

Jon Magnuson

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

6,201
citations

236925

25
h-index

361022

35
g-index

39
all docs

39
docs citations

39
times ranked

8074
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequencing and analysis of the biomass-degrading fungus <i>Trichoderma reesei</i> (syn. <i>Hypocrea</i>) Tj ETQq1 1	17.5	1516
2	The <i>Fusarium graminearum</i> Genome Reveals a Link Between Localized Polymorphism and Pathogen Specialization. <i>Science</i> , 2007, 317, 1400-1402.	12.6	837
3	Genome sequence of the model mushroom <i>Schizophyllum commune</i> . <i>Nature Biotechnology</i> , 2010, 28, 957-963.	17.5	490
4	The Microbial Opsin Family of Optogenetic Tools. <i>Cell</i> , 2011, 147, 1446-1457.	28.9	471
5	Comparative genomic analysis of the thermophilic biomass-degrading fungi <i>Myceliophthora thermophila</i> and <i>Thielavia terrestris</i> . <i>Nature Biotechnology</i> , 2011, 29, 922-927.	17.5	428
6	Comparative genomics of citric-acid-producing <i>Aspergillus niger</i> ATCC 1015 versus enzyme-producing CBS 513.88. <i>Genome Research</i> , 2011, 21, 885-897.	5.5	329
7	Widespread adenine N6-methylation of active genes in fungi. <i>Nature Genetics</i> , 2017, 49, 964-968.	21.4	292
8	Trichloroethene Reductive Dehalogenase from <i>Dehalococcoides ethenogenes</i> : Sequence of <i>tceA</i> and Substrate Range Characterization. <i>Applied and Environmental Microbiology</i> , 2000, 66, 5141-5147.	3.1	271
9	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
10	Tracking the roots of cellulase hyperproduction by the fungus <i>Trichoderma reesei</i> using massively parallel DNA sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16151-16156.	7.1	190
11	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
12	Determinants of protein hyperthermostability: purification and amino acid sequence of rubredoxin from the hyperthermophilic archaeobacterium <i>Pyrococcus furiosus</i> and secondary structure of the zinc adduct by NMR. <i>Biochemistry</i> , 1991, 30, 10885-10895.	2.5	175
13	Investigation of inter- and intraspecies variation through genome sequencing of <i>Aspergillus</i> section <i>Nigri</i> . <i>Nature Genetics</i> , 2018, 50, 1688-1695.	21.4	160
14	Linking secondary metabolites to gene clusters through genome sequencing of six diverse <i>Aspergillus</i> species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E753-E761.	7.1	126
15	A comparative genomics study of 23 <i>Aspergillus</i> species from section <i>Flavi</i> . <i>Nature Communications</i> , 2020, 11, 1106.	12.8	125
16	Characterization of functionalized nanoporous supports for protein confinement. <i>Nanotechnology</i> , 2006, 17, 5531-5538.	2.6	109
17	Hydrothermal Processing of Macroalgal Feedstocks in Continuous-Flow Reactors. <i>ACS Sustainable Chemistry and Engineering</i> , 2014, 2, 207-215.	6.7	101
18	The <i>Dunaliella salina</i> organelle genomes: large sequences, inflated with intronic and intergenic DNA. <i>BMC Plant Biology</i> , 2010, 10, 83.	3.6	98

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19	Review of the algal biology program within the National Alliance for Advanced Biofuels and Bioproducts. <i>Algal Research</i> , 2017, 22, 187-215.	4.6	69
20	Identification of Genes Associated with Morphology in <i>Aspergillus niger</i> by Using Suppression Subtractive Hybridization. <i>Applied and Environmental Microbiology</i> , 2004, 70, 2474-2485.	3.1	51
21	Differential Expression in <i>Phanerochaete chrysosporium</i> of Membrane-Associated Proteins Relevant to Lignin Degradation. <i>Applied and Environmental Microbiology</i> , 2008, 74, 7252-7257.	3.1	46
22	Proteomic and Functional Analysis of the Cellulase System Expressed by <i>Postia placenta</i> during Brown Rot of Solid Wood. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7933-7941.	3.1	46
23	Gene family expansions and transcriptome signatures uncover fungal adaptations to wood decay. <i>Environmental Microbiology</i> , 2021, 23, 5716-5732.	3.8	44
24	Fungal glycoside hydrolases for saccharification of lignocellulose: outlook for new discoveries fueled by genomics and functional studies. <i>Cellulose</i> , 2009, 16, 687-697.	4.9	32
25	Impact of <i>alg3</i> gene deletion on growth, development, pigment production, protein secretion, and functions of recombinant <i>Trichoderma reesei</i> cellobiohydrolases in <i>Aspergillus niger</i> . <i>Fungal Genetics and Biology</i> , 2013, 61, 120-132.	2.1	25
26	<i>Agrobacterium tumefaciens</i> -mediated transformation of oleaginous yeast <i>Lipomyces</i> species. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 6099-6110.	3.6	22
27	Fungal Ligninolytic Enzymes and Their Applications. <i>Microbiology Spectrum</i> , 2016, 4, .	3.0	19
28	Evolutionary innovations through gain and loss of genes in the ectomycorrhizal Boletales. <i>New Phytologist</i> , 2022, 233, 1383-1400.	7.3	19
29	A Green Nonsulfur Bacterium, <i>Dehalococcoides ethenogenes</i> , with the LexA Binding Sequence Found in Gram-Positive Organisms. <i>Journal of Bacteriology</i> , 2002, 184, 6073-6080.	2.2	17
30	Nitrogenase iron-molybdenum cofactor binding site: Protein conformational changes associated with cofactor binding. <i>Tetrahedron</i> , 1997, 53, 11971-11984.	1.9	12
31	Techno-economic analysis of corn stover fungal fermentation to ethanol. <i>Applied Energy</i> , 2013, 111, 657-668.	10.1	12
32	Proteomics for Validation of Automated Gene Model Predictions. <i>Methods in Molecular Biology</i> , 2009, 492, 447-452.	0.9	4
33	A Conversation with Blake Simmons, Vice President, Deconstruction Division, and Jon Magnuson, Director, Fungal Biotechnology Group, Joint BioEnergy Institute, Emeryville, CA. <i>Industrial Biotechnology</i> , 2013, 9, 108-112.	0.8	2
34	Approaches to understanding protein hypersecretion in fungi. <i>Fungal Biology Reviews</i> , 2016, 30, 145-151.	4.7	2