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Nucleic Acids Research

40, D26-D32

DOI: [10.1093/nar/gkr947](https://doi.org/10.1093/nar/gkr947)

Citation Report

#	ARTICLE	IF	CITATIONS
1	OrySPSSP: a comparative Platform for Small Secreted Proteins from rice and other plants. <i>Nucleic Acids Research</i> , 2012, 41, D1192-D1198.	6.5	18
2	The Genomes of the Fungal Plant Pathogens <i>Cladosporium fulvum</i> and <i>Dothistroma septosporum</i> Reveal Adaptation to Different Hosts and Lifestyles But Also Signatures of Common Ancestry. <i>PLoS Genetics</i> , 2012, 8, e1003088.	1.5	226
3	Diverse Lifestyles and Strategies of Plant Pathogenesis Encoded in the Genomes of Eighteen Dothideomycetes Fungi. <i>PLoS Pathogens</i> , 2012, 8, e1003037.	2.1	595
4	Four Novel Cellulose Synthase (CESA) Genes from Birch ( <i>Betula platyphylla</i> Suk.) Involved in Primary and Secondary Cell Wall Biosynthesis. <i>International Journal of Molecular Sciences</i> , 2012, 13, 12195-12212.	1.8	17
5	Transcription Factor Amr1 Induces Melanin Biosynthesis and Suppresses Virulence in <i>Alternaria brassicicola</i> . <i>PLoS Pathogens</i> , 2012, 8, e1002974.	2.1	91
6	Detecting Phylogenetic Signals in Eukaryotic Whole Genome Sequences. <i>Journal of Computational Biology</i> , 2012, 19, 945-956.	0.8	11
7	Perspectives in PDK1 evolution. <i>Plant Signaling and Behavior</i> , 2012, 7, 642-649.	1.2	15
8	The eIF4F and eIFiso4F Complexes of Plants: An Evolutionary Perspective. <i>Comparative and Functional Genomics</i> , 2012, 2012, 1-12.	2.0	58
9	A simple high performance liquid chromatography method for the measurement of nucleobases and the RNA and DNA content of cellular material. <i>Limnology and Oceanography: Methods</i> , 2012, 10, 608-616.	1.0	19
10	Genome sequence of the button mushroom <i>Agaricus bisporus</i> reveals mechanisms governing adaptation to a humic-rich ecological niche. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17501-17506.	3.3	359
11	Novel traits of <i>Trichoderma</i> predicted through the analysis of its secretome. <i>FEMS Microbiology Letters</i> , 2012, 337, 1-9.	0.7	106
12	Genome mining reveals the evolutionary origin and biosynthetic potential of basidiomycete polyketide synthases. <i>Fungal Genetics and Biology</i> , 2012, 49, 996-1003.	0.9	71
13	Transformation of the fungus <i>Absidia glauca</i> by complementation of a methionine auxotrophic strain affected in the homoserine acetyltransferase gene. <i>FEBS Open Bio</i> , 2012, 2, 197-201.	1.0	1
14	Comparative Genomics of the Lipid-body-membrane Proteins Oleosin, Caleosin and Steroleosin in Magnoliophyte, Lycophyte and Bryophyte. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 345-353.	3.0	21
15	Nucleic Acid-based Methods to Assess the Composition and Function of the Bowel Microbiota. <i>Gastroenterology Clinics of North America</i> , 2012, 41, 855-868.	1.0	5
16	The 2012 Nucleic Acids Research Database Issue and the online Molecular Biology Database Collection. <i>Nucleic Acids Research</i> , 2012, 40, D1-D8.	6.5	104
17	Biotin-Binding Proteins in the Defense of Mushrooms against Predators and Parasites. <i>Applied and Environmental Microbiology</i> , 2012, 78, 8485-8487.	1.4	20
18	The ins and outs of algal metal transport. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2012, 1823, 1531-1552.	1.9	173

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19	Genome Sequencing and Mapping Reveal Loss of Heterozygosity as a Mechanism for Rapid Adaptation in the Vegetable Pathogen <i>Phytophthora capsici</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 1350-1360.	1.4	264
20	In-depth proteomic analysis of a mollusc shell: acid-soluble and acid-insoluble matrix of the limpet <i>Lottia gigantea</i> . <i>Proteome Science</i> , 2012, 10, 28.	0.7	79
21	<i>Thermoascus aurantiacus</i> is a promising source of enzymes for biomass deconstruction under thermophilic conditions. <i>Biotechnology for Biofuels</i> , 2012, 5, 54.	6.2	88
22	Genomics of Algal Host-Virus Interactions. <i>Advances in Botanical Research</i> , 2012, , 343-381.	0.5	15
24	Comparative Pathogenomics Reveals Horizontally Acquired Novel Virulence Genes in Fungi Infecting Cereal Hosts. <i>PLoS Pathogens</i> , 2012, 8, e1002952.	2.1	176
25	Expanded Functional Diversity of Shaker K <sup>+</sup> Channels in Cnidarians Is Driven by Gene Expansion. <i>PLoS ONE</i> , 2012, 7, e51366.	1.1	29
26	The genome of wine yeast <i>Dekkera bruxellensis</i> provides a tool to explore its food-related properties. <i>International Journal of Food Microbiology</i> , 2012, 157, 202-209.	2.1	102
27	Toward genome-enabled mycology. <i>Mycologia</i> , 2013, 105, 1339-1349.	0.8	38
28	Distribution and bioinformatic analysis of the cerato-platanin protein family in Dikarya. <i>Mycologia</i> , 2013, 105, 1479-1488.	0.8	58
29	Antimicrobial Defenses and Resistance in Forest Trees: Challenges and Perspectives in a Genomic Era. <i>Annual Review of Phytopathology</i> , 2013, 51, 221-244.	3.5	66
30	<i>Trichoderma</i> Research in the Genome Era. <i>Annual Review of Phytopathology</i> , 2013, 51, 105-129.	3.5	370
31	Lignin-degrading peroxidases in Polyporales: an evolutionary survey based on 10 sequenced genomes. <i>Mycologia</i> , 2013, 105, 1428-1444.	0.8	134
32	Membrane cholesterol and sphingomyelin, and ostreolysin A are obligatory for pore-formation by a MACPF/CDC-like pore-forming protein, pleurotolysin B. <i>Biochimie</i> , 2013, 95, 1855-1864.	1.3	68
33	Genomewide analysis of polysaccharides degrading enzymes in 11 white- and brown-rot Polyporales provides insight into mechanisms of wood decay. <i>Mycologia</i> , 2013, 105, 1412-1427.	0.8	110
34	Evolution of protein indels in plants, animals and fungi. <i>BMC Evolutionary Biology</i> , 2013, 13, 140.	3.2	58
35	Gene make-up: rapid and massive intron gains after horizontal transfer of a bacterial $\alpha$ -amylase gene to Basidiomycetes. <i>BMC Evolutionary Biology</i> , 2013, 13, 40.	3.2	49
36	Comparative analysis of fungal genomes reveals different plant cell wall degrading capacity in fungi. <i>BMC Genomics</i> , 2013, 14, 274.	1.2	473
37	RNAseq versus genome-predicted transcriptomes: a large population of novel transcripts identified in an Illumina-454 Hydra transcriptome. <i>BMC Genomics</i> , 2013, 14, 204.	1.2	61

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38	5'-Serial Analysis of Gene Expression studies reveal a transcriptomic switch during fruiting body development in <i>Coprinopsis cinerea</i> . <i>BMC Genomics</i> , 2013, 14, 195.	1.2	65
39	PacC and pH-dependent transcriptome of the mycotrophic fungus <i>Trichoderma virens</i> . <i>BMC Genomics</i> , 2013, 14, 138.	1.2	63
40	The basidiomycete <i>Ustilago maydis</i> has two plasma membrane H <sup>+</sup> -ATPases related to fungi and plants. <i>Journal of Bioenergetics and Biomembranes</i> , 2013, 45, 477-490.	1.0	7
41	Diversity and evolution of ABC proteins in basidiomycetes. <i>Mycologia</i> , 2013, 105, 1456-1470.	0.8	16
42	Phylogenetic and phylogenomic overview of the Polyporales. <i>Mycologia</i> , 2013, 105, 1350-1373.	0.8	259
43	The Contribution of New Technologies Toward Understanding Plant-Fungus Symbioses. , 2013, , 201-214.		2
44	Comparative genomics and evolutionary analysis of hydrophobins from three species of wood-degrading fungi. <i>Mycologia</i> , 2013, 105, 1471-1478.	0.8	14
45	<i>Aspergillus</i> : Genomics of a Cosmopolitan Fungus. <i>Soil Biology</i> , 2013, , 89-126.	0.6	4
46	Aspects of nitrogen-fixing <i>Actinobacteria</i> , in particular free-living and symbiotic <i>Frankia</i> . <i>FEMS Microbiology Letters</i> , 2013, 342, 179-186.	0.7	157
47	Genome and transcriptome sequencing of the halophilic fungus <i>Wallemia ichthyophaga</i> : haloadaptations present and absent. <i>BMC Genomics</i> , 2013, 14, 617.	1.2	107
48	A novel type of light-harvesting antenna protein of red algal origin in algae with secondary plastids. <i>BMC Evolutionary Biology</i> , 2013, 13, 159.	3.2	32
49	Characterization of cytokinin signaling and homeostasis gene families in two hardwood tree species: <i>Populus trichocarpa</i> and <i>Prunus persica</i> . <i>BMC Genomics</i> , 2013, 14, 885.	1.2	38
50	Fungal genomes mining to discover novel sterol esterases and lipases as catalysts. <i>BMC Genomics</i> , 2013, 14, 712.	1.2	31
51	Targeting Genes of Cd Induced Oxidative Stress Response in Yeasts. <i>Biotechnology and Biotechnological Equipment</i> , 2013, 27, 3716-3724.	0.5	4
52	Using an RSP3 reporter gene system to investigate molecular regulation of hydrogenase expression in <i>Chlamydomonas reinhardtii</i> . <i>Algal Research</i> , 2013, 2, 341-351.	2.4	3
53	Spliceosome twin introns in fungal nuclear transcripts. <i>Fungal Genetics and Biology</i> , 2013, 57, 48-57.	0.9	16
54	Two-component signal transduction in <i>Agaricus bisporus</i> : A comparative genomic analysis with other basidiomycetes through the web-based tool BASID2CS. <i>Fungal Genetics and Biology</i> , 2013, 55, 77-84.	0.9	6
55	The response of <i>Mucor plumbeus</i> to pentachlorophenol: A toxicoproteomics study. <i>Journal of Proteomics</i> , 2013, 78, 159-171.	1.2	28

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56	Simple and efficient recycling of fungal selectable marker genes with the Cre-loxP recombination system via anastomosis. <i>Fungal Genetics and Biology</i> , 2013, 61, 1-8.	0.9	24
57	Oxygen regulation of alternative respiration in fungus <i>Phycomyces blakesleeana</i> : connection with phosphate metabolism. <i>Research in Microbiology</i> , 2013, 164, 770-778.	1.0	12
58	Contribution of phage-derived genomic islands to the virulence of facultative bacterial pathogens. <i>Environmental Microbiology</i> , 2013, 15, 307-312.	1.8	79
59	Ostreopexin: A hemopexin fold protein from the oyster mushroom, <i>Pleurotus ostreatus</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1468-1473.	1.1	3
60	A Practical Approach to Reconstruct Evolutionary History of Animal Sialyltransferases and Gain Insights into the Sequence-Function Relationships of Golgi-Glycosyltransferases. <i>Methods in Molecular Biology</i> , 2013, 1022, 73-97.	0.4	9
61	Mollusk shell structures and their formation mechanism. <i>Canadian Journal of Zoology</i> , 2013, 91, 349-366.	0.4	143
62	Phylogenetic analysis of fungal aquaporins provides insight into their possible role in water transport of mycorrhizal associations. <i>Botany</i> , 2013, 91, 495-504.	0.5	28
63	The function and evolution of the <i>Aspergillus</i> genome. <i>Trends in Microbiology</i> , 2013, 21, 14-22.	3.5	72
69	Structural and gene expression analyses of uptake hydrogenases and other proteins involved in nitrogenase protection in <i>Frankia</i> . <i>Journal of Biosciences</i> , 2013, 38, 703-712.	0.5	8
70	Comparative Genomics Analysis of <i>Trichoderma reesei</i> Strains. <i>Industrial Biotechnology</i> , 2013, 9, 352-367.	0.5	34
71	Orthologous lipoxygenases of <i>Pleurotus</i> spp. – A comparison of substrate specificity and sequence homology. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2013, 97, 189-195.	1.8	15
72	Genome Sequences of Industrially Relevant <i>Saccharomyces cerevisiae</i> Strain M3707, Isolated from a Sample of Distillers Yeast and Four Haploid Derivatives. <i>Genome Announcements</i> , 2013, 1, .	0.8	8
73	Metabolites Associated with Adaptation of Microorganisms to an Acidophilic, Metal-Rich Environment Identified by Stable-Isotope-Enabled Metabolomics. <i>MBio</i> , 2013, 4, e00484-12.	1.8	87
74	Comparative Genome Structure, Secondary Metabolite, and Effector Coding Capacity across <i>Cochliobolus</i> Pathogens. <i>PLoS Genetics</i> , 2013, 9, e1003233.	1.5	232
75	Structural, Biochemical, and Computational Characterization of the Glycoside Hydrolase Family 7 Cellobiohydrolase of the Tree-killing Fungus <i>Heterobasidion irregulare</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 5861-5872.	1.6	70
76	<i>Chlamydomonas</i> ODA10 is a conserved axonemal protein that plays a unique role in outer dynein arm assembly. <i>Molecular Biology of the Cell</i> , 2013, 24, 3689-3696.	0.9	33
77	CFGP 2.0: a versatile web-based platform for supporting comparative and evolutionary genomics of fungi and Oomycetes. <i>Nucleic Acids Research</i> , 2013, 41, D714-D719.	6.5	51
78	Computational identification of functional introns: high positional conservation of introns that harbor RNA genes. <i>Nucleic Acids Research</i> , 2013, 41, 5604-5613.	6.5	18

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79	Molecular evolution of peptidergic signaling systems in bilaterians. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2028-37.	3.3	362
80	OrthoDB: a hierarchical catalog of animal, fungal and bacterial orthologs. Nucleic Acids Research, 2013, 41, D358-D365.	6.5	333
81	Conserved MIP receptorâ€“ligand pair regulates <i>Platynereis</i> larval settlement. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 8224-8229.	3.3	128
82	A comparative hidden Markov model analysis pipeline identifies proteins characteristic of cereal-infecting fungi. BMC Genomics, 2013, 14, 807.	1.2	26
83	Chaperone-Usher Fimbriae of Escherichia coli. PLoS ONE, 2013, 8, e52835.	1.1	179
84	Assessment and Reconstruction of Novel HSP90 Genes: Duplications, Gains and Losses in Fungal and Animal Lineages. PLoS ONE, 2013, 8, e73217.	1.1	6
85	Phytophthora Have Distinct Endogenous Small RNA Populations That Include Short Interfering and microRNAs. PLoS ONE, 2013, 8, e77181.	1.1	88
86	Industrial Robustness: Understanding the Mechanism of Tolerance for the Populus Hydrolysate-Tolerant Mutant Strain of Clostridium thermocellum. PLoS ONE, 2013, 8, e78829.	1.1	21
87	Genome and Transcriptome Analysis of the Basidiomycetous Yeast Pseudozyma antarctica Producing Extracellular Glycolipids, Mannosylerythritol Lipids. PLoS ONE, 2014, 9, e86490.	1.1	45
88	F9 Fimbriae of Uropathogenic Escherichia coli Are Expressed at Low Temperature and Recognise GalÎ²1-3GlcNAc-Containing Glycans. PLoS ONE, 2014, 9, e93177.	1.1	43
89	Comparative Transcriptome Analysis of Four Prymnesiophyte Algae. PLoS ONE, 2014, 9, e97801.	1.1	34
90	Phylogenetic Analyses and Characterization of RNase X25 from Drosophila melanogaster Suggest a Conserved Housekeeping Role and Additional Functions for RNase T2 Enzymes in Protostomes. PLoS ONE, 2014, 9, e105444.	1.1	16
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92	Genome-Wide Macrosynteny among Fusarium Species in the Gibberella fujikuroi Complex Revealed by Amplified Fragment Length Polymorphisms. PLoS ONE, 2014, 9, e114682.	1.1	22
93	Nutritional control of body size through FoxO-Ultraspiracle mediated ecdysone biosynthesis. ELife, 2014, 3, .	2.8	157
94	Transcriptional Responses of the Bdtf1-Deletion Mutant to the Phytoalexin Brassinin in the Necrotrophic Fungus Alternaria brassicicola. Molecules, 2014, 19, 10717-10732.	1.7	10
96	From all to (nearly) none. Cellular Logistics, 2014, 4, e28114.	0.9	22
97	The unfolded protein response (UPR) pathway in <i>Cryptococcus</i> . Virulence, 2014, 5, 341-350.	1.8	23

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98	Fungal Genomics. <i>Advances in Botanical Research</i> , 2014, , 1-52.	0.5	25
99	Highly expressed captured genes and cross-kingdom domains present in Helitrons create novel diversity in <i>Pleurotus ostreatus</i> and other fungi. <i>BMC Genomics</i> , 2014, 15, 1071.	1.2	20
100	The GPCR repertoire in the demosponge <i>Amphimedon queenslandica</i> : insights into the GPCR system at the early divergence of animals. <i>BMC Evolutionary Biology</i> , 2014, 14, 270.	3.2	42
101	The separation between the 5' and 3' ends in long RNA molecules is short and nearly constant. <i>Nucleic Acids Research</i> , 2014, 42, 13963-13968.	6.5	30
102	A naturally occurring, noncanonical GTP aptamer made of simple tandem repeats. <i>RNA Biology</i> , 2014, 11, 682-692.	1.5	9
103	Influence of <i>Populus</i> Genotype on Gene Expression by the Wood Decay Fungus <i>Phanerochaete chrysosporium</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 5828-5835.	1.4	28
105	Analysis of the <i>Phlebiopsis gigantea</i> Genome, Transcriptome and Secretome Provides Insight into Its Pioneer Colonization Strategies of Wood. <i>PLoS Genetics</i> , 2014, 10, e1004759.	1.5	90
106	Origin and evolution of metal P-type ATPases in Plantae (Archaeplastida). <i>Frontiers in Plant Science</i> , 2013, 4, 544.	1.7	39
107	Diversifying selection in the wheat stem rust fungus acts predominantly on pathogen-associated gene families and reveals candidate effectors. <i>Frontiers in Plant Science</i> , 2014, 5, 372.	1.7	45
108	Comparative proteomic analysis of ovary for Chinese rare minnow ( <i>Gobiocypris rarus</i> ) exposed to chlorophenol chemicals. <i>Journal of Proteomics</i> , 2014, 110, 172-182.	1.2	9
109	Widespread occurrence of organelle genome-encoded 5S rRNAs including permuted molecules. <i>Nucleic Acids Research</i> , 2014, 42, 13764-13777.	6.5	129
110	MycoCosm portal: gearing up for 1000 fungal genomes. <i>Nucleic Acids Research</i> , 2014, 42, D699-D704.	6.5	1,187
111	Genome Sequence of the Mucoromycotina Fungus <i>Umbelopsis isabellina</i> , an Effective Producer of Lipids. <i>Genome Announcements</i> , 2014, 2, .	0.8	26
112	Genome sequencing of four <i>Aureobasidium pullulans</i> varieties: biotechnological potential, stress tolerance, and description of new species. <i>BMC Genomics</i> , 2014, 15, 549.	1.2	262
114	<i>Anadenanthera colubrina</i> (Vell.) Brenan produces steroidal substances that are active against <i>Alternaria alternata</i> (Fr.) Keissler and that may bind to oxysterol-binding proteins. <i>Pest Management Science</i> , 2014, 70, 1815-1822.	1.7	11
115	Fungal MACPF-Like Proteins and Aegerolysins: Bi-component Pore-Forming Proteins?. <i>Sub-Cellular Biochemistry</i> , 2014, 80, 271-291.	1.0	24
116	The genome portal of the Department of Energy Joint Genome Institute: 2014 updates. <i>Nucleic Acids Research</i> , 2014, 42, D26-D31.	6.5	590
117	Comparison of intracellular and secretion-based strategies for production of human $\beta$ -galactosidase A in the filamentous fungus <i>Trichoderma reesei</i> . <i>BMC Biotechnology</i> , 2014, 14, 91.	1.7	11

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119	<i>Fusarium oxysporum</i> . , 2014, , 99-119.		9
120	Discovering Functions of Unannotated Genes from a Transcriptome Survey of Wild Fungal Isolates. <i>MBio</i> , 2014, 5, e01046-13.	1.8	25
121	Gene Loss Rather Than Gene Gain Is Associated with a Host Jump from Monocots to Dicots in the Smut Fungus <i>Melanopsichium pennsylvanicum</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 2034-2049.	1.1	146
122	2 Genomics to Study Basal Lineage Fungal Biology: Phylogenomics Suggests a Common Origin. , 2014, , 31-60.		7
123	Molecular conservation of metazoan gut formation: evidence from expression of endomesoderm genes in <i>Capitella teleta</i> (Annelida). <i>EvoDevo</i> , 2014, 5, 39.	1.3	53
124	Pseudogenization in pathogenic fungi with different host plants and lifestyles might reflect their evolutionary past. <i>Molecular Plant Pathology</i> , 2014, 15, 133-144.	2.0	19
125	Strategies for mining fungal natural products. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2014, 41, 301-313.	1.4	168
126	Genome-wide identification, annotation and characterization of novel thermostable cytochrome P450 monooxygenases from the thermophilic biomass-degrading fungi <i>Thielavia terrestris</i> and <i>Myceliophthora thermophila</i> . <i>Genes and Genomics</i> , 2014, 36, 321-333.	0.5	15
127	Genome-wide identification and expression analysis of the mitogen-activated protein kinase gene family from banana suggest involvement of specific members in different stages of fruit ripening. <i>Functional and Integrative Genomics</i> , 2014, 14, 161-175.	1.4	47
128	The significance of cellulolytic enzymes produced by <i>Trichoderma</i> in opportunistic lifestyle of this fungus. <i>Journal of Basic Microbiology</i> , 2014, 54, S2-13.	1.8	62
129	Temporal Alterations in the Secretome of the Selective Ligninolytic Fungus <i>Ceriporiopsis subvermispora</i> during Growth on Aspen Wood Reveal This Organism's Strategy for Degrading Lignocellulose. <i>Applied and Environmental Microbiology</i> , 2014, 80, 2062-2070.	1.4	99
130	Point mutation of the xylose reductase (XR) gene reduces xylitol accumulation and increases citric acid production in <i>Aspergillus carbonarius</i> . <i>Journal of Industrial Microbiology and Biotechnology</i> , 2014, 41, 733-739.	1.4	22
131	Genome-scale analysis of demographic history and adaptive selection. <i>Protein and Cell</i> , 2014, 5, 99-112.	4.8	10
132	Automated alignment-based curation of gene models in filamentous fungi. <i>BMC Bioinformatics</i> , 2014, 15, 19.	1.2	9
133	Comparative analysis of secretomes in basidiomycete fungi. <i>Journal of Proteomics</i> , 2014, 102, 28-43.	1.2	84
134	Nikkomycin Z is an effective inhibitor of the chytrid fungus linked to global amphibian declines. <i>Fungal Biology</i> , 2014, 118, 48-60.	1.1	21
135	The Genome of the Foraminiferan <i>Reticulomyxa filosa</i> . <i>Current Biology</i> , 2014, 24, 11-18.	1.8	73



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136	A review of genomic data warehousing systems. <i>Briefings in Bioinformatics</i> , 2014, 15, 471-483.	3.2	22
137	Signature Protein of the PVC Superphylum. <i>Applied and Environmental Microbiology</i> , 2014, 80, 440-445.	1.4	20
138	Understanding the function of conserved variations in the catalytic loops of fungal glycoside hydrolase family 12. <i>Biotechnology and Bioengineering</i> , 2014, 111, 1494-1505.	1.7	15
139	<i>Klebsormidium flaccidum</i> genome reveals primary factors for plant terrestrial adaptation. <i>Nature Communications</i> , 2014, 5, 3978.	5.8	532
140	Essential Letters in the Fungal Alphabet. <i>Advances in Genetics</i> , 2014, 85, 201-253.	0.8	84
141	Observations on morphologic and genetic diversity in populations of <i>Filoboletus manipularis</i> (Fungi). <i>Trends in Microbiology</i> , 2014, 22, 101-107.	2.0	1
142	Conservation of Ca <sup>2+</sup> /Calmodulin Regulation across Na and Ca <sup>2+</sup> Channels. <i>Cell</i> , 2014, 157, 1657-1670.	13.5	91
143	Metatranscriptomic analysis of ectomycorrhizal roots reveals genes associated with <i>Glomerula</i> symbiosis: improved methodologies for assessing gene expression <i>in situ</i> . <i>Environmental Microbiology</i> , 2014, 16, 3730-3742.	1.8	71
144	Horizontal gene transfer and functional diversification of plant cell wall degrading polygalacturonases: Key events in the evolution of herbivory in beetles. <i>Insect Biochemistry and Molecular Biology</i> , 2014, 52, 33-50.	1.2	116
145	14 Agaricomycetes. <i>Journal of Fungi</i> , 2014, 1, 373-429.		88
146	Antifungal drug resistance evoked via RNAi-dependent epimutations. <i>Nature</i> , 2014, 513, 555-558.	13.7	147
147	Transcriptomic Responses of <i>Phanerochaete chrysosporium</i> to Oak Acetonic Extracts: Focus on a New Glutathione Transferase. <i>Applied and Environmental Microbiology</i> , 2014, 80, 6316-6327.	1.4	34
148	10 Pucciniomycotina. <i>Journal of Fungi</i> , 2014, 1, 271-294.		43
149	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Meloidogyne incana</i> . <i>New Phytologist</i> , 2014, 202, 554-564.	3.5	52
150	Identification of mycoparasitism-related genes against the phytopathogen <i>Sclerotinia sclerotiorum</i> through transcriptome and expression profile analysis in <i>Trichoderma harzianum</i> . <i>BMC Genomics</i> , 2014, 15, 204.	1.2	99
151	Zearalenone lactonohydrolase activity in Hypocreales and its evolutionary relationships within the epoxide hydrolase subset of a/b-hydrolases. <i>BMC Microbiology</i> , 2014, 14, 82.	1.3	34
152	Merging metagenomics and geochemistry reveals environmental controls on biological diversity and evolution. <i>BMC Ecology</i> , 2014, 14, 16.	3.0	24
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