

# Scott E Baker

## List of Publications by Year in descending order

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140  
papers

14,526  
citations

31902

53  
h-index

20307

116  
g-index

151  
all docs

151  
docs citations

151  
times ranked

12971  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.	13.7	1,442
2	Genome sequencing and analysis of the biomass-degrading fungus <i>Trichoderma reesei</i> (syn. <i>Hypocrea</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	9.4	1,116
3	The <i>Fusarium graminearum</i> Genome Reveals a Link Between Localized Polymorphism and Pathogen Specialization. <i>Science</i> , 2007, 317, 1400-1402.	6.0	837
4	Extensive sampling of basidiomycete genomes demonstrates inadequacy of the white-rot/brown-rot paradigm for wood decay fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9923-9928.	3.3	595
5	Comparative genome sequence analysis underscores mycoparasitism as the ancestral life style of <i>Trichoderma</i> . <i>Genome Biology</i> , 2011, 12, R40.	3.8	594
6	Genome, transcriptome, and secretome analysis of wood decay fungus <i>Postia placenta</i> supports unique mechanisms of lignocellulose conversion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1954-1959.	3.3	530
7	Structure and Function of Hemidesmosomes: More Than Simple Adhesion Complexes. <i>Journal of Investigative Dermatology</i> , 1999, 112, 411-418.	0.3	513
8	The Plant Cell Wallâ€œDecomposing Machinery Underlies the Functional Diversity of Forest Fungi. <i>Science</i> , 2011, 333, 762-765.	6.0	512
9	Genome sequence of the model mushroom <i>Schizophyllum commune</i> . <i>Nature Biotechnology</i> , 2010, 28, 957-963.	9.4	490
10	A versatile toolkit for high throughput functional genomics with <i>Trichoderma reesei</i> . <i>Biotechnology for Biofuels</i> , 2012, 5, 1.	6.2	434
11	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.	9.4	428
12	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus <i>Aspergillus</i> . <i>Genome Biology</i> , 2017, 18, 28.	3.8	417
13	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.	2.4	329
14	The putative protein methyltransferase LAE1 controls cellulase gene expression in <i>Trichoderma reesei</i> . <i>Molecular Microbiology</i> , 2012, 84, 1150-1164.	1.2	232
15	Comparative Genome Structure, Secondary Metabolite, and Effector Coding Capacity across <i>Cochliobolus</i> Pathogens. <i>PLoS Genetics</i> , 2013, 9, e1003233.	1.5	232
16	One Fungus, One Name: Defining the Genus <i>Fusarium</i> in a Scientifically Robust Way That Preserves Longstanding Use. <i>Phytopathology</i> , 2013, 103, 400-408.	1.1	219
17	<i>Aspergillus niger</i> genomics: Past, present and into the future. <i>Medical Mycology</i> , 2006, 44, 17-21.	0.3	200
18	The Genomes of Three Uneven Siblings: Footprints of the Lifestyles of Three <i>Trichoderma</i> Species. <i>Microbiology and Molecular Biology Reviews</i> , 2016, 80, 205-327.	2.9	194

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19	Tracking the roots of cellulase hyperproduction by the fungus <i>Trichoderma reesei</i> using massively parallel DNA sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16151-16156.	3.3	190
20	A parts list for fungal cellulosomes revealed by comparative genomics. Nature Microbiology, 2017, 2, 17087.	5.9	183
21	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. Current Biology, 2016, 26, 1577-1584.	1.8	175
22	Investigation of inter- and intraspecies variation through genome sequencing of <i>Aspergillus</i> section Nigri. Nature Genetics, 2018, 50, 1688-1695.	9.4	160
23	A Cell Signal Pathway Involving Laminin-5, $\beta$ 1 Integrin, and Mitogen-activated Protein Kinase Can Regulate Epithelial Cell Proliferation. Molecular Biology of the Cell, 1999, 10, 259-270.	0.9	146
24	Transcriptomic response of the mycoparasitic fungus <i>Trichoderma atroviride</i> to the presence of a fungal prey. BMC Genomics, 2009, 10, 567.	1.2	141
25	Regulation of amino-acid metabolism controls flux to lipid accumulation in <i>Yarrowia lipolytica</i> . Npj Systems Biology and Applications, 2016, 2, 16005.	1.4	141
26	Two Polyketide Synthase-Encoding Genes Are Required for Biosynthesis of the Polyketide Virulence Factor, $\beta$ -toxin, by <i>Cochliobolus heterostrophus</i> . Molecular Plant-Microbe Interactions, 2006, 19, 139-149.	1.4	135
27	101 Dothideomycetes genomes: A test case for predicting lifestyles and emergence of pathogens. Studies in Mycology, 2020, 96, 141-153.	4.5	135
28	Molecular genetic studies of a human epidermal autoantigen (the 180-kD bullous pemphigoid) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 39. evidence for an interaction between BP180 and alpha 6 integrin.. Journal of Cell Biology, 1995, 130, 117-125.	2.3	131
29	Linking secondary metabolites to gene clusters through genome sequencing of six diverse <i>Aspergillus</i> species. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E753-E761.	3.3	126
30	A comparative genomics study of 23 <i>Aspergillus</i> species from section Flavi. Nature Communications, 2020, 11, 1106.	5.8	125
31	Functional Analyses of <i>Trichoderma reesei</i> LAE1 Reveal Conserved and Contrasting Roles of This Regulator. G3: Genes, Genomes, Genetics, 2013, 3, 369-378.	0.8	109
32	Sequencing the fungal tree of life. New Phytologist, 2011, 190, 818-821.	3.5	107
33	Harnessing glycosylation to improve cellulase activity. Current Opinion in Biotechnology, 2012, 23, 338-345.	3.3	107
34	New Insight into the Ochratoxin A Biosynthetic Pathway through Deletion of a Nonribosomal Peptide Synthetase Gene in <i>Aspergillus carbonarius</i> . Applied and Environmental Microbiology, 2012, 78, 8208-8218.	1.4	99
35	Activation of an AP1-Like Transcription Factor of the Maize Pathogen <i>Cochliobolus heterostrophus</i> in Response to Oxidative Stress and Plant Signals. Eukaryotic Cell, 2005, 4, 443-454.	3.4	94
36	Circadian Proteomic Analysis Uncovers Mechanisms of Post-Transcriptional Regulation in Metabolic Pathways. Cell Systems, 2018, 7, 613-626.e5.	2.9	93

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37	Characterization of a polyketide synthase in <i>Aspergillus niger</i> whose product is a precursor for both dihydroxynaphthalene (DHN) melanin and naphtho-1 <sup>3</sup> -pyrone. <i>Fungal Genetics and Biology</i> , 2011, 48, 430-437.	0.9	91
38	Hemidesmosomes: Extracellular Matrix/Intermediate Filament Connectors. <i>Experimental Cell Research</i> , 1994, 213, 1-11.	1.2	90
39	Analytical and computational approaches to define the <i>Aspergillus niger</i> secretome. <i>Fungal Genetics and Biology</i> , 2009, 46, S153-S160.	0.9	87
40	What can comparative genomics tell us about species concepts in the genus <i>Aspergillus</i> ?. <i>Studies in Mycology</i> , 2007, 59, 11-17.	4.5	83
41	The Polyketide Synthase Gene <i>pks4</i> of <i>Trichoderma reesei</i> Provides Pigmentation and Stress Resistance. <i>Eukaryotic Cell</i> , 2013, 12, 1499-1508.	3.4	77
42	Phylogenomic analysis of polyketide synthase-encoding genes in <i>Trichoderma</i> . <i>Microbiology (United Kingdom)</i> 2017, 157, 1071-1081. <small>Tj ETQq0 0 0 ggBT /Overlock 10 Tf</small>	6.7	71
43	Structural reorganization of the fungal endoplasmic reticulum upon induction of mycotoxin biosynthesis. <i>Scientific Reports</i> , 2017, 7, 44296.	1.6	71
44	Purifying selection and birth-and-death evolution in the class II hydrophobin gene families of the ascomycete <i>Trichoderma/Hypocrea</i> . <i>BMC Evolutionary Biology</i> , 2008, 8, 4.	3.2	69
45	Novel Hydrophobins from <i>Trichoderma</i> Define a New Hydrophobin Subclass: Protein Properties, Evolution, Regulation and Processing. <i>Journal of Molecular Evolution</i> , 2011, 72, 339-351.	0.8	68
46	Rediscovery by Whole Genome Sequencing: Classical Mutations and Genome Polymorphisms in <i>Neurospora crassa</i> . <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 303-316.	0.8	68
47	Increased production of fatty acids and triglycerides in <i>Aspergillus oryzae</i> by enhancing expressions of fatty acid synthesis-related genes. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 269-281.	1.7	67
48	Morphogenetic Effects of Soluble Laminin-5 on Cultured Epithelial Cells and Tissue Explants. <i>Experimental Cell Research</i> , 1996, 228, 262-270.	1.2	66
49	The Production of Multiple Small Peptaibol Families by Single 14â€Module Peptide Synthetases in <i>Trichoderma</i> / <i>Hypocrea</i> . <i>Chemistry and Biodiversity</i> , 2012, 9, 499-535.	1.0	66
50	Identification of a Classical Mutant in the Industrial Host <i>Aspergillus niger</i> by Systems Genetics: LaeA Is Required for Citric Acid Production and Regulates the Formation of Some Secondary Metabolites. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 193-204.	0.8	65
51	Identification and characterization of the polyketide synthase involved in ochratoxin A biosynthesis in <i>Aspergillus carbonarius</i> . <i>International Journal of Food Microbiology</i> , 2014, 179, 10-17.	2.1	64
52	Mapping N-Linked Glycosylation Sites in the Secretome and Whole Cells of <i>Aspergillus niger</i> Using Hydrazide Chemistry and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2012, 11, 143-156.	1.8	62
53	Multi-omics analysis reveals regulators of the response to nitrogen limitation in <i>Yarrowia lipolytica</i> . <i>BMC Genomics</i> , 2016, 17, 138.	1.2	62
54	A molecular genetic toolbox for <i>Yarrowia lipolytica</i> . <i>Biotechnology for Biofuels</i> , 2017, 10, 2.	6.2	62

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55	Genetic and Genomic Dissection of the <i>Cochliobolus heterostrophus</i> Tox1 Locus Controlling Biosynthesis of the Polyketide Virulence Factor $\epsilon$ -toxin. <i>Advances in Genetics</i> , 2007, 57, 219-261.	0.8	56
56	Comprehensive Metabolomic, Lipidomic and Microscopic Profiling of <i>Yarrowia lipolytica</i> during Lipid Accumulation Identifies Targets for Increased Lipogenesis. <i>PLoS ONE</i> , 2015, 10, e0123188.	1.1	54
57	Phylogenomic and functional domain analysis of polyketide synthases in <i>Fusarium</i> . <i>Fungal Biology</i> , 2012, 116, 318-331.	1.1	50
58	Mixed-Effects Statistical Model for Comparative LC-MS Proteomics Studies. <i>Journal of Proteome Research</i> , 2008, 7, 1209-1217.	1.8	44
59	Genome sequencing and transcriptome analysis of <i>Trichoderma reesei</i> QM9978 strain reveals a distal chromosome translocation to be responsible for loss of <i>vib1</i> expression and loss of cellulase induction. <i>Biotechnology for Biofuels</i> , 2017, 10, 209.	6.2	43
60	Biomarker Candidate Identification in <i>Yersinia pestis</i> Using Organism-Wide Semiquantitative Proteomics. <i>Journal of Proteome Research</i> , 2006, 5, 3008-3017.	1.8	42
61	A new approach to Cas9-based genome editing in <i>Aspergillus niger</i> that is precise, efficient and selectable. <i>PLoS ONE</i> , 2019, 14, e0210243.	1.1	40
62	Anaerobic fungi: Neocallimastigomycota. <i>IMA Fungus</i> , 2010, 1, 181-185.	1.7	39
63	Leucine Biosynthesis Is Involved in Regulating High Lipid Accumulation in <i>Yarrowia lipolytica</i> . <i>MBio</i> , 2017, 8, .	1.8	38
64	<i>period-1</i> encodes an ATP-dependent RNA helicase that influences nutritional compensation of the <i>Neurospora</i> circadian clock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15707-15712.	3.3	37
65	<i>Dichomitus squalens</i> partially tailors its molecular responses to the composition of solid wood. <i>Environmental Microbiology</i> , 2018, 20, 4141-4156.	1.8	36
66	Exploiting proteomic data for genome annotation and gene model validation in <i>Aspergillus niger</i> . <i>BMC Genomics</i> , 2009, 10, 61.	1.2	35
67	Regulation of Yeast-to-Hyphae Transition in <i>Yarrowia lipolytica</i> . <i>MSphere</i> , 2018, 3, .	1.3	35
68	Comparative Genomics Analysis of <i>Trichoderma reesei</i> Strains. <i>Industrial Biotechnology</i> , 2013, 9, 352-367.	0.5	34
69	Fungal glycoside hydrolases for saccharification of lignocellulose: outlook for new discoveries fueled by genomics and functional studies. <i>Cellulose</i> , 2009, 16, 687-697.	2.4	32
70	Genome sequencing of the <i>Trichoderma reesei</i> QM9136 mutant identifies a truncation of the transcriptional regulator XYR1 as the cause for its cellulase-negative phenotype. <i>BMC Genomics</i> , 2015, 16, 326.	1.2	31
71	Regulation of Nitrogen Metabolism by GATA Zinc Finger Transcription Factors in <i>Yarrowia lipolytica</i> . <i>MSphere</i> , 2017, 2, .	1.3	29
72	Compartmentalized microchannel array for high-throughput analysis of single cell polarized growth and dynamics. <i>Scientific Reports</i> , 2015, 5, 16111.	1.6	28

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73	Genome Sequence and Annotation of <i>Trichoderma parareesei</i> , the Ancestor of the Cellulase Producer <i>Trichoderma reesei</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	28
74	Fungal genome sequencing and bioenergy. <i>Fungal Biology Reviews</i> , 2008, 22, 1-5.	1.9	27
75	Genetic Interaction Between Integrins and moleskin, a Gene Encoding a <i>Drosophila</i> Homolog of Importin-7. <i>Genetics</i> , 2002, 162, 285-296.	1.2	27
76	Genome Sequence of the Mucoromycotina Fungus <i>Umbelopsis isabellina</i> , an Effective Producer of Lipids. <i>Genome Announcements</i> , 2014, 2, .	0.8	26
77	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.	0.9	25
78	Multi-Omics Driven Metabolic Network Reconstruction and Analysis of Lignocellulosic Carbon Utilization in <i>Rhodospiridium toruloides</i> . <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 612832.	2.0	25
79	Resin-Assisted Enrichment of N-Terminal Peptides for Characterizing Proteolytic Processing. <i>Analytical Chemistry</i> , 2013, 85, 6826-6832.	3.2	24
80	Prediction of Metabolite Concentrations, Rate Constants and Post-Translational Regulation Using Maximum Entropy-Based Simulations with Application to Central Metabolism of <i>Neurospora crassa</i> . <i>Processes</i> , 2018, 6, 63.	1.3	24
81	Omics Analyses of <i>Trichoderma reesei</i> CBS999.97 and QM6a Indicate the Relevance of Female Fertility to Carbohydrate-Active Enzyme and Transporter Levels. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	22
82	Laminin-5 and modulation of keratin cytoskeleton arrangement in FG pancreatic carcinoma cells: Involvement of IFAP300 and evidence that laminin-5/cell interactions correlate with a dephosphorylation of $\beta$ 6A integrin. , 1997, 37, 271-286.		21
83	Duplications and losses of genes encoding known elements of the stress defence system of the <i>Aspergilli</i> contribute to the evolution of these filamentous fungi but do not directly influence their environmental stress tolerance. <i>Studies in Mycology</i> , 2018, 91, 23-36.	4.5	21
84	Essential pathway identification: from <i>in silico</i> analysis to potential antifungal targets in <i>Aspergillus fumigatus</i> . <i>Medical Mycology</i> , 2009, 47, S80-S87.	0.3	20
85	Ochratoxin A production by <i>Penicillium thymicola</i> . <i>Fungal Biology</i> , 2016, 120, 1041-1049.	1.1	20
86	<i>Thermoascus aurantiacus</i> is an Intriguing Host for the Industrial Production of Cellulases. <i>Current Biotechnology</i> , 2017, 6, 89-97.	0.2	20
87	Fungal Ligninolytic Enzymes and Their Applications. <i>Microbiology Spectrum</i> , 2016, 4, .	1.2	19
88	Protein hyperproduction in fungi by design. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 8621-8628.	1.7	19
89	Comparative Genomic Analysis of Ochratoxin A Biosynthetic Cluster in Producing Fungi: New Evidence of a Cyclase Gene Involvement. <i>Frontiers in Microbiology</i> , 2020, 11, 581309.	1.5	19
90	Draft Genome Sequence of <i>Neurospora crassa</i> Strain FGSC 73. <i>Genome Announcements</i> , 2015, 3, .	0.8	17

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91	An Overview of the Genus <i>Aspergillus</i> . <i>Mycology</i> , 2007, , 3-13.	0.5	16
92	Draft Genome Sequence of the Dimorphic Yeast <i>Yarrowia lipolytica</i> Strain W29. <i>Genome Announcements</i> , 2015, 3, .	0.8	16
93	Forward genetics screen coupled with whole-genome resequencing identifies novel gene targets for improving heterologous enzyme production in <i>Aspergillus niger</i> . <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 1797-1807.	1.7	15
94	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.	1.8	15
95	Increased production of free fatty acids in <i>Aspergillus oryzae</i> by disruption of a predicted acyl-CoA synthetase gene. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 3103-3113.	1.7	13
96	Diverse data supports the transition of filamentous fungal model organisms into the post-genomics era. <i>Mycology</i> , 2017, 8, 67-83.	2.0	13
97	Expression of naturally ionic liquid-tolerant thermophilic cellulases in <i>Aspergillus niger</i> . <i>PLoS ONE</i> , 2017, 12, e0189604.	1.1	13
98	The F-box protein gene <i>exo1</i> is a target for reverse engineering enzyme hypersecretion in filamentous fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	13
99	Correction for Riley et al., Extensive sampling of basidiomycete genomes demonstrates inadequacy of the white-rot/brown-rot paradigm for wood decay fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14959-14959.	3.3	12
100	Integration of Proteomics and Metabolomics Into the Design, Build, Test, Learn Cycle to Improve 3-Hydroxypropionic Acid Production in <i>Aspergillus pseudoterreus</i> . <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 603832.	2.0	12
101	Post-genomic approaches to understanding interactions between fungi and their environment. <i>IMA Fungus</i> , 2011, 2, 81-86.	1.7	11
102	The mitochondrial genome of the ethanol-metabolizing, wine cellar mold <i>Zasmidium cellare</i> is the smallest for a filamentous ascomycete. <i>Fungal Biology</i> , 2016, 120, 961-974.	1.1	11
103	Blocking hexose entry into glycolysis activates alternative metabolic conversion of these sugars and upregulates pentose metabolism in <i>Aspergillus nidulans</i> . <i>BMC Genomics</i> , 2018, 19, 214.	1.2	11
104	Evidence of the Involvement of a Cyclase Gene in the Biosynthesis of Ochratoxin A in <i>Aspergillus carbonarius</i> . <i>Toxins</i> , 2021, 13, 892.	1.5	11
105	The PS Integrins Are Required for a Regulatory Event during <i>Drosophila</i> Wing Morphogenesis. <i>Annals of the New York Academy of Sciences</i> , 1998, 857, 99-109.	1.8	10
106	Hydrogenosomes of Anaerobic Chytrids: An Alternative Way to Adapt to Anaerobic Environments. <i>Microbiology Monographs</i> , 2008, , 147-162.	0.3	10
107	Integrative quantitative-phase and airy light-sheet imaging. <i>Scientific Reports</i> , 2020, 10, 20150.	1.6	10
108	High-Throughput Large-Scale Targeted Proteomics Assays for Quantifying Pathway Proteins in <i>Pseudomonas putida</i> KT2440. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 603488.	2.0	10

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109	Deletion analysis of the itaconic acid biosynthesis gene cluster components in <i>Aspergillus pseudoterreus</i> ATCC32359. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 3981-3992.	1.7	10
110	Selection to sequence: opportunities in fungal genomics. <i>Environmental Microbiology</i> , 2009, 11, 2955-2958.	1.8	9
111	Hydrogenosomes of Anaerobic Fungi: An Alternative Way to Adapt to Anaerobic Environments. <i>Microbiology Monographs</i> , 2019, , 159-175.	0.3	8
112	Molecular Mechanisms of Plant-Microbe Interactions in the Rhizosphere as Targets for Improving Plant Productivity. <i>Rhizosphere Biology</i> , 2021, , 295-338.	0.4	8
113	Structural analysis of N- and O-glycans using ZIC-HILIC/dialysis coupled to NMR detection. <i>Fungal Genetics and Biology</i> , 2014, 72, 207-215.	0.9	7
114	Non-steady state mass action dynamics without rate constants: dynamics of coupled reactions using chemical potentials. <i>Physical Biology</i> , 2017, 14, 055003.	0.8	6
115	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.	1.8	6
116	<i>Aspergillus</i> : Genomics of a Cosmopolitan Fungus. <i>Soil Biology</i> , 2013, , 89-126.	0.6	4
117	Fungi and Industrial Biotechnology – A Special Issue for an Amazing Kingdom. <i>Industrial Biotechnology</i> , 2013, 9, 105-107.	0.5	4
118	Multimodal microfluidic platform for controlled culture and analysis of unicellular organisms. <i>Biomicrofluidics</i> , 2017, 11, 054104.	1.2	4
119	Re-routing of Sugar Catabolism Provides a Better Insight Into Fungal Flexibility in Using Plant Biomass-Derived Monomers as Substrates. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 644216.	2.0	4
120	Proteomics for Validation of Automated Gene Model Predictions. <i>Methods in Molecular Biology</i> , 2009, 492, 447-452.	0.4	4
121	Bayesian Inference for Integrating <i>Yarrowia lipolytica</i> Multiomics Datasets with Metabolic Modeling. <i>ACS Synthetic Biology</i> , 2021, 10, 2968-2981.	1.9	4
122	Proteome Studies of Filamentous Fungi. <i>Methods in Molecular Biology</i> , 2011, 722, 133-139.	0.4	3
123	Horizontal Gene Transfer in Fungi. <i>Grand Challenges in Biology and Biotechnology</i> , 2020, , 317-332.	2.4	3
124	Approaches to understanding protein hypersecretion in fungi. <i>Fungal Biology Reviews</i> , 2016, 30, 145-151.	1.9	2
125	Mycotoxins: A Fungal Genomics Perspective. <i>Methods in Molecular Biology</i> , 2017, 1542, 367-379.	0.4	2
126	Fungal Lignolytic Enzymes and Their Applications. , 2017, , 1049-1061.		2



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127	Strain Construction for Intracellular Metabolic Pathway Localization in <i>Y. lipolytica</i> . <i>Methods in Molecular Biology</i> , 2021, 2307, 147-157.	0.4	2
128	Comparative Genomics, Resequencing and Fast Forward Genetics in <i>Aspergillus</i> and <i>Penicillium</i> . , 2016, , 17-26.		2
129	Genomes to Proteomes. , 0, , 21-45.		1
130	Grand Challenges in Fungal Biotechnology. <i>Frontiers in Fungal Biology</i> , 2020, 1, .	0.9	1
131	Production of Biofuels From Biomass by Fungi. , 2021, , 555-576.		1
132	Genome and proteome analysis of industrial fungi. , 0, , 3-9.		0
133	Return of the Fungi. <i>Industrial Biotechnology</i> , 2013, 9, 328-330.	0.5	0
134	Multimodal microchannel and nanowell-based microfluidic platforms for bioimaging. , 2016, , .		0
135	Cloning and Expression of Heterologous Cellulases and Enzymes in <i>Aspergillus niger</i> . <i>Methods in Molecular Biology</i> , 2018, 1796, 123-133.	0.4	0
136	Prediction of Metabolite Concentrations, Rate Constants and Post-Translational Regulation of <i>Neurospora Crassa</i> using Maximum Entropy Optimizations and Reinforcement Learning. <i>Biophysical Journal</i> , 2019, 116, 130a-131a.	0.2	0
137	Fusing quantitative-phase imaging with airy light-sheet microscopy. , 2021, , .		0
138	Trichoderma and the biorefinery: from plant health to enzymes to biofuel production.. , 2013, , 222-229.		0
139	Phenotype to genotype in <i>Neurospora crassa</i> : Association of the scumbo phenotype with mutations in the gene encoding ceramide C9-methyltransferase. <i>Current Research in Microbial Sciences</i> , 2022, 3, 100117.	1.4	0
140	Major involvement of two laccase genes in conidial pigment biosynthesis in <i>Aspergillus oryzae</i> . <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 287-300.	1.7	0