

Felix Grewe

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

1,950
citations

304743

22
h-index

276875

41
g-index

51
all docs

51
docs citations

51
times ranked

1853
citing authors

#	ARTICLE	IF	CITATIONS
1	Should we hail the Red King? Evolutionary consequences of a mutualistic lifestyle in genomes of lichenized ascomycetes. <i>Ecology and Evolution</i> , 2022, 12, e8471.	1.9	4
2	Early stages of speciation with gene flow in the Amazilia Hummingbird (<i>Amazilia amazilia</i>) subspecies complex of Western South America. <i>Ecology and Evolution</i> , 2022, 12, e8895.	1.9	1
3	Interpreting phylogenetic conflict: Hybridization in the most speciose genus of lichen-forming fungi. <i>Molecular Phylogenetics and Evolution</i> , 2022, 174, 107543.	2.7	2
4	Using RADseq to understand the circum-Antarctic distribution of a lichenized fungus, <i>Pseudocyphellaria glabra</i> . <i>Journal of Biogeography</i> , 2021, 48, 78-90.	3.0	11
5	Population genomics of a reindeer lichen species from North American lichen woodlands. <i>American Journal of Botany</i> , 2021, 108, 159-171.	1.7	8
6	Effects of dispersal strategy and migration history on genetic diversity and population structure of Antarctic lichens. <i>Journal of Biogeography</i> , 2021, 48, 1635-1653.	3.0	13
7	Diversity of Xanthoparmelia (Parmeliaceae) species in Mexican xerophytic scrub vegetation, evidenced by molecular, morphological and chemistry data. <i>Anales Del Jardin Botanico De Madrid</i> , 2021, 78, e107.	0.4	2
8	Phylogenomic reconstruction addressing the Peltigeralean backbone (Lecanoromycetes, Ascomycota). <i>Fungal Diversity</i> , 2021, 110, 59.	12.3	3
9	Museum genomics reveals the Xerces blue butterfly (<i>Glaucopsyche xerces</i>) was a distinct species driven to extinction. <i>Biology Letters</i> , 2021, 17, 20210123.	2.3	15
10	The genomic basis of army ant chemosensory adaptations. <i>Molecular Ecology</i> , 2021, 30, 6627-6641.	3.9	9
11	On the nomenclature of the American clade of weasels (Carnivora: Mustelidae). <i>Journal of Animal Diversity</i> , 2021, 3, 1-8.	0.5	17
12	IMA Genome - F15. <i>IMA Fungus</i> , 2021, 12, 30.	3.8	8
13	Contributions to the phylogeny of Lepraria (Stereocaulaceae) species from the Southern Hemisphere, including three new species. <i>Bryologist</i> , 2021, 124, .	0.6	2
14	Species boundaries in the messy middle—A genome-scale validation of species delimitation in a recently diverged lineage of coastal fog desert lichen fungi. <i>Ecology and Evolution</i> , 2021, 11, 18615-18632.	1.9	6
15	Characterizing the ribosomal tandem repeat and its utility as a DNA barcode in lichen-forming fungi. <i>BMC Evolutionary Biology</i> , 2020, 20, 2.	3.2	16
16	Genome-Wide Analysis of Biosynthetic Gene Cluster Reveals Correlated Gene Loss with Absence of Usnic Acid in Lichen-Forming Fungi. <i>Genome Biology and Evolution</i> , 2020, 12, 1858-1868.	2.5	28
17	IMA Genome - F13. <i>IMA Fungus</i> , 2020, 11, 19.	3.8	13
18	Metagenomic data reveal diverse fungal and algal communities associated with the lichen symbiosis. <i>Symbiosis</i> , 2020, 82, 133-147.	2.3	34

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19	Using target enrichment sequencing to study the higher-level phylogeny of the largest lichen-forming fungi family: Parmeliaceae (Ascomycota). <i>IMA Fungus</i> , 2020, 11, 27.	3.8	7
20	Genome-scale data reveal the role of hybridization in lichen-forming fungi. <i>Scientific Reports</i> , 2020, 10, 1497.	3.3	26
21	Genome-scale data resolve ancestral rock-inhabiting lifestyle in Dothideomycetes (Ascomycota). <i>IMA Fungus</i> , 2019, 10, 19.	3.8	17
22	Multiple historical processes obscure phylogenetic relationships in a taxonomically difficult group (Lobariaceae, Ascomycota). <i>Scientific Reports</i> , 2019, 9, 8968.	3.3	32
23	Life in wood: preliminary phylogeny of deep-sea wood-boring bivalves (Xylophagaidae), with descriptions of three new genera and one new species. <i>Journal of Molluscan Studies</i> , 2019, 85, 232-243.	1.2	21
24	Lycophyte plastid genomics: extreme variation in GC , gene and intron content and multiple inversions between a direct and inverted orientation of the $rRNA$ repeat. <i>New Phytologist</i> , 2019, 222, 1061-1075.	7.3	51
25	Phylogenetic study and taxonomic revision of the <i>Xanthoparmelia mexicana</i> group, including the description of a new species (Parmeliaceae, Ascomycota). <i>MycKeys</i> , 2018, 40, 13-28.	1.9	4
26	Assessing phylogeny and historical biogeography of the largest genus of lichen-forming fungi, <i>Xanthoparmelia</i> (Parmeliaceae, Ascomycota). <i>Lichenologist</i> , 2018, 50, 299-312.	0.8	20
27	Phylogenomic analysis of 2556 single-copy protein-coding genes resolves most evolutionary relationships for the major clades in the most diverse group of lichen-forming fungi. <i>Fungal Diversity</i> , 2018, 92, 31-41.	12.3	19
28	Population genomic analyses of RAD sequences resolves the phylogenetic relationship of the lichen-forming fungal species <i>Usnea antarctica</i> and <i>Usnea aurantiacoatra</i> . <i>MycKeys</i> , 2018, 43, 91-113.	1.9	36
29	Reference-based RADseq resolves robust relationships among closely related species of lichen-forming fungi using metagenomic DNA. <i>Scientific Reports</i> , 2017, 7, 9884.	3.3	33
30	Loss of a Trans-splicing $nad1$ Intron from Geraniaceae and Transfer of the Maturase Gene $matR$ to the Nucleus in <i>Pelargonium</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 3193-3201.	2.5	22
31	Reverse U-to-C editing exceeds C-to-U RNA editing in some ferns – a monilophyte-wide comparison of chloroplast and mitochondrial RNA editing suggests independent evolution of the two processes in both organelles. <i>BMC Evolutionary Biology</i> , 2016, 16, 134.	3.2	64
32	Laser capture microdissection microscopy and genome sequencing of the avian malaria parasite, <i>Plasmodium relictum</i> . <i>Parasitology Research</i> , 2016, 115, 4503-4510.	1.6	20
33	Resolving evolutionary relationships in lichen-forming fungi using diverse phylogenomic datasets and analytical approaches. <i>Scientific Reports</i> , 2016, 6, 22262.	3.3	42
34	The Reverse Transcriptase/RNA Maturase Protein MatR Is Required for the Splicing of Various Group II Introns in Brassicaceae Mitochondria. <i>Plant Cell</i> , 2016, 28, 2805-2829.	6.6	91
35	<i>Ginkgo</i> and <i>Welwitschia</i> Mitogenomes Reveal Extreme Contrasts in Gymnosperm Mitochondrial Evolution. <i>Molecular Biology and Evolution</i> , 2016, 33, 1448-1460.	8.9	151
36	Monilophyte mitochondrial $rps1$ genes carry a unique group II intron that likely originated from an ancient paralog in $rpl2$. <i>Rna</i> , 2016, 22, 1338-1348.	3.5	11

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37	Dynamic evolution of <i>Geranium</i> mitochondrial genomes through multiple horizontal and intracellular gene transfers. <i>New Phytologist</i> , 2015, 208, 570-583.	7.3	84
38	Horsetails are the sister group to all other monilophytes and Marattiales are sister to leptosporangiate ferns. <i>Molecular Phylogenetics and Evolution</i> , 2015, 90, 140-149.	2.7	56
39	Extreme Features of the <i>Galdieria sulphuraria</i> Organellar Genomes: A Consequence of Polyextremophily?. <i>Genome Biology and Evolution</i> , 2015, 7, 367-380.	2.5	31
40	Variable Frequency of Plastid RNA Editing among Ferns and Repeated Loss of Uridine-to-Cytidine Editing from Vascular Plants. <i>PLoS ONE</i> , 2015, 10, e0117075.	2.5	58
41	Predominant and Substoichiometric Isomers of the Plastid Genome Coexist within <i>Juniperus</i> Plants and Have Shifted Multiple Times during Cupressophyte Evolution. <i>Genome Biology and Evolution</i> , 2014, 6, 580-590.	2.5	91
42	Comparative analysis of 11 Brassicales mitochondrial genomes and the mitochondrial transcriptome of <i>Brassica oleracea</i> . <i>Mitochondrion</i> , 2014, 19, 135-143.	3.4	81
43	Complete plastid genomes from <i>Ophioglossum californicum</i> , <i>Psilotum nudum</i> , and <i>Equisetum hyemale</i> reveal an ancestral land plant genome structure and resolve the position of Equisetales among monilophytes. <i>BMC Evolutionary Biology</i> , 2013, 13, 8.	3.2	91
44	Mitochondrial Genome Evolution in the Plant Lineage. , 2011, , 3-29.		35
45	Extreme RNA Editing in Coding Islands and Abundant Microsatellites in Repeat Sequences of <i>Selaginella moellendorffii</i> Mitochondria: The Root of Frequent Plant mtDNA Recombination in Early Tracheophytes. <i>Genome Biology and Evolution</i> , 2011, 3, 344-358.	2.5	164
46	A unique transcriptome: 1782 positions of RNA editing alter 1406 codon identities in mitochondrial mRNAs of the lycophyte <i>Isoetes engelmannii</i> . <i>Nucleic Acids Research</i> , 2011, 39, 2890-2902.	14.5	102
47	Introducing the plant RNA editing prediction and analysis computer tool PREPACT and an update on RNA editing site nomenclature. <i>Current Genetics</i> , 2010, 56, 189-201.	1.7	50
48	A trans-splicing group I intron and tRNA-hyperediting in the mitochondrial genome of the lycophyte <i>Isoetes engelmannii</i> . <i>Nucleic Acids Research</i> , 2009, 37, 5093-5104.	14.5	139
49	Ancestors of Trans-Splicing Mitochondrial Introns Support Serial Sister Group Relationships of Hornworts and Mosses with Vascular Plants. <i>Molecular Biology and Evolution</i> , 2004, 22, 117-125.	8.9	104