

Ad Wiebenga

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

4,005
citations

361413

20
h-index

552781

26
g-index

26
all docs

26
docs citations

26
times ranked

4795
citing authors

#	ARTICLE	IF	CITATIONS
1	The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. Science, 2012, 336, 1715-1719.	12.6	1,424
2	The Plant Cell Wallâ€“Decomposing Machinery Underlies the Functional Diversity of Forest Fungi. Science, 2011, 333, 762-765.	12.6	512
3	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus <i>Aspergillus</i> . Genome Biology, 2017, 18, 28.	8.8	417
4	Comparative genomics of <i>Ceriporiopsis subvermispora</i> and <i>Phanerochaete chrysosporium</i> provide insight into selective ligninolysis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5458-5463.	7.1	259
5	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. Current Biology, 2016, 26, 1577-1584.	3.9	175
6	Investigation of inter- and intraspecies variation through genome sequencing of <i>Aspergillus</i> section <i>Nigri</i> . Nature Genetics, 2018, 50, 1688-1695.	21.4	160
7	Comparative genomics of the white-rot fungi, <i>Phanerochaete carnosae</i> and <i>P. chrysosporium</i> , to elucidate the genetic basis of the distinct wood types they colonize. BMC Genomics, 2012, 13, 444.	2.8	125
8	A comparative genomics study of 23 <i>Aspergillus</i> species from section <i>Flavi</i> . Nature Communications, 2020, 11, 1106.	12.8	125
9	Closely related fungi employ diverse enzymatic strategies to degrade plant biomass. Biotechnology for Biofuels, 2015, 8, 107.	6.2	111
10	Carbohydrate-active enzymes from the zygomycete fungus <i>Rhizopus oryzae</i> : a highly specialized approach to carbohydrate degradation depicted at genome level. BMC Genomics, 2011, 12, 38.	2.8	105
11	The genome of the white-rot fungus <i>Pycnoporus cinnabarinus</i> : a basidiomycete model with a versatile arsenal for lignocellulosic biomass breakdown. BMC Genomics, 2014, 15, 486.	2.8	91
12	Genomic and transcriptomic analysis of <i>Laccaria bicolor</i> CAZome reveals insights into polysaccharides remodelling during symbiosis establishment. Fungal Genetics and Biology, 2014, 72, 168-181.	2.1	81
13	Protease and lipase activities of fungal and bacterial strains derived from an artisanal raw ewe's milk cheese. International Journal of Food Microbiology, 2016, 237, 17-27.	4.7	72
14	An enzyme cocktail for efficient protoplast formation in <i>Aspergillus niger</i> . Journal of Microbiological Methods, 2009, 76, 305-306.	1.6	59
15	<i>Aspergillus niger</i> RhaR, a regulator involved in L-rhamnose release and catabolism. Applied Microbiology and Biotechnology, 2014, 98, 5531-40.	3.6	56
16	Genetic Interaction of <i>Aspergillus nidulans</i> galR, xlnR and araR in Regulating D-Galactose and L-Arabinose Release and Catabolism Gene Expression. PLoS ONE, 2015, 10, e0143200.	2.5	41
17	Carbohydrate utilization and metabolism is highly differentiated in <i>Agaricus bisporus</i> . BMC Genomics, 2013, 14, 663.	2.8	35
18	Genomic and Genetic Insights Into a Cosmopolitan Fungus, <i>Paecilomyces variotii</i> (Eurotiales). Frontiers in Microbiology, 2018, 9, 3058.	3.5	35

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19	<i>Penicillium subrubescens</i> is a promising alternative for <i>Aspergillus niger</i> in enzymatic plant biomass saccharification. <i>New Biotechnology</i> , 2016, 33, 834-841.	4.4	27
20	Macroalgae Derived Fungi Have High Abilities to Degrade Algal Polymers. <i>Microorganisms</i> , 2020, 8, 52.	3.6	24
21	Secretion of small proteins is species-specific within <i>Aspergillus</i> sp. <i>Microbial Biotechnology</i> , 2017, 10, 323-329.	4.2	23
22	Colonies of the fungus <i>Aspergillus niger</i> are highly differentiated to adapt to local carbon source variation. <i>Environmental Microbiology</i> , 2020, 22, 1154-1166.	3.8	15
23	Genetic transformation of the white-rot fungus <i>Dichomitus squalens</i> using a new commercial protoplasting cocktail. <i>Journal of Microbiological Methods</i> , 2017, 143, 38-43.	1.6	12
24	Physiological background of the remarkably high Cd ²⁺ tolerance of the <i>Aspergillus fumigatus</i> Af293 strain. <i>Journal of Basic Microbiology</i> , 2018, 58, 957-967.	3.3	10
25	High resolution visualization and exo-proteomics reveal the physiological role of XlnR and AraR in plant biomass colonization and degradation by <i>Aspergillus niger</i> . <i>Environmental Microbiology</i> , 2017, 19, 4587-4598.	3.8	6
26	Transcriptome analysis of <i>Aspergillus niger</i> xlnR and xkiA mutants grown on corn Stover and soybean hulls reveals a highly complex regulatory network. <i>BMC Genomics</i> , 2019, 20, 853.	2.8	5