

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	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
2	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
3	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
4	Production of Biofuels From Biomass by Fungi. , 2021, , 555-576.		1
5	Fusing quantitative-phase imaging with airy light-sheet microscopy. , 2021, , .		0
6	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
7	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
8	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
9	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
10	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
11	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
12	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
13	Grand Challenges in Fungal Biotechnology. <i>Frontiers in Fungal Biology</i> , 2020, 1, .	0.9	1
14	Integrative quantitative-phase and airy light-sheet imaging. <i>Scientific Reports</i> , 2020, 10, 20150.	1.6	10
15	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
16	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
17	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
18	A comparative genomics study of 23 <i>Aspergillus</i> species from section Flavi. <i>Nature Communications</i> , 2020, 11, 1106.	5.8	125

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19	101 Dothideomycetes genomes: A test case for predicting lifestyles and emergence of pathogens. <i>Studies in Mycology</i> , 2020, 96, 141-153.	4.5	135
20	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
21	Horizontal Gene Transfer in Fungi. <i>Grand Challenges in Biology and Biotechnology</i> , 2020, , 317-332.	2.4	3
22	Hydrogenosomes of Anaerobic Fungi: An Alternative Way to Adapt to Anaerobic Environments. <i>Microbiology Monographs</i> , 2019, , 159-175.	0.3	8
23	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
24	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
25	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
26	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.	3.3	126
27	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
28	Circadian Proteomic Analysis Uncovers Mechanisms of Post-Transcriptional Regulation in Metabolic Pathways. <i>Cell Systems</i> , 2018, 7, 613-626.e5.	2.9	93
29	Regulation of Yeast-to-Hyphae Transition in <i>Yarrowia lipolytica</i> . <i>MSphere</i> , 2018, 3, .	1.3	35
30	<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
31	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.	9.4	160
32	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
33	Protein hyperproduction in fungi by design. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 8621-8628.	1.7	19
34	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
35	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
36	A molecular genetic toolbox for <i>Yarrowia lipolytica</i> . <i>Biotechnology for Biofuels</i> , 2017, 10, 2.	6.2	62

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37	Regulation of Nitrogen Metabolism by GATA Zinc Finger Transcription Factors in <i>Yarrowia lipolytica</i> . <i>MSphere</i> , 2017, 2, .	1.3	29
38	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
39	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
40	Leucine Biosynthesis Is Involved in Regulating High Lipid Accumulation in <i>Yarrowia lipolytica</i> . <i>MBio</i> , 2017, 8, .	1.8	38
41	A parts list for fungal cellulosomes revealed by comparative genomics. <i>Nature Microbiology</i> , 2017, 2, 17087.	5.9	183
42	Structural reorganization of the fungal endoplasmic reticulum upon induction of mycotoxin biosynthesis. <i>Scientific Reports</i> , 2017, 7, 44296.	1.6	71
43	Mycotoxins: A Fungal Genomics Perspective. <i>Methods in Molecular Biology</i> , 2017, 1542, 367-379.	0.4	2
44	Multimodal microfluidic platform for controlled culture and analysis of unicellular organisms. <i>Biomicrofluidics</i> , 2017, 11, 054104.	1.2	4
45	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
46	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
47	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
48	Fungal Ligninolytic Enzymes and Their Applications. , 2017, , 1049-1061.		2
49	<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
50	Expression of naturally ionic liquid-tolerant thermophilic cellulases in <i>Aspergillus niger</i> . <i>PLoS ONE</i> , 2017, 12, e0189604.	1.1	13
51	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
52	Identification of a Classical Mutant in the Industrial Host <i>Aspergillus niger</i> by Systems Genetics: <i>LaeA</i> 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
53	Fungal Ligninolytic Enzymes and Their Applications. <i>Microbiology Spectrum</i> , 2016, 4, .	1.2	19
54	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. <i>Current Biology</i> , 2016, 26, 1577-1584.	1.8	175

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55	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
56	Ochratoxin A production by <i>Penicillium thymicola</i> . <i>Fungal Biology</i> , 2016, 120, 1041-1049.	1.1	20
57	Approaches to understanding protein hypersecretion in fungi. <i>Fungal Biology Reviews</i> , 2016, 30, 145-151.	1.9	2
58	Regulation of amino-acid metabolism controls flux to lipid accumulation in <i>Yarrowia lipolytica</i> . <i>Npj Systems Biology and Applications</i> , 2016, 2, 16005.	1.4	141
59	Multimodal microchannel and nanowell-based microfluidic platforms for bioimaging. , 2016, , .		0
60	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
61	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
62	Comparative Genomics, Resequencing and Fast Forward Genetics in <i>Aspergillus</i> and <i>Penicillium</i> . , 2016, , 17-26.		2
63	Compartmentalized microchannel array for high-throughput analysis of single cell polarized growth and dynamics. <i>Scientific Reports</i> , 2015, 5, 16111.	1.6	28
64	Draft Genome Sequence of the Dimorphic Yeast <i>Yarrowia lipolytica</i> Strain W29. <i>Genome Announcements</i> , 2015, 3, .	0.8	16
65	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
66	<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
67	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
68	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
69	Draft Genome Sequence of <i>Neurospora crassa</i> Strain FGSC 73. <i>Genome Announcements</i> , 2015, 3, .	0.8	17
70	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
71	Genome Sequence of the Mucoromycotina Fungus <i>Umbelopsis isabellina</i> , an Effective Producer of Lipids. <i>Genome Announcements</i> , 2014, 2, .	0.8	26
72	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

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73	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
74	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
75	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
76	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
77	<i>Aspergillus</i> : Genomics of a Cosmopolitan Fungus. <i>Soil Biology</i> , 2013, , 89-126.	0.6	4
78	Return of the Fungi. <i>Industrial Biotechnology</i> , 2013, 9, 328-330.	0.5	0
79	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
80	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
81	Fungi and Industrial Biotechnology – A Special Issue for an Amazing Kingdom. <i>Industrial Biotechnology</i> , 2013, 9, 105-107.	0.5	4
82	Resin-Assisted Enrichment of N-Terminal Peptides for Characterizing Proteolytic Processing. <i>Analytical Chemistry</i> , 2013, 85, 6826-6832.	3.2	24
83	Comparative Genomics Analysis of <i>Trichoderma reesei</i> Strains. <i>Industrial Biotechnology</i> , 2013, 9, 352-367.	0.5	34
84	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
85	Comparative Genome Structure, Secondary Metabolite, and Effector Coding Capacity across <i>Cochliobolus</i> Pathogens. <i>PLoS Genetics</i> , 2013, 9, e1003233.	1.5	232
86	Functional Analyses of <i>Trichoderma reesei</i> LAE1 Reveal Conserved and Contrasting Roles of This Regulator. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 369-378.	0.8	109
87	<i>Trichoderma</i> and the biorefinery: from plant health to enzymes to biofuel production.. , 2013, , 222-229.		0
88	Phylogenomic analysis of polyketide synthase-encoding genes in <i>Trichoderma</i> . <i>Microbiology (United Kingdom)</i> , 2013, 153, 1077-1087.	0.7	71
89	New Insight into the Ochratoxin A Biosynthetic Pathway through Deletion of a Nonribosomal Peptide Synthetase Gene in <i>Aspergillus carbonarius</i> . <i>Applied and Environmental Microbiology</i> , 2012, 78, 8208-8218.	1.4	99
90	Phylogenomic and functional domain analysis of polyketide synthases in <i>Fusarium</i> . <i>Fungal Biology</i> , 2012, 116, 318-331.	1.1	50

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91	Harnessing glycosylation to improve cellulase activity. <i>Current Opinion in Biotechnology</i> , 2012, 23, 338-345.	3.3	107
92	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
93	A versatile toolkit for high throughput functional genomics with <i>Trichoderma reesei</i> . <i>Biotechnology for Biofuels</i> , 2012, 5, 1.	6.2	434
94	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
95	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
96	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
97	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
98	Characterization of a polyketide synthase in <i>Aspergillus niger</i> whose product is a precursor for both dihydroxynaphthalene (DHN) melanin and naphtho-î³-pyrone. <i>Fungal Genetics and Biology</i> , 2011, 48, 430-437.	0.9	91
99	Proteome Studies of Filamentous Fungi. <i>Methods in Molecular Biology</i> , 2011, 722, 133-139.	0.4	3
100	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
101	Sequencing the fungal tree of life. <i>New Phytologist</i> , 2011, 190, 818-821.	3.5	107
102	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
103	Post-genomic approaches to understanding interactions between fungi and their environment. <i>IMA Fungus</i> , 2011, 2, 81-86.	1.7	11
104	The Plant Cell Wallâ€™Decomposing Machinery Underlies the Functional Diversity of Forest Fungi. <i>Science</i> , 2011, 333, 762-765.	6.0	512
105	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
106	Anaerobic fungi: Neocallimastigomycota. <i>IMA Fungus</i> , 2010, 1, 181-185.	1.7	39
107	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.	13.7	1,442
108	Genome sequence of the model mushroom <i>Schizophyllum commune</i> . <i>Nature Biotechnology</i> , 2010, 28, 957-963.	9.4	490

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109	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
110	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
111	Exploiting proteomic data for genome annotation and gene model validation in <i>Aspergillus niger</i> . BMC Genomics, 2009, 10, 61.	1.2	35
112	Fungal glycoside hydrolases for saccharification of lignocellulose: outlook for new discoveries fueled by genomics and functional studies. Cellulose, 2009, 16, 687-697.	2.4	32
113	Selection to sequence: opportunities in fungal genomics. Environmental Microbiology, 2009, 11, 2955-2958.	1.8	9
114	Genome, transcriptome, and secretome analysis of wood decay fungus <i>Postia placenta</i> supports unique mechanisms of lignocellulose conversion. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1954-1959.	3.3	530
115	Analytical and computational approaches to define the <i>Aspergillus niger</i> secretome. Fungal Genetics and Biology, 2009, 46, S153-S160.	0.9	87
116	Essential pathway identification: from <i>in silico</i> analysis to potential antifungal targets in <i>Aspergillus fumigatus</i> . Medical Mycology, 2009, 47, S80-S87.	0.3	20
117	Proteomics for Validation of Automated Gene Model Predictions. Methods in Molecular Biology, 2009, 492, 447-452.	0.4	4
118	Fungal genome sequencing and bioenergy. Fungal Biology Reviews, 2008, 22, 1-5.	1.9	27
119	Genome sequencing and analysis of the biomass-degrading fungus <i>Trichoderma reesei</i> (syn. <i>Hypocrea</i>) Tj ETQq1 1 0.784314 rgBT /Over	9.4	1,116
120	Purifying selection and birth-and-death evolution in the class II hydrophobin gene families of the ascomycete <i>Trichoderma/Hypocrea</i> . BMC Evolutionary Biology, 2008, 8, 4.	3.2	69
121	Mixed-Effects Statistical Model for Comparative LC-MS Proteomics Studies. Journal of Proteome Research, 2008, 7, 1209-1217.	1.8	44
122	Hydrogenosomes of Anaerobic Chytrids: An Alternative Way to Adapt to Anaerobic Environments. Microbiology Monographs, 2008, , 147-162.	0.3	10
123	Genetic and Genomic Dissection of the <i>Cochliobolus heterostrophus</i> Tox1 Locus Controlling Biosynthesis of the Polyketide Virulence Factor ϵ -toxin. Advances in Genetics, 2007, 57, 219-261.	0.8	56
124	An Overview of the Genus <i>Aspergillus</i> . Mycology, 2007, , 3-13.	0.5	16
125	The <i>Fusarium graminearum</i> Genome Reveals a Link Between Localized Polymorphism and Pathogen Specialization. Science, 2007, 317, 1400-1402.	6.0	837
126	What can comparative genomics tell us about species concepts in the genus <i>Aspergillus</i> ?. Studies in Mycology, 2007, 59, 11-17.	4.5	83

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127	Aspergillus niger genomics: Past, present and into the future. <i>Medical Mycology</i> , 2006, 44, 17-21.	0.3	200
128	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
129	Two Polyketide Synthase-Encoding Genes Are Required for Biosynthesis of the Polyketide Virulence Factor, T-toxin, by <i>Cochliobolus heterostrophus</i> . <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 139-149.	1.4	135
130	Activation of an AP1-Like Transcription Factor of the Maize Pathogen <i>Cochliobolus heterostrophus</i> in Response to Oxidative Stress and Plant Signals. <i>Eukaryotic Cell</i> , 2005, 4, 443-454.	3.4	94
131	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
132	A Cell Signal Pathway Involving Laminin-5, $\alpha 3 \beta 1$ Integrin, and Mitogen-activated Protein Kinase Can Regulate Epithelial Cell Proliferation. <i>Molecular Biology of the Cell</i> , 1999, 10, 259-270.	0.9	146
133	Structure and Function of Hemidesmosomes: More Than Simple Adhesion Complexes. <i>Journal of Investigative Dermatology</i> , 1999, 112, 411-418.	0.3	513
134	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
135	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 $\alpha 6$ integrin. , 1997, 37, 271-286.		21
136	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
137	Molecular genetic studies of a human epidermal autoantigen (the 180-kD bullous pemphigoid) Tj ETQq1 1 0.784314 rgBT /Overlock 10 evidence for an interaction between BP180 and alpha 6 integrin.. <i>Journal of Cell Biology</i> , 1995, 130, 117-125.	2.3	131
138	Hemidesmosomes: Extracellular Matrix/Intermediate Filament Connectors. <i>Experimental Cell Research</i> , 1994, 213, 1-11.	1.2	90
139	Genome and proteome analysis of industrial fungi. , 0, , 3-9.		0
140	Genomes to Proteomes. , 0, , 21-45.		1