

# Jon Magnuson

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

34  
papers

4,705  
citations

23  
h-index

39  
g-index

39  
ext. papers

5,682  
ext. citations

13.8  
avg, IF

4.18  
L-index

#	Paper	IF	Citations
34	Gene family expansions and transcriptome signatures uncover fungal adaptations to wood decay. <i>Environmental Microbiology</i> , <b>2021</b> , 23, 5716-5732	5.2	15
33	A comparative genomics study of 23 <i>Aspergillus</i> species from section Flavi. <i>Nature Communications</i> , <b>2020</b> , 11, 1106	17.4	54
32	Large-scale genome sequencing of mycorrhizal fungi provides insights into the early evolution of symbiotic traits. <i>Nature Communications</i> , <b>2020</b> , 11, 5125	17.4	86
31	Comparative genomics and transcriptomics depict ericoid mycorrhizal fungi as versatile saprotrophs and plant mutualists. <i>New Phytologist</i> , <b>2018</b> , 217, 1213-1229	9.8	99
30	Linking secondary metabolites to gene clusters through genome sequencing of six diverse species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, E753-E761	11.5	78
29	Investigation of inter- and intraspecies variation through genome sequencing of <i>Aspergillus</i> section Nigri. <i>Nature Genetics</i> , <b>2018</b> , 50, 1688-1695	36.3	100
28	Review of the algal biology program within the National Alliance for Advanced Biofuels and Bioproducts. <i>Algal Research</i> , <b>2017</b> , 22, 187-215	5	50
27	Widespread adenine N6-methylation of active genes in fungi. <i>Nature Genetics</i> , <b>2017</b> , 49, 964-968	36.3	181
26	<i>Agrobacterium tumefaciens</i> -mediated transformation of oleaginous yeast <i>Lipomyces</i> species. <i>Applied Microbiology and Biotechnology</i> , <b>2017</b> , 101, 6099-6110	5.7	17
25	Approaches to understanding protein hypersecretion in fungi. <i>Fungal Biology Reviews</i> , <b>2016</b> , 30, 145-1516.8		2
24	Fungal Ligninolytic Enzymes and Their Applications. <i>Microbiology Spectrum</i> , <b>2016</b> , 4,	8.9	17
23	Hydrothermal Processing of Macroalgal Feedstocks in Continuous-Flow Reactors. <i>ACS Sustainable Chemistry and Engineering</i> , <b>2014</b> , 2, 207-215	8.3	84
22	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> , <b>2013</b> , 9, 108-112	1.3	2
21	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> , <b>2013</b> , 61, 120-32	3.9	20
20	Techno-economic analysis of corn stover fungal fermentation to ethanol. <i>Applied Energy</i> , <b>2013</b> , 111, 657-668		11
19	Comparative genomics of citric-acid-producing <i>Aspergillus niger</i> ATCC 1015 versus enzyme-producing CBS 513.88. <i>Genome Research</i> , <b>2011</b> , 21, 885-97	9.7	266
18	The microbial opsin family of optogenetic tools. <i>Cell</i> , <b>2011</b> , 147, 1446-57	56.2	388

17	Comparative genomic analysis of the thermophilic biomass-degrading fungi <i>Myceliophthora thermophila</i> and <i>Thielavia terrestris</i> . <i>Nature Biotechnology</i> , <b>2011</b> , 29, 922-7	44.5	324
16	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> , <b>2011</b> , 77, 7933-41	4.8	37
15	Genome sequence of the model mushroom <i>Schizophyllum commune</i> . <i>Nature Biotechnology</i> , <b>2010</b> , 28, 957-63	44.5	381
14	The <i>Dunaliella salina</i> organelle genomes: large sequences, inflated with intronic and intergenic DNA. <i>BMC Plant Biology</i> , <b>2010</b> , 10, 83	5.3	88
13	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> , <b>2009</b> , 106, 16151-6	11.5	164
12	Fungal glycoside hydrolases for saccharification of lignocellulose: outlook for new discoveries fueled by genomics and functional studies. <i>Cellulose</i> , <b>2009</b> , 16, 687-697	5.5	23
11	Proteomics for validation of automated gene model predictions. <i>Methods in Molecular Biology</i> , <b>2009</b> , 492, 447-52	1.4	3
10	Genome sequencing and analysis of the biomass-degrading fungus <i>Trichoderma reesei</i> (syn. <i>Hypocrea jecorina</i> ). <i>Nature Biotechnology</i> , <b>2008</b> , 26, 553-60	44.5	920
9	Differential expression in <i>Phanerochaete chrysosporium</i> of membrane-associated proteins relevant to lignin degradation. <i>Applied and Environmental Microbiology</i> , <b>2008</b> , 74, 7252-7	4.8	41
8	The <i>Fusarium graminearum</i> genome reveals a link between localized polymorphism and pathogen specialization. <i>Science</i> , <b>2007</b> , 317, 1400-2	33.3	668
7	Characterization of functionalized nanoporous supports for protein confinement. <i>Nanotechnology</i> , <b>2006</b> , 17, 5531-8	3.4	100
6	Identification of genes associated with morphology in <i>Aspergillus niger</i> by using suppression subtractive hybridization. <i>Applied and Environmental Microbiology</i> , <b>2004</b> , 70, 2474-85	4.8	45
5	A green nonsulfur bacterium, <i>Dehalococcoides ethenogenes</i> , with the LexA binding sequence found in gram-positive organisms. <i>Journal of Bacteriology</i> , <b>2002</b> , 184, 6073-80	3.5	17
4	Trichloroethene reductive dehalogenase from <i>Dehalococcoides ethenogenes</i> : sequence of <i>tceA</i> and substrate range characterization. <i>Applied and Environmental Microbiology</i> , <b>2000</b> , 66, 5141-7	4.8	242
3	Nitrogenase iron-molybdenum cofactor binding site: Protein conformational changes associated with cofactor binding. <i>Tetrahedron</i> , <b>1997</b> , 53, 11971-11984	2.4	11
2	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> , <b>1991</b> , 30, 10885-95	3.2	156
1	Multiplexed CRISPR-Cas9 based genome editing of <i>Rhodosporidium toruloides</i>		1