

Laszlo Irinyi

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

2,697
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304743

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53
docs citations

53
times ranked

3708
citing authors

#	ARTICLE	IF	CITATIONS
1	Overview of Phoma-Like Fungi on Important Legumes (Papilionaceous Plants)., 2022, , 65-89.		1
2	In depth search of the Sequence Read Archive database reveals global distribution of the emerging pathogenic fungus <i>Scenedosporium aurantiacum</i> . Medical Mycology, 2022, 60, .	0.7	2
3	Inferring Species Compositions of Complex Fungal Communities from Long- and Short-Read Sequence Data. MBio, 2022, 13, e0244421.	4.1	2
4	Finding a Needle in a Haystack – In Silico Search for Environmental Traces of <i>Candida auris</i> . Japanese Journal of Infectious Diseases, 2022, 75, 490-495.	1.2	8
5	Fungal taxonomy and sequence-based nomenclature. Nature Microbiology, 2021, 6, 540-548.	13.3	101
6	Mycosands: Fungal diversity and abundance in beach sand and recreational waters – Relevance to human health. Science of the Total Environment, 2021, 781, 146598.	8.0	24
7	Long-Reads-Based Metagenomics in Clinical Diagnosis With a Special Focus on Fungal Infections. Frontiers in Microbiology, 2021, 12, 708550.	3.5	9
8	Long-read sequencing based clinical metagenomics for the detection and confirmation of <i>Pneumocystis jirovecii</i> directly from clinical specimens: A paradigm shift in mycological diagnostics. Medical Mycology, 2020, 58, 650-660.	0.7	28
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	Consensus Multilocus Sequence Typing Scheme for <i>Pneumocystis jirovecii</i> . Journal of Fungi (Basel), 2020, 6, 107.	3.5	7
11	Genetic Heterogeneity of Australian <i>Candida auris</i> Isolates: Insights From a Nonoutbreak Setting Using Whole-Genome Sequencing. Open Forum Infectious Diseases, 2020, 7, ofaa158.	0.9	12
12	FungalTraits: a user-friendly traits database of fungi and fungus-like stramenopiles. Fungal Diversity, 2020, 105, 1-16.	12.3	387
13	Metatranscriptomics as a tool to identify fungal species and subspecies in mixed communities – a proof of concept under laboratory conditions. IMA Fungus, 2019, 10, 12.	3.8	20
14	The mycobiome of Australian tree hollows in relation to the <i>Cryptococcus gattii</i> and <i>C. neoformans</i> species complexes. Ecology and Evolution, 2019, 9, 9684-9700.	1.9	7
15	Dual DNA Barcoding for the Molecular Identification of the Agents of Invasive Fungal Infections. Frontiers in Microbiology, 2019, 10, 1647.	3.5	40
16	Genetic differences in <i>Chlamydia pecorum</i> between neighbouring sub-populations of koalas (<i>Phascolarctos cinereus</i>). Veterinary Microbiology, 2019, 231, 264-270.	1.9	14
17	Preliminary study of the oral mycobiome of children with and without dental caries. Journal of Oral Microbiology, 2019, 11, 1536182.	2.7	30
18	Database establishment for the secondary fungal DNA barcode<i>translational elongation factor 1 α <td>2.0</td> <td>41</td>	2.0	41

#	ARTICLE	IF	CITATIONS
19	Scedosporium and Lomentospora: an updated overview of underrated opportunists. Medical Mycology, 2018, 56, S102-S125.	0.7	186
20	Taxonomic annotation of public fungal ITS sequences from the built environment – a report from an April 10–11, 2017 workshop (Aberdeen, UK). MycoKeys, 2018, 28, 65-82.	1.9	33
21	Online Databases for Taxonomy and Identification of Pathogenic Fungi and Proposal for a Cloud-Based Dynamic Data Network Platform. Journal of Clinical Microbiology, 2017, 55, 1011-1024.	3.9	43
22	DNA barcoding of fungi causing infections in humans and animals. Fungal Biology, 2016, 120, 125-136.	2.5	67
23	Medical and veterinary mycology. Microbiology Australia, 2015, 36, 42.	0.4	0
24	Diversity of Cryphonectria parasitica populations from the Carpathian Basin. Acta Microbiologica Et Immunologica Hungarica, 2015, 62, 247-266.	0.8	3
25	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.	4.4	416
26	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.	0.7	252
27	DNA barcoding of human and animal pathogenic fungi: the ISHAM-ITS database. Microbiology Australia, 2015, 36, 44.	0.4	1
28	Phoma-like fungi on soybeans. Critical Reviews in Microbiology, 2014, 40, 49-62.	6.1	14
29	Advances in Taxonomy of Genus Phoma: Polyphyletic Nature and Role of Phenotypic Traits and Molecular Systematics. Indian Journal of Microbiology, 2014, 54, 123-128.	2.7	28
30	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.	3.0	272
31	FIRST DETECTION OF THE CHESTNUT BLIGHT FUNGUS ON SESSILE OAK IN UKRAINE. Acta Horticulturae, 2014, , 199-204.	0.2	0
32	NEW DATA OF CRYPHONECTRIA PARASITICA (MURR.) BARR POPULATION IN CARPATHIAN-BASIN. Acta Horticulturae, 2014, , 43-49.	0.2	0
33	MycoBank gearing up for new horizons. IMA Fungus, 2013, 4, 371-379.	3.8	170
34	Genetic diversity of a Botrytis cinerea cryptic species complex in Hungary. Microbiological Research, 2012, 167, 283-291.	5.3	43
35	Cytochrome b diversity of Hungarian Botrytis cinerea strains. Agrártudományi Közlemények, 2010, , 18-21.	0.3	0
36	Dieback of apricot plantations caused by 'Ca. Phytoplasma prunorum' in Borsod-Abaúj-Zemplén county (Northern-Hungary). Agrártudományi Közlemények, 2010, , 34-41.	0.3	0

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37	Laboratory diagnoses of the isolates of chestnut blight disease fungus <i>Cryphonectria parasitica</i> (MURR. BARR). <i>Agrártudományi Közlemények</i> , 2010, , 45-52.	0.3	0
38	Taxonomical re-evaluation of Phoma-like soybean pathogenic fungi. <i>Mycological Research</i> , 2009, 113, 249-260.	2.5	26
39	Phoma Saccardo: Distribution, secondary metabolite production and biotechnological applications. <i>Critical Reviews in Microbiology</i> , 2009, 35, 182-196.	6.1	43
40	Phylogenetic studies of soybean pathogen Phoma species by Bayesian analysis. <i>Agrártudományi Közlemények</i> , 2009, , 53-61.	0.3	0
41	Awns and flag leaf contribution towards grain yield in spring wheat (<i>Triticum aestivum</i> L.). <i>Cereal Research Communications</i> , 2008, 36, 65-76.	1.6	54
42	Phylogenetic studies of Phoma species by maximum likelihood analysis. <i>Agrártudományi Közlemények</i> , 2008, , 37-46.	0.3	0
43	Phylogenetic analysis of Phoma species. <i>Agrártudományi Közlemények</i> , 2007, , 100-107.	0.3	0
44	Combined application of methods to taxonomic identification of <i>Saccharomyces</i> strains in fermenting botrytized grape must. <i>Journal of Applied Microbiology</i> , 2005, 98, 971-979.	3.1	47
45	Studies of Expression of Peptaibol Synthetase of <i>Trichoderma reesei</i> . <i>Agrártudományi Közlemények</i> , 2005, , 188-190.	0.3	0
46	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