

Scott E Baker

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.

140
papers

11,084
citations

49
h-index

104
g-index

150
ext. papers

13,293
ext. citations

7.7
avg, IF

5.59
L-index

#	Paper	IF	Citations
140	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	3.3	
139	Evidence of the Involvement of a Cyclase Gene in the Biosynthesis of Ochratoxin A in .. <i>Toxins</i> , 2021 , 13,	4.9	2
138	Bayesian Inference for Integrating Multiomics Datasets with Metabolic Modeling. <i>ACS Synthetic Biology</i> , 2021 , 10, 2968-2981	5.7	1
137	Molecular Mechanisms of Plant-Microbe Interactions in the Rhizosphere as Targets for Improving Plant Productivity. <i>Rhizosphere Biology</i> , 2021 , 295-338	0.8	2
136	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	5.8	1
135	Integration of Proteomics and Metabolomics Into the Design, Build, Test, Learn Cycle to Improve 3-Hydroxypropionic Acid Production in. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021 , 9, 603832	5.8	1
134	The F-box protein gene - 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,	11.5	2
133	Strain Construction for Intracellular Metabolic Pathway Localization in <i>Y. lipolytica</i> . <i>Methods in Molecular Biology</i> , 2021 , 2307, 147-157	1.4	0
132	Production of Biofuels From Biomass by Fungi 2021 , 555-576		0
131	Major involvement of two laccase genes in conidial pigment biosynthesis in <i>Aspergillus oryzae</i> . <i>Applied Microbiology and Biotechnology</i> , 2021 , 106, 287	5.7	
130	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	5.7	3
129	A comparative genomics study of 23 <i>Aspergillus</i> species from section Flavi. <i>Nature Communications</i> , 2020 , 11, 1106	17.4	54
128	101 genomes: A test case for predicting lifestyles and emergence of pathogens. <i>Studies in Mycology</i> , 2020 , 96, 141-153	22.2	63
127	Horizontal Gene Transfer in Fungi. <i>Grand Challenges in Biology and Biotechnology</i> , 2020 , 317-332	2.4	2
126	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	5.2	7
125	Grand Challenges in Fungal Biotechnology. <i>Frontiers in Fungal Biology</i> , 2020 , 1,	0.3	1
124	Integrative quantitative-phase and airy light-sheet imaging. <i>Scientific Reports</i> , 2020 , 10, 20150	4.9	4

123	High-Throughput Large-Scale Targeted Proteomics Assays for Quantifying Pathway Proteins in KT2440. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 603488	5.8	3
122	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	5.7	8
121	Multi-Omics Driven Metabolic Network Reconstruction and Analysis of Lignocellulosic Carbon Utilization in. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 612832	5.8	8
120	Hydrogenosomes of Anaerobic Fungi: An Alternative Way to Adapt to Anaerobic Environments. <i>Microbiology Monographs</i> , 2019 , 159-175	0.8	5
119	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	3.7	29
118	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	5.7	9
117	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> , 2018 , 115, E753-E761	11.5	78
116	Protein hyperproduction in fungi by design. <i>Applied Microbiology and Biotechnology</i> , 2018 , 102, 8621-8628	5.7	12
115	Prediction of Metabolite Concentrations, Rate Constants and Post-Translational Regulation Using Maximum Entropy-Based Simulations with Application to Central Metabolism of. <i>Processes</i> , 2018 , 6,	2.9	8
114	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	4.5	10
113	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	22.2	8
112	Circadian Proteomic Analysis Uncovers Mechanisms of Post-Transcriptional Regulation in Metabolic Pathways. <i>Cell Systems</i> , 2018 , 7, 613-626.e5	10.6	46
111	Regulation of Yeast-to-Hyphae Transition in <i>Yarrowia lipolytica</i> . <i>MSphere</i> , 2018 , 3,	5	20
110	<i>Dichomitus squalens</i> partially tailors its molecular responses to the composition of solid wood. <i>Environmental Microbiology</i> , 2018 , 20, 4141-4156	5.2	19
109	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	36.3	100
108	Cloning and Expression of Heterologous Cellulases and Enzymes in <i>Aspergillus niger</i> . <i>Methods in Molecular Biology</i> , 2018 , 1796, 123-133	1.4	
107	A molecular genetic toolbox for. <i>Biotechnology for Biofuels</i> , 2017 , 10, 2	7.8	41
106	Regulation of Nitrogen Metabolism by GATA Zinc Finger Transcription Factors in. <i>MSphere</i> , 2017 , 2,	5	19

105	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	18.3	261
104	Diverse data supports the transition of filamentous fungal model organisms into the post-genomics era. <i>Mycology</i> , 2017 , 8, 67-83	3.7	7
103	Leucine Biosynthesis Is Involved in Regulating High Lipid Accumulation in. <i>MBio</i> , 2017 , 8,	7.8	29
102	A parts list for fungal cellulosomes revealed by comparative genomics. <i>Nature Microbiology</i> , 2017 , 2, 17087	26.6	111
101	Structural reorganization of the fungal endoplasmic reticulum upon induction of mycotoxin biosynthesis. <i>Scientific Reports</i> , 2017 , 7, 44296	4.9	46
100	Mycotoxins: A Fungal Genomics Perspective. <i>Methods in Molecular Biology</i> , 2017 , 1542, 367-379	1.4	2
99	Multimodal microfluidic platform for controlled culture and analysis of unicellular organisms. <i>Biomicrofluidics</i> , 2017 , 11, 054104	3.2	1
98	Non-steady state mass action dynamics without rate constants: dynamics of coupled reactions using chemical potentials. <i>Physical Biology</i> , 2017 , 14, 055003	3	5
97	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	5.2	5
96	Expression of naturally ionic liquid-tolerant thermophilic cellulases in <i>Aspergillus niger</i> . <i>PLoS ONE</i> , 2017 , 12, e0189604	3.7	8
95	Genome sequencing and transcriptome analysis of QM9978 strain reveals a distal chromosome translocation to be responsible for loss of expression and loss of cellulase induction. <i>Biotechnology for Biofuels</i> , 2017 , 10, 209	7.8	32
94	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,	4.8	14
93	Fungal Ligninolytic Enzymes and Their Applications 2017 , 1049-1061		2
92	<i>Thermoascus aurantiacus</i> is an Intriguing Host for the Industrial Production of Cellulases. <i>Current Biotechnology</i> , 2017 , 6, 89-97	0.6	16
91	Approaches to understanding protein hypersecretion in fungi. <i>Fungal Biology Reviews</i> , 2016 , 30, 145-1516.8		2
90	Regulation of amino-acid metabolism controls flux to lipid accumulation in. <i>Npj Systems Biology and Applications</i> , 2016 , 2, 16005	5	106
89	Multi-omics analysis reveals regulators of the response to nitrogen limitation in <i>Yarrowia lipolytica</i> . <i>BMC Genomics</i> , 2016 , 17, 138	4.5	45
88	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	13.2	118

87	Comparative Genomics, Resequencing and Fast Forward Genetics in <i>Aspergillus</i> and <i>Penicillium</i> 2016 , 17-26		2
86	Fungal Ligninolytic Enzymes and Their Applications. <i>Microbiology Spectrum</i> , 2016 , 4,	8.9	17
85	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. <i>Current Biology</i> , 2016 , 26, 1577-1584	6.3	119
84	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	2.8	8
83	Ochratoxin A production by <i>Penicillium thymicola</i> . <i>Fungal Biology</i> , 2016 , 120, 1041-1049	2.8	13
82	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,		21
81	Draft Genome Sequence of <i>Neurospora crassa</i> Strain FGSC 73. <i>Genome Announcements</i> , 2015 , 3,		12
80	Compartmentalized microchannel array for high-throughput analysis of single cell polarized growth and dynamics. <i>Scientific Reports</i> , 2015 , 5, 16111	4.9	20
79	Draft Genome Sequence of the Dimorphic Yeast <i>Yarrowia lipolytica</i> Strain W29. <i>Genome Announcements</i> , 2015 , 3,		15
78	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	4.5	25
77	period-1 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, 15707-12	11.5	16
76	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, 3103-13	5.7	11
75	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	3.7	44
74	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> , 2015 , 6, 193-204	3.2	42
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, 10-7	5.8	60
72	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	3.9	6
71	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, 9923-8	11.5	461
70	Genome Sequence of the Mucoromycotina Fungus <i>Umbelopsis isabellina</i> , an Effective Producer of Lipids. <i>Genome Announcements</i> , 2014 , 2,		12

69	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	11.5	8
68	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, 269-81	5.7	57
67	<i>Aspergillus</i> : Genomics of a Cosmopolitan Fungus. <i>Soil Biology</i> , 2013 , 89-126	1	2
66	Return of the Fungi. <i>Industrial Biotechnology</i> , 2013 , 9, 328-330	1.3	
65	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, 120-32	3.9	20
64	One fungus, one name: defining the genus <i>Fusarium</i> in a scientifically robust way that preserves longstanding use. <i>Phytopathology</i> , 2013 , 103, 400-8	3.8	155
63	Fungi and Industrial Biotechnology [A Special Issue for an Amazing Kingdom. <i>Industrial Biotechnology</i> , 2013 , 9, 105-107	1.3	4
62	Resin-assisted enrichment of N-terminal peptides for characterizing proteolytic processing. <i>Analytical Chemistry</i> , 2013 , 85, 6826-32	7.8	20
61	<i>Aspergilli</i> and Biomass-Degrading Fungi 2013 , 63-87		0
60	Comparative Genomics Analysis of <i>Trichoderma reesei</i> Strains. <i>Industrial Biotechnology</i> , 2013 , 9, 352-367	1.3	27
59	The polyketide synthase gene <i>pks4</i> of <i>Trichoderma reesei</i> provides pigmentation and stress resistance. <i>Eukaryotic Cell</i> , 2013 , 12, 1499-508		61
58	Comparative genome structure, secondary metabolite, and effector coding capacity across <i>Cochliobolus</i> pathogens. <i>PLoS Genetics</i> , 2013 , 9, e1003233	6	161
57	Functional analyses of <i>Trichoderma reesei</i> LAE1 reveal conserved and contrasting roles of this regulator. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 369-78	3.2	86
56	<i>Trichoderma</i> and the biorefinery: from plant health to enzymes to biofuel production. 2013 , 222-229		
55	The putative protein methyltransferase LAE1 controls cellulase gene expression in <i>Trichoderma reesei</i> . <i>Molecular Microbiology</i> , 2012 , 84, 1150-64	4.1	170
54	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, 8208-18	4.8	87
53	Phylogenomic and functional domain analysis of polyketide synthases in <i>Fusarium</i> . <i>Fungal Biology</i> , 2012 , 116, 318-31	2.8	41
52	Harnessing glycosylation to improve cellulase activity. <i>Current Opinion in Biotechnology</i> , 2012 , 23, 338-45	1.4	96

51	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, 143-56	5.6	53
50	A versatile toolkit for high throughput functional genomics with <i>Trichoderma reesei</i> . <i>Biotechnology for Biofuels</i> , 2012 , 5, 1	7.8	318
49	The production of multiple small peptaibol families by single 14-module Peptide synthetases in <i>Trichoderma/Hypocrea</i> . <i>Chemistry and Biodiversity</i> , 2012 , 9, 499-535	2.5	58
48	Phylogenomic analysis of polyketide synthase-encoding genes in <i>Trichoderma</i> . <i>Microbiology (United Kingdom)</i> , 2012 , 158, 147-154	2.9	67
47	Comparative genomics of citric-acid-producing <i>Aspergillus niger</i> ATCC 1015 versus enzyme-producing CBS 513.88. <i>Genome Research</i> , 2011 , 21, 885-97	9.7	266
46	Comparative genome sequence analysis underscores mycoparasitism as the ancestral life style of <i>Trichoderma</i> . <i>Genome Biology</i> , 2011 , 12, R40	18.3	448
45	Characterization of a polyketide synthase in <i>Aspergillus niger</i> whose product is a precursor for both dihydroxynaphthalene (DHN) melanin and naphthopyrone. <i>Fungal Genetics and Biology</i> , 2011 , 48, 430-7	3.9	77
44	Proteome studies of filamentous fungi. <i>Methods in Molecular Biology</i> , 2011 , 722, 133-9	1.4	1
43	Comparative genomic analysis of the thermophilic biomass-degrading fungi <i>Myceliophthora thermophila</i> and <i>Thielavia terrestris</i> . <i>Nature Biotechnology</i> , 2011 , 29, 922-7	44.5	324
42	Sequencing the fungal tree of life. <i>New Phytologist</i> , 2011 , 190, 818-821	9.8	91
41	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, 339-51	3.1	54
40	Post-genomic approaches to understanding interactions between fungi and their environment. <i>IMA Fungus</i> , 2011 , 2, 81-6	6.8	9
39	The plant cell wall-decomposing machinery underlies the functional diversity of forest fungi. <i>Science</i> , 2011 , 333, 762-5	33.3	417
38	Rediscovery by Whole Genome Sequencing: Classical Mutations and Genome Polymorphisms in <i>Neurospora crassa</i> . <i>G3: Genes, Genomes, Genetics</i> , 2011 , 1, 303-16	3.2	54
37	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010 , 464, 367-73	50.4	1085
36	Genome sequence of the model mushroom <i>Schizophyllum commune</i> . <i>Nature Biotechnology</i> , 2010 , 28, 957-63	44.5	381
35	Anaerobic fungi: Neocallimastigomycota. <i>IMA Fungus</i> , 2010 , 1, 181-5	6.8	37
34	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, 16151-6	11.5	164

33	Transcriptomic response of the mycoparasitic fungus <i>Trichoderma atroviride</i> to the presence of a fungal prey. <i>BMC Genomics</i> , 2009 , 10, 567	4.5	118
32	Exploiting proteomic data for genome annotation and gene model validation in <i>Aspergillus niger</i> . <i>BMC Genomics</i> , 2009 , 10, 61	4.5	32
31	Fungal glycoside hydrolases for saccharification of lignocellulose: outlook for new discoveries fueled by genomics and functional studies. <i>Cellulose</i> , 2009 , 16, 687-697	5.5	23
30	Selection to sequence: opportunities in fungal genomics. <i>Environmental Microbiology</i> , 2009 , 11, 2955-8	5.2	8
29	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, 1954-9	11.5	479
28	Analytical and computational approaches to define the <i>Aspergillus niger</i> secretome. <i>Fungal Genetics and Biology</i> , 2009 , 46 Suppl 1, S153-S160	3.9	77
27	Essential pathway identification: from in silico analysis to potential antifungal targets in <i>Aspergillus fumigatus</i> . <i>Medical Mycology</i> , 2009 , 47 Suppl 1, S80-7	3.9	15
26	Proteomics for validation of automated gene model predictions. <i>Methods in Molecular Biology</i> , 2009 , 492, 447-52	1.4	3
25	Genome sequencing and analysis of the biomass-degrading fungus <i>Trichoderma reesei</i> (syn. <i>Hypocrea jecorina</i>). <i>Nature Biotechnology</i> , 2008 , 26, 553-60	44.5	920
24	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	59
23	Mixed-effects statistical model for comparative LC-MS proteomics studies. <i>Journal of Proteome Research</i> , 2008 , 7, 1209-17	5.6	35
22	Hydrogenosomes of Anaerobic Chytrids: An Alternative Way to Adapt to Anaerobic Environments. <i>Microbiology Monographs</i> , 2008 , 147-162	0.8	10
21	Fungal genome sequencing and bioenergy. <i>Fungal Biology Reviews</i> , 2008 , 22, 1-5	6.8	19
20	<i>Aspergillus</i> in the genomic era 2008 ,		17
19	Genetic and genomic dissection of the <i>Cochliobolus heterostrophus</i> Tox1 locus controlling biosynthesis of the polyketide virulence factor T-toxin. <i>Advances in Genetics</i> , 2007 , 57, 219-61	3.3	47
18	An Overview of the Genus <i>Aspergillus</i> . <i>Mycology</i> , 2007 , 3-13		5
17	The <i>Fusarium graminearum</i> genome reveals a link between localized polymorphism and pathogen specialization. <i>Science</i> , 2007 , 317, 1400-2	33.3	668
16	What can comparative genomics tell us about species concepts in the genus <i>Aspergillus</i> ?. <i>Studies in Mycology</i> , 2007 , 59, 11-7	22.2	70

15	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, 139-49	3.6	108
14	<i>Aspergillus niger</i> genomics: past, present and into the future. <i>Medical Mycology</i> , 2006 , 44 Suppl 1, S17-21	3.9	155
13	Biomarker candidate identification in <i>Yersinia pestis</i> using organism-wide semiquantitative proteomics. <i>Journal of Proteome Research</i> , 2006 , 5, 3008-17	5.6	40
12	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, 443-54		90
11	Genetic interaction between integrins and moleskin, a gene encoding a <i>Drosophila</i> homolog of importin-7. <i>Genetics</i> , 2002 , 162, 285-96	4	26
10	A cell signal pathway involving laminin-5, alpha3beta1 integrin, and mitogen-activated protein kinase can regulate epithelial cell proliferation. <i>Molecular Biology of the Cell</i> , 1999 , 10, 259-70	3.5	135
9	Structure and function of hemidesmosomes: more than simple adhesion complexes. <i>Journal of Investigative Dermatology</i> , 1999 , 112, 411-8	4.3	428
8	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	6.5	9
7	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 6A integrin. <i>Cytoskeleton</i> , 1997 , 37, 271-86		20
6	Morphogenetic effects of soluble laminin-5 on cultured epithelial cells and tissue explants. <i>Experimental Cell Research</i> , 1996 , 228, 262-70	4.2	63
5	Molecular genetic studies of a human epidermal autoantigen (the 180-kD bullous pemphigoid antigen/BP180): identification of functionally important sequences within the BP180 molecule and evidence for an interaction between BP180 and alpha 6 integrin. <i>Journal of Cell Biology</i> , 1995 , 130, 117-25	7.3	120
4	Hemidesmosomes: extracellular matrix/intermediate filament connectors. <i>Experimental Cell Research</i> , 1994 , 213, 1-11	4.2	84
3	Genomes to Proteomes21-45		
2	Genome and proteome analysis of industrial fungi3-9		
1	Fungal Cell Factories205-219		4