Laszlo Irinyi

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4527814/publications.pdf

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46	2,697	304743	345221
papers	citations	22 h-index	36 g-index

53	53	53	3708
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	FungalTraits: a user-friendly traits database of fungi and fungus-like stramenopiles. Fungal Diversity, 2020, 105, 1-16.	12.3	387
3	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
4	International Society of Human and Animal Mycology (ISHAM)-ITS reference DNA barcoding databaseâ€"the quality controlled standard tool for routine identification of human and animal pathogenic fungi. Medical Mycology, 2015, 53, 313-337.	0.7	252
5	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
6	Scedosporium and Lomentospora: an updated overview of underrated opportunists. Medical Mycology, 2018, 56, S102-S125.	0.7	186
7	MycoBank gearing up for new horizons. IMA Fungus, 2013, 4, 371-379.	3.8	170
8	Fungal taxonomy and sequence-based nomenclature. Nature Microbiology, 2021, 6, 540-548.	13.3	101
9	DNA barcoding of fungi causing infections in humans and animals. Fungal Biology, 2016, 120, 125-136.	2.5	67
10	Awns and flag leaf contribution towards grain yield in spring wheat (Triticum aestivumL.). Cereal Research Communications, 2008, 36, 65-76.	1.6	54
11	Combined application of methods to taxonomic identification of Saccharomyces strains in fermenting botrytized grape must. Journal of Applied Microbiology, 2005, 98, 971-979.	3.1	47
12	Phoma Saccardo: Distribution, secondary metabolite production and biotechnological applications. Critical Reviews in Microbiology, 2009, 35, 182-196.	6.1	43
13	Genetic diversity of a Botrytis cinerea cryptic species complex in Hungary. Microbiological Research, 2012, 167, 283-291.	5.3	43
14	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
15	Database establishment for the secondary fungal DNA barcodetranslational elongation factor 1Î±(TEF1Î±). Genome, 2019, 62, 160-169.	2.0	41
16	Dual DNA Barcoding for the Molecular Identification of the Agents of Invasive Fungal Infections. Frontiers in Microbiology, 2019, 10, 1647.	3.5	40
17	Taxonomic annotation of public fungal ITS sequences from the built environment â€“ a report from an April 10â€"11, 2017 workshop (Aberdeen, UK). MycoKeys, 2018, 28, 65-82.	1.9	33
18	Preliminary study of the oral mycobiome of children with and without dental caries. Journal of Oral Microbiology, 2019, 11, 1536182.	2.7	30

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19	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
20	Long-read sequencing based clinical metagenomics for the detection and confirmation of Pneumocystis jirovecii directly from clinical specimens: A paradigm shift in mycological diagnostics. Medical Mycology, 2020, 58, 650-660.	0.7	28
21	Taxonomical re-evaluation of Phoma-like soybean pathogenic fungi. Mycological Research, 2009, 113, 249-260.	2.5	26
22	Mycosands: Fungal diversity and abundance in beach sand and recreational waters â€" Relevance to human health. Science of the Total Environment, 2021, 781, 146598.	8.0	24
23	Metatranscriptomics as a tool to identify fungal species and subspecies in mixed communities â€" a proof of concept under laboratory conditions. IMA Fungus, 2019, 10, 12.	3.8	20
24	Annotating public fungal ITS sequences from the built environment according to the MIxS-Built Environment standard â€" a report from a May 23-24, 2016 workshop (Gothenburg, Sweden). MycoKeys, 0, 16, 1-15.	1.9	16
25	Phoma-like fungi on soybeans. Critical Reviews in Microbiology, 2014, 40, 49-62.	6.1	14
26	Genetic differences in Chlamydia pecorum between neighbouring sub-populations of koalas (Phascolarctos cinereus). Veterinary Microbiology, 2019, 231, 264-270.	1.9	14
27	Genetic Heterogeneity of Australian Candida auris Isolates: Insights From a Nonoutbreak Setting Using Whole-Genome Sequencing. Open Forum Infectious Diseases, 2020, 7, ofaa158.	0.9	12
28	Long-Reads-Based Metagenomics in Clinical Diagnosis With a Special Focus on Fungal Infections. Frontiers in Microbiology, 2021, 12, 708550.	3.5	9
29	Finding a Needle in a Haystack â€" In Silico Search for Environmental Traces of <i>Candida auris </i>. Japanese Journal of Infectious Diseases, 2022, 75, 490-495.	1.2	8
30	The mycobiome of Australian tree hollows in relation to theCryptococcus gattiiandC.Âneoformansspecies complexes. Ecology and Evolution, 2019, 9, 9684-9700.	1.9	7
31	Consensus Multilocus Sequence Typing Scheme for Pneumocystis jirovecii. Journal of Fungi (Basel,) Tj ETQq1 1 0.784314 rgBT /Overlo	3.5	7
32	Diversity of Cryphonectria parasitica populations from the Carpathian Basin. Acta Microbiologica Et Immunologica Hungarica, 2015, 62, 247-266.	0.8	3
33	In depth search of the Sequence Read Archive database reveals global distribution of the emerging pathogenic fungus Scedosporium aurantiacum. Medical Mycology, 2022, 60, .	0.7	2
34	Inferring Species Compositions of Complex Fungal Communities from Long- and Short-Read Sequence Data. MBio, 2022, 13, e0244421.	4.1	2
35	DNA barcoding of human and animal pathogenic fungi: the ISHAM-ITS database. Microbiology Australia, 2015, 36, 44.	0.4	1
36	Overview of Phoma-Like Fungi on Important Legumes (Papilionaceous Plants). , 2022, , 65-89.		1

#	Article	IF	Citations
37	Medical and veterinary mycology. Microbiology Australia, 2015, 36, 42.	0.4	0
38	Studies of Expression of Peptaibol Synthetase of Trichoderma reesei. AgrÃ¡rtudomÃ¡nyi KÃ¶zlemÃ©nyek, 2005, , 188-190.	0.3	0
39	Phylogenetic analysis of Phoma species. AgrÃ¡rtudomÃ¡nyi KÃ¶zlemÃ©nyek, 2007, , 100-107.	0.3	0
40	Phylogenetic studies of Phoma species by maximum likelihood analysis. AgrÃ¡rtudomÃ¡nyi KÃ¶zlemÃ©nyek, 2008, , 37-46.	0.3	0
41	Phylogenetic studies of soybean pathogen Phoma species by Bayesian analysis. AgrÃ¡rtudomÃ¡nyi KÃ¶zlemÃ©nyek, 2009, , 53-61.	0.3	0
42	Cytochrome b diversity of Hungarian Botrytis cinerea strains. AgrÃ¡rtudomÃ¡nyi KÃ¶zlemÃ©nyek, 2010, , 18-21.	0.3	0
43	Dieback of apricot plantations caused by 'Ca. Phytoplasma prunorum' in Borsod-AbaÃºj-ZemplÃ©n county (Northern-Hungary). AgrÃ¡rtudomÃ¡nyi KÃ¶zlemÃ©nyek, 2010, , 34-41.	0.3	0
44	Laboratory diagnoses of the isolates of chestnut blight disease fungus Cryphonectria parasitica (MURR. BARR). AgrÃ¡rtudomÃ¡nyi KÃ¶zlemÃ©nyek, 2010, , 45-52.	0.3	0
45	FIRST DETECTION OF THE CHESTNUT BLIGHT FUNGUS ON SESSILE OAK IN UKRAINE. Acta Horticulturae, 2014, , 199-204.	0.2	0
46	NEW DATA OF CRYPHONECTRIA PARASITICA (MURR.) BARR POPULATION IN CARPATHIAN-BASIN. Acta Horticulturae, 2014, , 43-49.	0.2	0