

László G Nagy

List of Publications by Year in descending order

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Version: 2024-02-01

82
papers

7,401
citations

136950

32
h-index

79698

73
g-index

100
all docs

100
docs citations

100
times ranked

7837
citing authors

#	ARTICLE	IF	CITATIONS
1	The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 2012, 336, 1715-1719.	12.6	1,424
2	Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 2015, 47, 410-415.	21.4	870
3	Extensive sampling of basidiomycete genomes demonstrates inadequacy of the white-rot/brown-rot paradigm for wood decay fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9923-9928.	7.1	595
4	FungalTraits: a user-friendly traits database of fungi and fungus-like stramenopiles. <i>Fungal Diversity</i> , 2020, 105, 1-16.	12.3	387
5	Genome sequence of the button mushroom <i>Agaricus bisporus</i> reveals mechanisms governing adaptation to a humic-rich ecological niche. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17501-17506.	7.1	359
6	Large-scale genome sequencing of mycorrhizal fungi provides insights into the early evolution of symbiotic traits. <i>Nature Communications</i> , 2020, 11, 5125.	12.8	258
7	Notes, outline and divergence times of Basidiomycota. <i>Fungal Diversity</i> , 2019, 99, 105-367.	12.3	256
8	Comparative Genomics of Early-Diverging Mushroom-Forming Fungi Provides Insights into the Origins of Lignocellulose Decay Capabilities. <i>Molecular Biology and Evolution</i> , 2016, 33, 959-970.	8.9	213
9	Long-term thermal sensitivity of Earth's tropical forests. <i>Science</i> , 2020, 368, 869-874.	12.6	198
10	Megaphylogeny resolves global patterns of mushroom evolution. <i>Nature Ecology and Evolution</i> , 2019, 3, 668-678.	7.8	187
11	Genome expansion and lineage-specific genetic innovations in the forest pathogenic fungus <i>Armillaria</i> . <i>Nature Ecology and Evolution</i> , 2017, 1, 1931-1941.	7.8	145
12	Evolution of novel wood decay mechanisms in Agaricales revealed by the genome sequences of <i>Fistulina hepatica</i> and <i>Cylindrobasidium torrendii</i> . <i>Fungal Genetics and Biology</i> , 2015, 76, 78-92.	2.1	141
13	Comparative genomics provides insights into the lifestyle and reveals functional heterogeneity of dark septate endophytic fungi. <i>Scientific Reports</i> , 2018, 8, 6321.	3.3	138
14	Lignin-degrading peroxidases in Polyporales: an evolutionary survey based on 10 sequenced genomes. <i>Mycologia</i> , 2013, 105, 1428-1444.	1.9	134
15	Latent homology and convergent regulatory evolution underlies the repeated emergence of yeasts. <i>Nature Communications</i> , 2014, 5, 4471.	12.8	133
16	Transcriptomic atlas of mushroom development reveals conserved genes behind complex multicellularity in fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7409-7418.	7.1	115
17	Global maps of soil temperature. <i>Global Change Biology</i> , 2022, 28, 3110-3144.	9.5	113
18	Re-Mind the Gap! Insertion-Deletion Data Reveal Neglected Phylogenetic Potential of the Nuclear Ribosomal Internal Transcribed Spacer (ITS) of Fungi. <i>PLoS ONE</i> , 2012, 7, e49794.	2.5	97

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19	Peizizomycetes genomes reveal the molecular basis of ectomycorrhizal truffle lifestyle. <i>Nature Ecology and Evolution</i> , 2018, 2, 1956-1965.	7.8	95
20	Complex multicellularity in fungi: evolutionary convergence, single origin, or both?. <i>Biological Reviews</i> , 2018, 93, 1778-1794.	10.4	92
21	Comparative genomics reveals the origin of fungal hyphae and multicellularity. <i>Nature Communications</i> , 2019, 10, 4080.	12.8	80
22	Where is the unseen fungal diversity hidden? A study of <i>Mortierella</i> reveals a large contribution of reference collections to the identification of fungal environmental sequences. <i>New Phytologist</i> , 2011, 191, 789-794.	7.3	79
23	Genetic Bases of Fungal White Rot Wood Decay Predicted by Phylogenomic Analysis of Correlated Gene-Phenotype Evolution. <i>Molecular Biology and Evolution</i> , 2017, 34, 35-44.	8.9	65
24	Fruiting body form, not nutritional mode, is the major driver of diversification in mushroom-forming fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 32528-32534.	7.1	65
25	The global abundance of tree palms. <i>Global Ecology and Biogeography</i> , 2020, 29, 1495-1514.	5.8	62
26	Understanding the Evolutionary Processes of Fungal Fruiting Bodies: Correlated Evolution and Divergence Times in the Psathyrellaceae. <i>Systematic Biology</i> , 2011, 60, 303-317.	5.6	56
27	Genomics and Development of <i>Lentinus tigrinus</i> : A White-Rot Wood-Decaying Mushroom with Dimorphic Fruiting Bodies. <i>Genome Biology and Evolution</i> , 2018, 10, 3250-3261.	2.5	53
28	Comparative genomics reveals unique wood decay strategies and fruiting body development in the Schizophyllaceae. <i>New Phytologist</i> , 2019, 224, 902-915.	7.3	53
29	Gene family expansions and transcriptome signatures uncover fungal adaptations to wood decay. <i>Environmental Microbiology</i> , 2021, 23, 5716-5732.	3.8	44
30	NFAP2, a novel cysteine-rich anti-yeast protein from <i>Neosartorya fischeri</i> NRRL 181: isolation and characterization. <i>AMB Express</i> , 2016, 6, 75.	3.0	43
31	Molecular identification of <i>Trichoderma</i> species associated with <i>Pleurotus ostreatus</i> and natural substrates of the oyster mushroom. <i>FEMS Microbiology Letters</i> , 2009, 300, 58-67.	1.8	42
32	Data Partitions, Bayesian Analysis and Phylogeny of the Zygomycetous Fungal Family Mortierellaceae, Inferred from Nuclear Ribosomal DNA Sequences. <i>PLoS ONE</i> , 2011, 6, e27507.	2.5	37
33	Iteratively Refined Guide Trees Help Improving Alignment and Phylogenetic Inference in the Mushroom Family Bolbitiaceae. <i>PLoS ONE</i> , 2013, 8, e56143.	2.5	34
34	Model Choice, Missing Data, and Taxon Sampling Impact Phylogenomic Inference of Deep Basidiomycota Relationships. <i>Systematic Biology</i> , 2020, 69, 17-37.	5.6	34
35	Novel phylogenetic methods are needed for understanding gene function in the era of mega-scale genome sequencing. <i>Nucleic Acids Research</i> , 2020, 48, 2209-2219.	14.5	32
36	Morphological characterization of clades of the Psathyrellaceae (Agaricales) inferred from a multigene phylogeny. <i>Mycological Progress</i> , 2013, 12, 505-517.	1.4	31

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37	Phylogenetic relationships and morphological evolution in <i>Lentinus</i> , <i>Polyporellus</i> and <i>Neofavolus</i> , emphasizing southeastern Asian taxa. <i>Mycologia</i> , 2015, 107, 460-474.	1.9	31
38	Six Key Traits of Fungi: Their Evolutionary Origins and Genetic Bases. <i>Microbiology Spectrum</i> , 2017, 5, .	3.0	31
39	<i>Mycena</i> genomes resolve the evolution of fungal bioluminescence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31267-31277.	7.1	30
40	The Evolution of Defense Mechanisms Correlate with the Explosive Diversification of Autodigesting <i>Coprinellus</i> Mushrooms (Agaricales, Fungi). <i>Systematic Biology</i> , 2012, 61, 595-607.	5.6	29
41	Evolution: Complex Multicellular Life with 5,500 Genes. <i>Current Biology</i> , 2017, 27, R609-R612.	3.9	29
42	<i>Armillaria</i> . <i>Current Biology</i> , 2018, 28, R297-R298.	3.9	29
43	No Indication of Strict Host Associations in a Widespread Mycoparasite: Grapevine Powdery Mildew (<i>Erysiphe necator</i>) Is Attacked by Phylogenetically Distant <i>Ampelomyces</i> Strains in the Field. <i>Phytopathology</i> , 2012, 102, 707-716.	2.2	28
44	The evolution of autodigestion in the mushroom family Psathyrellaceae (Agaricales) inferred from Maximum Likelihood and Bayesian methods. <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 1037-1048.	2.7	27
45	Phylogeny and species delimitation in the genus <i>Coprinellus</i> with special emphasis on the haired species. <i>Mycologia</i> , 2012, 104, 254-275.	1.9	25
46	Fungi took a unique evolutionary route to multicellularity: Seven key challenges for fungal multicellular life. <i>Fungal Biology Reviews</i> , 2020, 34, 151-169.	4.7	25
47	Unmatched Level of Molecular Convergence among Deeply Divergent Complex Multicellular Fungi. <i>Molecular Biology and Evolution</i> , 2020, 37, 2228-2240.	8.9	23
48	Hallmarks of Basidiomycete Soft- and White-Rot in Wood-Decay -Omics Data of Two <i>Armillaria</i> Species. <i>Microorganisms</i> , 2021, 9, 149.	3.6	23
49	Evolutionary transition to the ectomycorrhizal habit in the genomes of a hyperdiverse lineage of mushroom-forming fungi. <i>New Phytologist</i> , 2022, 233, 2294-2309.	7.3	21
50	Transcriptome data reveal conserved patterns of fruiting body development and response to heat stress in the mushroom-forming fungus <i>Flammulina filiformis</i> . <i>PLoS ONE</i> , 2020, 15, e0239890.	2.5	20
51	Ectomycorrhizal Plant-Fungal Co-invasions as Natural Experiments for Connecting Plant and Fungal Traits to Their Ecosystem Consequences. <i>Frontiers in Forests and Global Change</i> , 2020, 3, .	2.3	20
52	Type studies and nomenclatural revisions in <i>Parasola</i> (Psathyrellaceae) and related taxa. <i>Mycotaxon</i> , 2010, 112, 103-141.	0.3	19
53	Evolutionary innovations through gain and loss of genes in the ectomycorrhizal Boletales. <i>New Phytologist</i> , 2022, 233, 1383-1400.	7.3	19
54	Gene age shapes the transcriptional landscape of sexual morphogenesis in mushroom-forming fungi (Agaricomycetes). <i>ELife</i> , 2022, 11, .	6.0	18

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55	Phylogenetic analyses of <i>Coprinopsis</i> sections <i>Lanatuli</i> and <i>Atramentarii</i> identify multiple species within morphologically defined taxa. <i>Mycologia</i> , 2013, 105, 112-124.	1.9	17
56	Fungal Phylogeny in the Age of Genomics: Insights Into Phylogenetic Inference From Genome-Scale Datasets. <i>Advances in Genetics</i> , 2017, 100, 49-72.	1.8	16
57	A new β -glucosidase gene from the zygomycete fungus <i>Rhizomucor miehei</i> . <i>Antonie Van Leeuwenhoek</i> , 2010, 97, 1-10.	1.7	14
58	Molecular identification and antifungal susceptibility of <i>Curvularia australiensis</i> , <i>C. hawaiiensis</i> and <i>C. Aspicifera</i> isolated from human eye infections. <i>Mycoses</i> , 2015, 58, 603-609.	4.0	14
59	A common soil temperature threshold for the upper limit of alpine grasslands in European mountains. <i>Alpine Botany</i> , 2021, 131, 41-52.	2.4	13
60	Evolutionary Morphogenesis of Sexual Fruiting Bodies in Basidiomycota: Toward a New Evo-Devo Synthesis. <i>Microbiology and Molecular Biology Reviews</i> , 2022, 86, e0001921.	6.6	13
61	<i>Coprinellus radicellus</i> , a new species with northern distribution. <i>Mycological Progress</i> , 2011, 10, 363-371.	1.4	10
62	Six Key Traits of Fungi: Their Evolutionary Origins and Genetic Bases. , 2017, , 35-56.		10
63	Many roads to convergence. <i>Science</i> , 2018, 361, 125-126.	12.6	10
64	<i>Psathyroma</i> , a new genus in Hymenogastraceae described from New Zealand. <i>Mycologia</i> , 2016, 108, 397-404.	1.9	9
65	The genus <i>Parasola</i> : phylogeny and the description of three new species. <i>Mycologia</i> , 2017, 109, 1-10.	1.9	8
66	Type studies and fourteen new North American species of <i>Cortinarius</i> section <i>Anomali</i> reveal high continental species diversity. <i>Mycological Progress</i> , 2021, 20, 1399-1439.	1.4	5
67	Reappraisal of the Genus <i>Exsudoporus</i> (Boletaceae) Worldwide Based on Multi-Gene Phylogeny, Morphology and Biogeography, and Insights on <i>Amoenoboletus</i> . <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 101.	3.5	5
68	Radiation of mushroom-forming fungi correlates with novel modes of protecting sexual fruiting bodies. <i>Fungal Biology</i> , 2022, 126, 556-565.	2.5	5
69	Fungal Phylogenomics. <i>Methods in Molecular Biology</i> , 2018, 1775, 251-266.	0.9	4
70	Homology modeling and phylogenetic relationships of catalases of an opportunistic pathogen <i>Rhizopus oryzae</i> . <i>Life Sciences</i> , 2012, 91, 115-126.	4.3	2
71	Mycology: Rediscovery of a lost model fungus highlights the origin of mycorrhizal symbioses. <i>Current Biology</i> , 2021, 31, R342-R344.	3.9	1
72	Evolution of opposing regulatory interactions underlies the emergence of eukaryotic cell cycle checkpoints. <i>Scientific Reports</i> , 2021, 11, 11122.	3.3	1

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73	Nitrogen pulses increase fungal pathogens in Amazonian lowland tropical rain forests. Journal of Ecology, 2022, 110, 1775-1789.	4.0	1
74	Assessment of selective logging impacts using UAV, Landsat, and Sentinel data in the Brazilian Amazon rainforest. Journal of Applied Remote Sensing, 2022, 16, .	1.3	0
75	Title is missing!. , 2020, 15, e0239890.		0
76	Title is missing!. , 2020, 15, e0239890.		0
77	Title is missing!. , 2020, 15, e0239890.		0
78	Title is missing!. , 2020, 15, e0239890.		0
79	Title is missing!. , 2020, 15, e0239890.		0
80	Title is missing!. , 2020, 15, e0239890.		0
81	Title is missing!. , 2020, 15, e0239890.		0
82	Title is missing!. , 2020, 15, e0239890.		0