Tuan A Duong

List of Publications by Year
in descending order

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72	6,560	218677	91884
papers	citations	26 h-index	69 g-index

72	72	72	7881
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6241-6246.	7.1	4,012
2	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
3	Fungal Planet description sheets: 214â€“280. Persoonia: Molecular Phylogeny and Evolution of Fungi, 2014, 32, 184-306.	4.4	229
4	Redefining Ceratocystis and allied genera. Studies in Mycology, 2014, 79, 187-219.	7.2	216
5	The divorce of Sporothrix and Ophiostoma: solution to a problematic relationship. Studies in Mycology, 2016, 83, 165-191.	7.2	169
6	Fungal Planet description sheets: 371â€“399. Persoonia: Molecular Phylogeny and Evolution of Fungi, 2015, 35, 264-327.	4.4	133
7	Phylogeny and taxonomy of species in theGrosmannia serpenscomplex. Mycologia, 2012, 104, 715-732.	1.9	67
8	Draft genome sequences of Ceratocystis eucalypticola, Chrysoporthe cubensis, C. deuterocubensis, Davidsoniella virescens, Fusarium temperatum, Graphilbum fragrans, Penicillium nordicum, and Thielaviopsis musarum. IMA Fungus, 2015, 6, 493-506.	3.8	57
9	New and Interesting Fungi. 4. Fungal Systematics and Evolution, 2021, 7, 255-343.	2.2	53
10	Large Shift in Symbiont Assemblage in the Invasive Red Turpentine Beetle. PLoS ONE, 2013, 8, e78126.	2.5	51
11	Development of a Nested Quantitative Real-Time PCR for Detecting Phytophthora cinnamomi in Persea americana Rootstocks. Plant Disease, 2013, 97, 1012-1017.	1.4	50
12	Characterization of the mating-type genes in Leptographium procerum and Leptographium profanum. Fungal Biology, 2013, 117, 411-421.	2.5	46
13	MAT gene idiomorphs suggest a heterothallic sexual cycle in a predominantly asexual and important pine pathogen. Fungal Genetics and Biology, 2014, 62, 55-61.	2.1	46
14	Draft genome sequences of Chrysoporthe austroafricana, Diplodia scrobiculata, Fusarium nygamai, Leptographium lundbergii, Limonomyces culmigenus, Stagonosporopsis tanaceti, and Thielaviopsis punctulata. IMA Fungus, 2015, 6, 233-248.	3.8	46
15	Taxonomy and phylogeny of the Leptographium procerum complex, including Leptographium sinense sp. nov. and Leptographium longiconidiophorum sp. nov.. Antonie Van Leeuwenhoek, 2015, 107, 547-563.	1.7	46
16	Hawksworthiomyces gen. nov. (Ophiostomatales), illustrates the urgency for a decision on how to name novel taxa known only from environmental nucleic acid sequences (ENAS). Fungal Biology, 2016, 120, 1323-1340.	2.5	44
17	Grosmannia and Leptographium spp. associated with conifer-infesting bark beetles in Finland and Russia, including Leptographium taigense sp. nov.. Antonie Van Leeuwenhoek, 2012, 102, 375-399.	1.7	43
18	Ophiostomatoid fungi associated with conifer-infesting beetles and their phoretic mites in Yunnan, China. MycoKeys, 2017, 28, 19-64.	1.9	43

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19	A new genus and species for the globally important, multihost root pathogen Thielaviopsis basicola. Plant Pathology, 2018, 67, 871-882.	2.4	42
20	IMA Genome-F 6. IMA Fungus, 2016, 7, 217-227.	3.8	39
21	Reconsideration of species boundaries and proposed DNA barcodes for Calonectria. Studies in Mycology, 2020, 97, 100106.	7.2	39
22	Draft genome of Cercospora zeina, Fusarium pininemorale, Hawksworthiomyces lignivorus, Huntiella decipiens and Ophiostoma ips. IMA Fungus, 2017, 8, 385-396.	3.8	37
23	Draft genome sequence of Annulohypoxylon stygium, Aspergillus mulundensis, Berkeleyomyces basicola (syn. Thielaviopsis basicola), Ceratocystis smalleyi, two Cercospora beticola strains, Coleophoma cylindrospora, Fusarium fracticaudum, Phialophora cf. hyalina, and Morchella septimelata. IMA Fungus, 2018, 9, 199-223.	3.8	37
24	Bretziella, a new genus to accommodate the oak wilt fungus, Ceratocystis fagacearum (Microascales,) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.9	36
25	Draft genome sequences for Ceratocystis fagacearum, C. harringtonii, Grosmannia penicillata, and Huntiella bhutanensis. IMA Fungus, 2016, 7, 317-323.	3.8	31
26	Nine draft genome sequences of Claviceps purpurea s.lat., including C. arundinis, C. humidiphila, and C. cf. spartinae, pseudomolecules for the pitch canker pathogen Fusarium circinatum, draft genome of Davidsoniella eucalypti, Grosmannia galeiformis, Quambalaria eucalypti, and Teratosphaeria destructans. IMA Fungus, 2018, 9, 401-418.	3.8	31
27	New species of Ophiostomatales from Scolytinae and Platypodinae beetles in the Cape Floristic Region, including the discovery of the sexual state of Raffaelea. Antonie Van Leeuwenhoek, 2015, 108, 933-950.	1.7	30
28	Armillaria root rot fungi host single-stranded RNA viruses. Scientific Reports, 2021, 11, 7336.	3.3	30
29	Ophiostomatoid fungi associated with the spruce bark beetle Ips typographus, including 11 new species from China. Persoonia: Molecular Phylogeny and Evolution of Fungi, 2019, 42, 50-74.	4.4	28
30	Fungal associates of the lodgepole pine beetle, Dendroctonus murrayanae. Antonie Van Leeuwenhoek, 2011, 100, 231-244.	1.7	27
31	Genome of the destructive oomycete Phytophthora cinnamomi provides insights into its pathogenicity and adaptive potential. BMC Genomics, 2021, 22, 302.	2.8	24
32	Cornuvesica: A little known mycophilic genus with a unique biology and unexpected new species. Fungal Biology, 2015, 119, 615-630.	2.5	22
33	New microsatellite markers for population studies of Phytophthora cinnamomi, an important global pathogen. Scientific Reports, 2017, 7, 17631.	3.3	20
34	Bark beetle mycobiome: collaboratively defined research priorities on a widespread insect-fungus symbiosis. Symbiosis, 2020, 81, 101-113.	2.3	20
35	Multigene phylogenies of Ophiostomataceae associated with Monterey pine bark beetles in Spain reveal three new fungal species. Mycologia, 2014, 106, 119-132.	1.9	19
36	Mating strategy and mating type distribution in six global populations of the Eucalyptus foliar pathogen Teratosphaeria destructans. Fungal Genetics and Biology, 2020, 137, 103350.	2.1	19

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37	Draft genome sequences of five Calonectria species from Eucalyptus plantations in China, Celoporthe dispersa, Sporothrix phasma and Alectoria sarmentosa. IMA Fungus, 2019, 10, 22.	3.8	17
38	Diversity and bioactivities of nostocacean cyanobacteria isolated from paddy soil in Vietnam. Systematic and Applied Microbiology, 2017, 40, 470-481.	2.8	16
39	IMA Genome - F13. IMA Fungus, 2020, 11, 19.	3.8	13
40	Putative origins of the fungus Leptographium procerum. Fungal Biology, 2017, 121, 82-94.	2.5	12
41	Black root rot: a long known but little understood disease. Plant Pathology, 2019, 68, 834-842.	2.4	12
42	IMA Genome-F 11. IMA Fungus, 2019, 10, 13.	3.8	12
43	Chromium sequencing: the doors open for genomics of obligate plant pathogens. BioTechniques, 2018, 65, 253-257.	1.8	11
44	Heterothallism revealed in the root rot fungi Berkeleyomyces basicola and B.Ârouxiae. Fungal Biology, 2018, 122, 1031-1040.	2.5	11
45	Genomic analysis of the aggressive tree pathogen Ceratocystis albifundus. Fungal Biology, 2019, 123, 351-363.	2.5	11
46	Eucalyptus scab and shoot malformation: A new and serious foliar disease of Eucalyptus caused by Elsinoe necatrix sp. nov.. Plant Pathology, 2021, 70, 1230-1242.	2.4	11
47	Fungal associates of an invasive pine-infesting bark beetle, Dendroctonus valens, including seven new Ophiostomatalean fungi. Persoonia: Molecular Phylogeny and Evolution of Fungi, 2020, 45, 177-195.	4.4	10
48	Mating type markers reveal high levels of heterothallism in Leptographium sensu lato. Fungal Biology, 2016, 120, 538-546.	2.5	9
49	The granulate ambrosia beetle, Xylosandrus crassiusculus (Coleoptera: Curculionidae, Scolytinae), and its fungal symbiont found in South Africa . Zootaxa, 2020, 4838, 427-435.	0.5	9
50	Genome comparisons suggest an association between Ceratocystis host adaptations and effector clusters in unique transposable element families. Fungal Genetics and Biology, 2020, 143, 103433.	2.1	9
51	Ras2 is important for growth and pathogenicity in Fusarium circinatum. Fungal Genetics and Biology, 2021, 150, 103541.	2.1	9
52	Microsatellite and mating type markers reveal unexpected patterns of genetic diversity in the pine rootâ€infecting fungus Grosmannia alacris. Plant Pathology, 2015, 64, 235-242.	2.4	8
53	Wounds on Rapanea melanophloeos provide habitat for a large diversity of Ophiostomatales including four new species. Antonie Van Leeuwenhoek, 2016, 109, 877-894.	1.7	8
54	IMA Genome - F15. IMA Fungus, 2021, 12, 30.	3.8	8

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55	Population genomics reveals historical and ongoing recombination in the Fusarium oxysporum species complex. Studies in Mycology, 2021, 99, 100132-100132.	7.2	8
56	Ophiostomatalean fungi associated with wood boring beetles in South Africa including two new species. Antonie Van Leeuwenhoek, 2021, 114, 667-686.	1.7	7
57	Ophiostomatoid fungi associated with mites phoretic on bark beetles in Qinghai, China. IMA Fungus, 2020, 11, 15.	3.8	6
58	Filamentous Fungi and Yeasts Associated with Mites Phoretic on Ips typographus in Eastern Finland. Forests, 2021, 12, 743.	2.1	6
59	IMA genome - F14. IMA Fungus, 2021, 12, 5.	3.8	5
60	Four New Species of Harringtonia: Unravelling the Laurel Wilt Fungal Genus. Journal of Fungi (Basel,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.5	5
61	New ophiostomatoid fungi from wounds on storm-damaged trees in Afromontane forests of the Cape Floristic Region. Mycological Progress, 2020, 19, 81-95.	1.4	4
62	Population Diversity and Genetic Structure Reveal Patterns of Host Association and Anthropogenic Impact for the Globally Important Fungal Tree Pathogen Ceratocystis manginecans. Journal of Fungi (Basel, Switzerland), 2021, 7, 759.	3.5	4
63	IMA Genome - F16. IMA Fungus, 2022, 13, 3.	3.8	4
64	Intra-Species Genomic Variation in the Pine Pathogen Fusarium circinatum. Journal of Fungi (Basel,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.5	4
65	Population genetic analyses of Phytophthora cinnamomi reveals three lineages and movement between natural vegetation and avocado orchards in South Africa. Phytopathology, 2022, , .	2.2	3
66	Molecular basis of cycloheximide resistance in the Ophiostomatales revealed. Current Genetics, 2022, 68, 505-514.	1.7	3
67	A new Leptographium species from the roots of declining Pinus sylvestris in Switzerland. Forest Pathology, 2017, 47, e12346.	1.1	2
68	Phylogenetic and phylogenomic analyses reveal two new genera and three new species of ophiostomatalean fungi from termite fungus combs. Mycologia, 2021, 113, 1-19.	1.9	2
69	Microsatellite markers for Grosmannia alacris (Ophiostomataceae, Ascomycota) and other species in the G. serpens complex. American Journal of Botany, 2012, 99, e216-9.	1.7	1
70	The relevance of studying insectâ€“nematode interactions for human disease. Pathogens and Global Health, 2022, 116, 140-145.	2.3	1
71	Ophiostomatoid fungi including a new species associated with Asian larch bark beetle Ips subelongatus, in Heilongjiang (Northeast China). Fungal Systematics and Evolution, 2021, 8, 155-161.	2.2	1
72	(2592) Proposal to conserve Endoconidiophora fagacearum (Bretziella fagacearum, Ceratocystis) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.7	0