

Anna Lipzen

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

3,401
citations

279778

23
h-index

168376

53
g-index

64
all docs

64
docs citations

64
times ranked

4077
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	Comparative genomics and transcriptomics depict ericoid mycorrhizal fungi as versatile saprotrophs and plant mutualists. <i>New Phytologist</i> , 2018, 217, 1213-1229.	7.3	185
4	Ectomycorrhizal ecology is imprinted in the genome of the dominant symbiotic fungus <i>Cenococcum geophilum</i> . <i>Nature Communications</i> , 2016, 7, 12662.	12.8	156
5	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
6	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , 2021, 590, 438-444.	27.8	144
7	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
8	The <i>Physcomitrella patens</i> gene atlas project: large-scale RNA-seq based expression data. <i>Plant Journal</i> , 2018, 95, 168-182.	5.7	115
9	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
10	The genomic landscape of molecular responses to natural drought stress in <i>Panicum hallii</i> . <i>Nature Communications</i> , 2018, 9, 5213.	12.8	101
11	Genetic isolation between two recently diverged populations of a symbiotic fungus. <i>Molecular Ecology</i> , 2015, 24, 2747-2758.	3.9	100
12	Strand-Specific RNA-Seq Analyses of Fruiting Body Development in <i>Coprinopsis cinerea</i> . <i>PLoS ONE</i> , 2015, 10, e0141586.	2.5	95
13	Genome-wide association analysis of stalk biomass and anatomical traits in maize. <i>BMC Plant Biology</i> , 2019, 19, 45.	3.6	77
14	The regulatory and transcriptional landscape associated with carbon utilization in a filamentous fungus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 6003-6013.	7.1	75
15	A new reference genome for <i>Sorghum bicolor</i> reveals high levels of sequence similarity between sweet and grain genotypes: implications for the genetics of sugar metabolism. <i>BMC Genomics</i> , 2019, 20, 420.	2.8	73
16	Genomic Analysis Enlightens Agaricales Lifestyle Evolution and Increasing Peroxidase Diversity. <i>Molecular Biology and Evolution</i> , 2021, 38, 1428-1446.	8.9	72
17	Genetic determinants of endophytism in the <i>Arabidopsis</i> root mycobiome. <i>Nature Communications</i> , 2021, 12, 7227.	12.8	58
18	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

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19	Gene-rich UV sex chromosomes harbor conserved regulators of sexual development. <i>Science Advances</i> , 2021, 7, .	10.3	53
20	Gene family expansions and transcriptome signatures uncover fungal adaptations to wood decay. <i>Environmental Microbiology</i> , 2021, 23, 5716-5732.	3.8	44
21	Comparative genomics reveals dynamic genome evolution in host specialist ectomycorrhizal fungi. <i>New Phytologist</i> , 2021, 230, 774-792.	7.3	37
22	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus <i>Pycnoporus</i> . <i>DNA Research</i> , 2020, 27, .	3.4	32
23	Genome-wide role of codon usage on transcription and identification of potential regulators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	30
24	Genomic characterization of three marine fungi, including <i>Emericellopsis atlantica</i> sp. nov. with signatures of a generalist lifestyle and marine biomass degradation. <i>IMA Fungus</i> , 2021, 12, 21.	3.8	23
25	Ecological generalism drives hyperdiversity of secondary metabolite gene clusters in xylarialean endophytes. <i>New Phytologist</i> , 2022, 233, 1317-1330.	7.3	23
26	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
27	Evolutionary innovations through gain and loss of genes in the ectomycorrhizal Boletales. <i>New Phytologist</i> , 2022, 233, 1383-1400.	7.3	19
28	IMITATION SWITCH is required for normal chromatin structure and gene repression in PRC2 target domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	18
29	Comparative Genomics of the Ectomycorrhizal Sister Species <i>Rhizopogon vinicolor</i> and <i>Rhizopogon vesiculosus</i> (Basidiomycota: Boletales) Reveals a Divergence of the Mating Type <i>B</i> Locus. <i>Genes, Genomes, Genetics</i> , 2017, 7, 1775-1789.	1.8	17
30	Symbiotic nitrogen fixation in the reproductive structures of a basidiomycete fungus. <i>Current Biology</i> , 2021, 31, 3905-3914.e6.	3.9	17
31	Single-parent expression drives dynamic gene expression complementation in maize hybrids. <i>Plant Journal</i> , 2021, 105, 93-107.	5.7	16
32	Population genomics provides insights into the genetic basis of adaptive evolution in the mushroom-forming fungus <i>Lentinula edodes</i> . <i>Journal of Advanced Research</i> , 2022, 38, 91-106.	9.5	16
33	CreA-mediated repression of gene expression occurs at low monosaccharide levels during fungal plant biomass conversion in a time and substrate dependent manner. <i>Cell Surface</i> , 2021, 7, 100050.	3.0	16
34	Comparative genomics reveals a dynamic genome evolution in the ectomycorrhizal milk-cap (<i>Lactarius</i>) mushrooms. <i>New Phytologist</i> , 2022, 235, 306-319.	7.3	14
35	Defining the eco-enzymological role of the fungal strain <i>Coniochaeta</i> sp. 2T2.1 in a tripartite lignocellulolytic microbial consortium. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	12
36	Comparative genomics of pyrophilous fungi reveals a link between fire events and developmental genes. <i>Environmental Microbiology</i> , 2021, 23, 99-109.	3.8	12

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37	Integrative genomics reveals paths to sex dimorphism in <i>Salix purpurea</i> L. Horticulture Research, 2021, 8, 170.	6.3	12
38	Abscisic acid supports colonization of <i>Eucalyptus grandis</i> roots by the mutualistic ectomycorrhizal fungus <i>Pisolithus microcarpus</i> . New Phytologist, 2022, 233, 966-982.	7.3	12
39	Light-responsive expression atlas reveals the effects of light quality and intensity in <i>Kalanchoë fedtschenkoi</i> , a plant with crassulacean acid metabolism. GigaScience, 2020, 9, .	6.4	11
40	Revisiting a "simple" fungal metabolic pathway reveals redundancy, complexity and diversity. Microbial Biotechnology, 2021, 14, 2525-2537.	4.2	10
41	Phylogenomics and Comparative Genomics Highlight Specific Genetic Features in <i>Ganoderma</i> Species. Journal of Fungi (Basel, Switzerland), 2022, 8, 311.	3.5	10
42	The Transcription Factor Roc1 Is a Key Regulator of Cellulose Degradation in the Wood-Decaying Mushroom <i>Schizophyllum commune</i> . MBio, 2022, 13, .	4.1	10
43	A Multiomic Approach to Understand How <i>Pleurotus eryngii</i> Transforms Non-Woody Lignocellulosic Material. Journal of Fungi (Basel, Switzerland), 2021, 7, 426.	3.5	9
44	The Ancient Salicoid Genome Duplication Event: A Platform for Reconstruction of De Novo Gene Evolution in <i>Populus trichocarpa</i> . Genome Biology and Evolution, 2021, 13, .	2.5	9
45	Genomic Signatures of a Major Adaptive Event in the Pathogenic Fungus <i>Melampsora larici-populina</i> . Genome Biology and Evolution, 2022, 14, .	2.5	9
46	Detailed analysis of the D-galactose catabolic pathways in <i>Aspergillus niger</i> reveals complexity at both metabolic and regulatory level. Fungal Genetics and Biology, 2022, 159, 103670.	2.1	7
47	Salinity tolerance mechanisms of an Arctic Pelagophyte using comparative transcriptomic and gene expression analysis. Communications Biology, 2022, 5, .	4.4	7
48	Evidence for Lignocellulose-Decomposing Enzymes in the Genome and Transcriptome of the Aquatic Hyphomycete <i>Clavariopsis aquatica</i> . Journal of Fungi (Basel, Switzerland), 2021, 7, 854.	3.5	6
49	Omics analyses and biochemical study of <i>Phlebiopsis gigantea</i> elucidate its degradation strategy of wood extractives. Scientific Reports, 2021, 11, 12528.	3.3	5
50	Cryptic genetic structure and copy number variation in the ubiquitous forest symbiotic fungus <i>Cenococcum geophilum</i> . Environmental Microbiology, 2021, 23, 6536-6556.	3.8	5
51	Unraveling the regulation of sugar beet pulp utilization in the industrially relevant fungus <i>Aspergillus niger</i> . IScience, 2022, 25, 104065.	4.1	5
52	Succession of physiological stages hallmarks the transcriptomic response of the fungus <i>Aspergillus niger</i> to lignocellulose. Biotechnology for Biofuels, 2020, 13, 69.	6.2	4
53	Annotated Genome Sequence of the High-Biomass-Producing Yellow-Green Alga <i>Tribonema minus</i> . Microbiology Resource Announcements, 2021, 10, e0032721.	0.6	4
54	GalR, GalX and AraR co-regulate galactose and arabinose utilization in <i>Aspergillus nidulans</i> . Microbial Biotechnology, 2022, 15, 1839-1851.	4.2	4

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55	High-Quality Draft Nuclear and Mitochondrial Genome Sequence of <i>Fusarium oxysporum</i> f. sp. <i>albedinis</i> strain 9, the Causal Agent of Bayoud Disease on Date Palm. <i>Plant Disease</i> , 2022, 106, 1974-1976.	1.4	3
56	Draft genome sequences of strains CBS6241 and CBS6242 of the basidiomycetous yeast <i>Filobasidium floriforme</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	0
57	Enemy or ally: a genomic approach to elucidate the lifestyle of <i>Phyllosticta citrichinaensis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	0
58	Near-Complete Genome Sequence of <i>Zygosaccharomyces rouxii</i> NRRL Y-64007, a Yeast Capable of Growing on Lignocellulosic Hydrolysates. <i>Microbiology Resource Announcements</i> , 2022, , e0005022.	0.6	0