.	1.9	10
47	↗ Evidence for further non-coding RNA genes in the fungal rDNA region. <i>MycoKeys</i> , 0, 90, 203-213.	1.9	3