

Jeffrey P Townsend

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7128597/publications.pdf>

Version: 2024-02-01

193
papers

11,825
citations

44066

48
h-index

33889

99
g-index

215
all docs

215
docs citations

215
times ranked

15401
citing authors

#	ARTICLE	IF	CITATIONS
1	Environmental and sex-specific molecular signatures of glioma causation. <i>Neuro-Oncology</i> , 2022, 24, 29-36.	1.2	12
2	Heavy mutagenesis by tobacco leads to lung adenocarcinoma tumors with KRAS G12 mutations other than G12D, leading KRAS G12D tumors to "on average" to exhibit a lower mutation burden. <i>Lung Cancer</i> , 2022, 166, 265-269.	2.0	3
3	Premetastatic shifts of endogenous and exogenous mutational processes support consolidative therapy in EGFR-driven lung adenocarcinoma. <i>Cancer Letters</i> , 2022, 526, 346-351.	7.2	10
4	The Prognostic Value of an RT-PCR Test for Severe Acute Respiratory SyndromeâCoronavirus 2 (SARS-CoV-2) Is Contingent on Timing across Disease Time Course in addition to Assay Sensitivity. <i>Journal of Molecular Diagnostics</i> , 2022, 24, 101-103.	2.8	4
5	Quarantine and testing strategies to ameliorate transmission due to travel during the COVID-19 pandemic: a modelling study. <i>Lancet Regional Health - Europe, The</i> , 2022, 14, 100304.	5.6	20
6	Sequencing and Analysis of the Entire Genome of the Mycoparasitic Bioeffector Fungus <i>Trichoderma asperelloides</i> Strain T 203 (Hypocreales). <i>Microbiology Resource Announcements</i> , 2022, 11, e0099521.	0.6	4
7	Attribution of Cancer Origins to Endogenous, Exogenous, and Preventable Mutational Processes. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	14
8	Cancer Relevance of Human Genes. <i>Journal of the National Cancer Institute</i> , 2022, 114, 988-995.	6.3	2
9	Transcriptional Divergence Underpinning Sexual Development in the Fungal Class Sordariomycetes. <i>MBio</i> , 2022, 13, .	4.1	4
10	Secondary Metabolism Gene Clusters Exhibit Increasingly Dynamic and Differential Expression during Asexual Growth, Conidiation, and Sexual Development in <i>Neurospora crassa</i> . <i>MSystems</i> , 2022, 7, .	3.8	2
11	A phylogenetic approach to study the evolution of somatic mutational processes in cancer. <i>Communications Biology</i> , 2022, 5, .	4.4	3
12	Comparative analyses of eighteen rapid antigen tests and RT-PCR for COVID-19 quarantine and surveillance-based isolation. <i>Communications Medicine</i> , 2022, 2, .	4.2	13
13	The durability of natural infection and vaccine-induced immunity against future infection by SARS-CoV-2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	47
14	APOBEC mutagenesis and selection for NFE2L2 contribute to the origin of lung squamous-cell carcinoma. <i>Lung Cancer</i> , 2022, , .	2.0	1
15	Chemsearch: collaborative compound libraries with structure-aware browsing. <i>Bioinformatics Advances</i> , 2021, 1, .	2.4	1
16	Optimal COVID-19 quarantine and testing strategies. <i>Nature Communications</i> , 2021, 12, 356.	12.8	164
17	Identifying modules of cooperating cancer drivers. <i>Molecular Systems Biology</i> , 2021, 17, e9810.	7.2	13
18	The GUL-1 Protein Binds Multiple RNAs Involved in Cell Wall Remodeling and Affects the MAK-1 Pathway in <i>Neurospora crassa</i> . <i>Frontiers in Fungal Biology</i> , 2021, 2, .	2.0	4

#	ARTICLE	IF	CITATIONS
19	Mechanistic basis of post-treatment control of SIV after anti- H^27 antibody therapy. PLoS Computational Biology, 2021, 17, e1009031.	3.2	4
20	The somatic molecular evolution of cancer: Mutation, selection, and epistasis. Progress in Biophysics and Molecular Biology, 2021, 165, 56-65.	2.9	11
21	Comparative Genomics within and across Bilaterians Illuminates the Evolutionary History of ALK and LTK Proto-Oncogene Origination and Diversification. Genome Biology and Evolution, 2021, 13, .	2.5	6
22	The durability of immunity against reinfection by SARS-CoV-2: a comparative evolutionary study. Lancet Microbe, The, 2021, 2, e666-e675.	7.3	147
23	Implementation of Syringe Services Programs to Prevent Rapid Human Immunodeficiency Virus Transmission in Rural Counties in the United States: A Modeling Study. Clinical Infectious Diseases, 2020, 70, 1096-1102.	5.8	27
24	Re: Ming-Jun Shi, Xiang-Yu Meng, Philippe Lamy, et al. APOBEC-mediated Mutagenesis as a Likely Cause of FGFR3 S249C Mutation Over-representation in Bladder Cancer. Eur Urol 2019;76:9â€“13. European Urology, 2020, 77, e24-e25.	1.9	4
25	Molecular Biology and Evolution of Cancer: From Discovery to Action. Molecular Biology and Evolution, 2020, 37, 320-326.	8.9	43
26	Transfer RNA methyltransferase gene NSUN2 mRNA expression modifies the effect of T cell activation score on patient survival in head and neck squamous carcinoma. Oral Oncology, 2020, 101, 104554.	1.5	18
27	Non-Coding Mutations in Urothelial Bladder Cancer: Biological and Clinical Relevance and Potential Utility as Biomarkers. Bladder Cancer, 2020, 6, 211-213.	0.4	4
28	Germline variant burden in cancer genes correlates with age at diagnosis and somatic mutation burden. Nature Communications, 2020, 11, 2438.	12.8	52
29	Dogs and pigs are transport hosts of <i>Necator americanus</i> : Molecular evidence for a zoonotic mechanism of human hookworm transmission in Ghana. Zoonoses and Public Health, 2020, 67, 474-483.	2.2	9
30	Unmatched Level of Molecular Convergence among Deeply Divergent Complex Multicellular Fungi. Molecular Biology and Evolution, 2020, 37, 2228-2240.	8.9	23
31	Getting quantitative on the effects of somatic mutation on cancer. Oncoscience, 2020, 7, 83-84.	2.2	0
32	85. The Impact of Carbapenem-Sparing Interventions on the Evolution of Resistance in Pseudomonas aeruginosa in the USA. Open Forum Infectious Diseases, 2020, 7, S59-S60.	0.9	0
33	Getting quantitative on the effects of somatic mutation on cancer. Oncoscience, 2020, 7, 83-84.	2.2	0
34	Optimal Rates for Phylogenetic Inference and Experimental Design in the Era of Genome-Scale Data Sets. Systematic Biology, 2019, 68, 145-156.	5.6	51
35	GEM-NET: Lessons in Multi-Institution Teamwork Using Collaboration Software. ACS Central Science, 2019, 5, 1159-1169.	11.3	2
36	Modelling microbial infection to address global health challenges. Nature Microbiology, 2019, 4, 1612-1619.	13.3	34

#	ARTICLE	IF	CITATIONS
37	Wagging the long tail of drivers of prostate cancer. PLoS Genetics, 2019, 15, e1007820.	3.5	5
38	Comparative Genomics and Transcriptomics During Sexual Development Gives Insight Into the Life History of the Cosmopolitan Fungus <i>Fusarium neocosmosporiellum</i> . Frontiers in Microbiology, 2019, 10, 1247.	3.5	15
39	A multigene phylogeny toward a new phylogenetic classification of Leotiomyces. IMA Fungus, 2019, 10, 1.	3.8	140
40	Combined Aurora Kinase A (AURKA) and WEE1 Inhibition Demonstrates Synergistic Antitumor Effect in Squamous Cell Carcinoma of the Head and Neck. Clinical Cancer Research, 2019, 25, 3430-3442.	7.0	51
41	Metabolism and Development during Conidial Germination in Response to a Carbon-Nitrogen-Rich Synthetic or a Natural Source of Nutrition in <i>Neurospora crassa</i> . MBio, 2019, 10, .	4.1	21
42	EPID-26. SEX-SPECIFIC GLIOMA MOLECULAR SIGNATURES. Neuro-Oncology, 2019, 21, vi80-vi80.	1.2	2
43	Integrative Activity of Mating Loci, Environmentally Responsive Genes, and Secondary Metabolism Pathways during Sexual Development of <i>Chaetomium globosum</i> . MBio, 2019, 10, .	4.1	7
44	APOBEC-induced mutations and their cancer effect size in head and neck squamous cell carcinoma. Oncogene, 2019, 38, 3475-3487.	5.9	81
45	The landscape of novel and complementary targets for immunotherapy: an analysis of gene expression in the tumor microenvironment. Oncotarget, 2019, 10, 4532-4545.	1.8	8
46	Modeling Approaches Toward Understanding Infectious Disease Transmission. , 2019, , 227-243.		4
47	La g��n��alogie d��une tumeur. Pourlascience Fr, 2019, N�� 495 - janvier, 44-52.	0.0	0
48	Using evolutionary genomics, transcriptomics, and systems biology to reveal gene networks underlying fungal development. Fungal Biology Reviews, 2018, 32, 249-264.	4.7	22
49	Neutral Theory and the Somatic Evolution of Cancer. Molecular Biology and Evolution, 2018, 35, 1308-1315.	8.9	26
50	Heterogeneity and mutation in KRAS and associated oncogenes: evaluating the potential for the evolution of resistance to targeting of KRAS G12C. Oncogene, 2018, 37, 2444-2455.	5.9	31
51	Primary hepatic neuroendocrine carcinoma: report of two cases and literature review. BMC Clinical Pathology, 2018, 18, 3.	1.8	23
52	The Cancer Tree. Scientific American, 2018, 318, 34-41.	1.0	0
53	Light sensing by opsins and fungal ecology: NOP��1 modulates entry into sexual reproduction in response to environmental cues. Molecular Ecology, 2018, 27, 216-232.	3.9	43
54	Effect Sizes of Somatic Mutations in Cancer. Journal of the National Cancer Institute, 2018, 110, 1171-1177.	6.3	71

#	ARTICLE	IF	CITATIONS
55	Lvr, a Signaling System That Controls Global Gene Regulation and Virulence in Pathogenic <i>Leptospira</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 45.	3.9	19
56	Genomic Comparison Among Global Isolates of <i>L. interrogans</i> Serovars Copenhageni and Icterohaemorrhagiae Identified Natural Genetic Variation Caused by an Indel. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 193.	3.9	39
57	CDKN2A Copy Number Loss Is an Independent Prognostic Factor in HPV-Negative Head and Neck Squamous Cell Carcinoma. <i>Frontiers in Oncology</i> , 2018, 8, 95.	2.8	36
58	Somatic evolutionary timings of driver mutations. <i>BMC Cancer</i> , 2018, 18, 85.	2.6	20
59	Developmental Dynamics of Long Noncoding RNA Expression during Sexual Fruiting Body Formation in <i>Fusarium graminearum</i> . <i>MBio</i> , 2018, 9, .	4.1	37
60	Potential effectiveness of long-acting injectable pre-exposure prophylaxis for HIV prevention in men who have sex with men: a modelling study. <i>Lancet HIV</i> , 2018, 5, e498-e505.	4.7	37
61	Analysis of mutation, selection, and epistasis: an informed approach to cancer clinical trials. <i>Oncotarget</i> , 2018, 9, 22243-22253.	1.8	15
62	New insights on the sister lineage of percomorph fishes with an anchored hybrid enrichment dataset. <i>Molecular Phylogenetics and Evolution</i> , 2017, 110, 27-38.	2.7	40
63	Distributions of Mutational Effects and the Estimation of Directional Selection in Divergent Lineages of <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2017, 206, 2105-2117.	2.9	6
64	Radiation-Specific Clinical Data Should Be Included in Existing Large-Scale Genomic Datasets. <i>International Journal of Radiation Oncology Biology Physics</i> , 2017, 98, 8-10.	0.8	4
65	MA16.02 Mutational Landscape of TKI Naïve and Resistant EGFR Mutant Lung Adenocarcinomas. <i>Journal of Thoracic Oncology</i> , 2017, 12, S435.	1.1	0
66	Detection of Regional Variation in Selection Intensity within Protein-Coding Genes Using DNA Sequence Polymorphism and Divergence. <i>Molecular Biology and Evolution</i> , 2017, 34, 3006-3022.	8.9	10
67	The Likelihood of Heterogeneity or Additional Mutation to Compromise Targeting of KRAS G12C. <i>Journal of Thoracic Oncology</i> , 2017, 12, S1538.	1.1	1
68	Effect Sizes of Somatic Mutations in Lung Cancer: Identifying New Targets and Prioritizing Old Ones. <i>Journal of Thoracic Oncology</i> , 2017, 12, S1542-S1543.	1.1	1
69	Maximizing Power in Phylogenetics and Phylogenomics: A Perspective Illuminated by Fungal Big Data. <i>Advances in Genetics</i> , 2017, 100, 1-47.	1.8	28
70	PhyloOncology: Understanding cancer through phylogenetic analysis. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2017, 1867, 101-108.	7.4	22
71	Mutation profiles in early-stage lung squamous cell carcinoma with clinical follow-up and correlation with markers of immune function. <i>Annals of Oncology</i> , 2017, 28, 83-89.	1.2	97
72	Whole-exome sequencing and immune profiling of early-stage lung adenocarcinoma with fully annotated clinical follow-up. <i>Annals of Oncology</i> , 2017, 28, 75-82.	1.2	159

#	ARTICLE	IF	CITATIONS
73	CDKN2A copy number loss in HPV- and HPV+ head and neck cancer to indicate poor prognosis: An integrated genomic and clinical TCGA analysis.. Journal of Clinical Oncology, 2017, 35, 6060-6060.	1.6	1
74	The ancestral levels of transcription and the evolution of sexual phenotypes in filamentous fungi. PLoS Genetics, 2017, 13, e1006867.	3.5	46
75	Quantifying Transmission of <i>Clostridium difficile</i> within and outside Healthcare Settings. Emerging Infectious Diseases, 2016, 22, 608-616.	4.3	48
76	Determinants of Human African Trypanosomiasis Elimination via Paratransgenesis. PLoS Neglected Tropical Diseases, 2016, 10, e0004465.	3.0	21
77	PhyInformR: phylogenetic experimental design and phylogenomic data exploration in R. BMC Evolutionary Biology, 2016, 16, 262.	3.2	39
78	One Health approach to cost-effective rabies control in India. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14574-14581.	7.1	63
79	Cost-effectiveness of next-generation vaccines: The case of pertussis. Vaccine, 2016, 34, 3405-3411.	3.8	3
80	Retrospective Analysis of the 2014–2015 Ebola Epidemic in Liberia. American Journal of Tropical Medicine and Hygiene, 2016, 94, 833-839.	1.4	10
81	PathScore: a web tool for identifying altered pathways in cancer data. Bioinformatics, 2016, 32, 3688-3690.	4.1	9
82	A comprehensive phylogeny of birds (Aves) using targeted next-generation DNA sequencing. Nature, 2016, 534, S7-S8.	27.8	872
83	Climatic and evolutionary drivers of phase shifts in the plague epidemics of colonial India. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14601-14608.	7.1	18
84	Vaccination strategies against respiratory syncytial virus. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13239-13244.	7.1	70
85	Cost-Effectiveness of Pertussis Vaccination During Pregnancy in the United States. American Journal of Epidemiology, 2016, 183, 1159-1170.	3.4	43
86	The Fast-Evolving <i>phy-2</i> Gene Modulates Sexual Development in Response to Light in the Model Fungus <i>Neurospora crassa</i> . MBio, 2016, 7, e02148.	4.1	37
87	The Impact of Enhanced Screening and Treatment on Hepatitis C in the United States. Clinical Infectious Diseases, 2016, 62, 298-304.	5.8	46
88	Optimizing age of cytomegalovirus screening and vaccination to avert congenital disease in the US. Vaccine, 2016, 34, 225-229.	3.8	9
89	Future Perspectives and Challenges of Fungal Systematics in the Age of Big Data. Fungal Biology, 2016, , 25-46.	0.6	16
90	Early and multiple origins of metastatic lineages within primary tumors. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 2140-2145.	7.1	157

#	ARTICLE	IF	CITATIONS
91	Abstract 142: Mutation and immune profiles in early-stage lung squamous cell carcinoma. Cancer Research, 2016, 76, 142-142.	0.9	1
92	Abstract 89: Whole-exome sequencing and immune profiling of early-stage lung adenocarcinoma. , 2016, , .		0
93	Quantitative analyses and modelling to support achievement of the 2020 goals for nine neglected tropical diseases. Parasites and Vectors, 2015, 8, 630.	2.5	80
94	Solving the ecological puzzle of mycorrhizal associations using data from annotated collections and environmental samples – an example of saddle fungi. Environmental Microbiology Reports, 2015, 7, 658-667.	2.4	18
95	Under-reporting and case fatality estimates for emerging epidemics. BMJ, The, 2015, 350, h1115-h1115.	6.0	38
96	Integrating Community-Based Interventions to Reverse the Convergent TB/HIV Epidemics in Rural South Africa. PLoS ONE, 2015, 10, e0126267.	2.5	21
97	H-CLAP: hierarchical clustering within a linear array with an application in genetics. Statistical Applications in Genetics and Molecular Biology, 2015, 14, 125-41.	0.6	0
98	Harnessing Case Isolation and Ring Vaccination to Control Ebola. PLoS Neglected Tropical Diseases, 2015, 9, e0003794.	3.0	31
99	Utility of characters evolving at diverse rates of evolution to resolve quartet trees with unequal branch lengths: analytical predictions of long-branch effects. BMC Evolutionary Biology, 2015, 15, 86.	3.2	24
100	Gene Expression Evolves under a House-of-Cards Model of Stabilizing Selection. Molecular Biology and Evolution, 2015, 32, 2130-2140.	8.9	70
101	Impact of bed capacity on spatiotemporal shifts in Ebola transmission. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14125-14126.	7.1	6
102	Inferring the Origin of Metastases from Cancer Phylogenies. Cancer Research, 2015, 75, 4021-4025.	0.9	43
103	A comprehensive phylogeny of birds (Aves) using targeted next-generation DNA sequencing. Nature, 2015, 526, 569-573.	27.8	1,341
104	Epidemiological and Viral Genomic Sequence Analysis of the 2014 Ebola Outbreak Reveals Clustered Transmission. Clinical Infectious Diseases, 2015, 60, 1079-1082.	5.8	59
105	Neural Gene Expression Profiles and Androgen Levels Underlie Alternative Reproductive Tactics in the Ocellated Wrasse, <i>Symphodus ocellatus</i> . Ethology, 2015, 121, 152-167.	1.1	32
106	Genomic and Gene-Expression Comparisons among Phage-Resistant Type-IV Pilus Mutants of <i>Pseudomonas syringae</i> pathovar phaseolicola. PLoS ONE, 2015, 10, e0144514.	2.5	11
107	Gene Expression Differences among Three <i>Neurospora</i> Species Reveal Genes Required for Sexual Reproduction in <i>Neurospora crassa</i> . PLoS ONE, 2014, 9, e110398.	2.5	39
108	The impact of incorporating molecular evolutionary model into predictions of phylogenetic signal and noise. Frontiers in Ecology and Evolution, 2014, 2, .	2.2	7

#	ARTICLE	IF	CITATIONS
109	Detecting rare gene transfer events in bacterial populations. <i>Frontiers in Microbiology</i> , 2014, 4, 415.	3.5	43
110	Genome-Wide Characterization of Light-Regulated Genes in <i>Neurospora crassa</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1731-1745.	1.8	82
111	Cellular Superspreaders: An Epidemiological Perspective on HIV Infection inside the Body. <i>PLoS Pathogens</i> , 2014, 10, e1004092.	4.7	20
112	GENETIC CHANGES IN RADIATION-ASSOCIATED MENINGIOMA. <i>Neuro-Oncology</i> , 2014, 16, iii1-iii1.	1.2	1
113	Global Gene Expression and Focused Knockout Analysis Reveals Genes Associated with Fungal Fruiting Body Development in <i>Neurospora crassa</i> . <i>Eukaryotic Cell</i> , 2014, 13, 154-169.	3.4	66
114	Strategies for containing Ebola in West Africa. <i>Science</i> , 2014, 346, 991-995.	12.6	244
115	The peopling of the African continent and the diaspora into the new world. <i>Current Opinion in Genetics and Development</i> , 2014, 29, 120-132.	3.3	45
116	Phylogenetic informativeness reconciles ray-finned fish molecular divergence times. <i>BMC Evolutionary Biology</i> , 2014, 14, 169.	3.2	77
117	Probabilistic uncertainty analysis of epidemiological modeling to guide public health intervention policy. <i>Epidemics</i> , 2014, 6, 37-45.	3.0	29
118	Phylogenetic and phylogenomic overview of the Polyporales. <i>Mycologia</i> , 2013, 105, 1350-1373.	1.9	259
119	Epidemiological mechanisms of genetic resistance to kuru. <i>Journal of the Royal Society Interface</i> , 2013, 10, 20130331.	3.4	4
120	Cost-effectiveness of a community-based intervention for reducing the transmission of <i>Schistosoma haematobium</i> and HIV in Africa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7952-7957.	7.1	35
121	Response to: The relative utility of sequence divergence and phylogenetic informativeness profiling in phylogenetic study design. <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 436.	2.7	3
122	Optimal targeting of seasonal influenza vaccination toward younger ages is robust to parameter uncertainty. <i>Vaccine</i> , 2013, 31, 3079-3089.	3.8	13
123	Evaluating Phylogenetic Informativeness as a Predictor of Phylogenetic Signal for Metazoan, Fungal, and Mammalian Phylogenomic Data Sets. <i>BioMed Research International</i> , 2013, 2013, 1-14.	1.9	17
124	Potential Cost-Effectiveness of Schistosomiasis Treatment for Reducing HIV Transmission in Africa – The Case of Zimbabwean Women. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2346.	3.0	33
125	Sex-linked transcriptional divergence in the hermaphrodite fungus <i>Neurospora tetrasperma</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20130862.	2.6	26
126	AuthorReward: increasing community curation in biological knowledge wikis through automated authorship quantification. <i>Bioinformatics</i> , 2013, 29, 1837-1839.	4.1	10

#	ARTICLE	IF	CITATIONS
127	Yeast response to LA virus indicates coadapted global gene expression during mycoviral infection. FEMS Yeast Research, 2013, 13, 162-179.	2.3	27
128	Optimized primers and other critical conditions for efficient fusion PCR to generate knockout vectors in filamentous fungi.. Fungal Genetics Reports, 2013, 60, 1-10.	0.6	1
129	Potential for Rabies Control through Dog Vaccination in Wildlife-Abundant Communities of Tanzania. PLoS Neglected Tropical Diseases, 2012, 6, e1796.	3.0	46
130	Resampling QTL Effects in the QTL Sign Test Leads to Incongruous Sensitivity to Variance in Effect Size. G3: Genes, Genomes, Genetics, 2012, 2, 905-911.	1.8	10
131	The influence of altruism on influenza vaccination decisions. Journal of the Royal Society Interface, 2012, 9, 2234-2243.	3.4	168
132	A Test for Selection Employing Quantitative Trait Locus and Mutation Accumulation Data. Genetics, 2012, 190, 1533-1545.	2.9	19
133	Reevaluation of Epidemiological Data Demonstrates That It Is Consistent With Cross-Immunity Among Human Papillomavirus Types. Journal of Infectious Diseases, 2012, 206, 1291-1298.	4.0	30
134	Abundant Gene-by-Environment Interactions in Gene Expression Reaction Norms to Copper within Saccharomyces cerevisiae. Genome Biology and Evolution, 2012, 4, 1061-1079.	2.5	37
135	Phylogenetic Signal and Noise: Predicting the Power of a Data Set to Resolve Phylogeny. Systematic Biology, 2012, 61, 835.	5.6	120
136	Differential impact of nutrition on developmental and metabolic gene expression during fruiting body development in Neurospora crassa. Fungal Genetics and Biology, 2012, 49, 405-413.	2.1	33
137	Sex-specific gene expression during asexual development of Neurospora crassa. Fungal Genetics and Biology, 2012, 49, 533-543.	2.1	31
138	Transcriptome analyses during fruiting body formation in Fusarium graminearum and Fusarium verticillioides reflect species life history and ecology. Fungal Genetics and Biology, 2012, 49, 663-673.	2.1	78
139	Codon Deviation Coefficient: a novel measure for estimating codon usage bias and its statistical significance. BMC Bioinformatics, 2012, 13, 43.	2.6	53
140	Analyses of expressed sequence tags in Neurospora reveal rapid evolution of genes associated with the early stages of sexual reproduction in fungi. BMC Evolutionary Biology, 2012, 12, 229.	3.2	12
141	Controlling Antimicrobial Resistance through Targeted, Vaccine-Induced Replacement of Strains. PLoS ONE, 2012, 7, e50688.	2.5	20
142	Assessing the Probability of Detection of Horizontal Gene Transfer Events in Bacterial Populations. Frontiers in Microbiology, 2012, 3, 27.	3.5	26
143	RBE controls microRNA164 expression to effect floral organogenesis. Development (Cambridge), 2012, 139, 2161-2169.	2.5	69
144	Taxon Sampling and the Optimal Rates of Evolution for Phylogenetic Inference. Systematic Biology, 2011, 60, 358-365.	5.6	87

#	ARTICLE	IF	CITATIONS
145	Getting the Most Out of Your Fungal Microarray Data: Two Cost- and Time-Effective Methods. <i>Methods in Molecular Biology</i> , 2011, 722, 61-77.	0.9	0
146	Tasting Soil Fungal Diversity with Earth Tongues: Phylogenetic Test of SATÅ© Alignments for Environmental ITS Data. <i>PLoS ONE</i> , 2011, 6, e19039.	2.5	32
147	SIR2 and other genes are abundantly expressed in long-lived natural segregants for replicative aging of the budding yeast <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2011, 11, 345-355.	2.3	10
148	PhyDesign: an online application for profiling phylogenetic informativeness. <i>BMC Evolutionary Biology</i> , 2011, 11, 152.	3.2	174
149	Phylogenetic informativeness profiling of 12 genes for 28 vertebrate taxa without divergence dates. <i>Molecular Phylogenetics and Evolution</i> , 2011, 60, 271-272.	2.7	19
150	Retrospective evidence for a biological cost of vancomycin resistance determinants in the absence of glycopeptide selective pressures. <i>Journal of Antimicrobial Chemotherapy</i> , 2011, 66, 608-610.	3.0	51
151	Multi-targeted priming for genome-wide gene expression assays. <i>BMC Genomics</i> , 2010, 11, 477.	2.8	14
152	Identification of new molecular markers for assembling the eukaryotic tree of life. <i>Molecular Phylogenetics and Evolution</i> , 2010, 55, 1177-1182.	2.7	14
153	LOX: inferring Level Of eXpression from diverse methods of census sequencing. <i>Bioinformatics</i> , 2010, 26, 1918-1919.	4.1	30
154	Northern species of earth tongue genus <i>Thuemenidium</i> revisited, considering morphology, ecology and molecular phylogeny. <i>Mycologia</i> , 2010, 102, 1089-1095.	1.9	11
155	Optimal Selection of Gene and Ingroup Taxon Sampling for Resolving Phylogenetic Relationships. <i>Systematic Biology</i> , 2010, 59, 446-457.	5.6	70
156	The filamentous fungal gene expression database (FFGED). <i>Fungal Genetics and Biology</i> , 2010, 47, 199-204.	2.1	32
157	Maximum-Likelihood Model Averaging To Profile Clustering of Site Types across Discrete Linear Sequences. <i>PLoS Computational Biology</i> , 2009, 5, e1000421.	3.2	17
158	Evolution of Reproductive Morphology in Leaf Endophytes. <i>PLoS ONE</i> , 2009, 4, e4246.	2.5	31
159	Measuring Transcription Factorâ€“Binding Site Turnover: A Maximum Likelihood Approach Using Phylogenies. <i>Genome Biology and Evolution</i> , 2009, 1, 85-98.	2.5	17
160	The Ascomycota Tree of Life: A Phylum-wide Phylogeny Clarifies the Origin and Evolution of Fundamental Reproductive and Ecological Traits. <i>Systematic Biology</i> , 2009, 58, 224-239.	5.6	581
161	Evolving gene expression: from G to E to GÃ—E. <i>Trends in Ecology and Evolution</i> , 2009, 24, 649-658.	8.7	134
162	Factors affecting the reversal of antimicrobial-drug resistance. <i>Lancet Infectious Diseases</i> , The, 2009, 9, 357-364.	9.1	112

#	ARTICLE	IF	CITATIONS
163	Article Commentary: Snapshots of Tree Space. <i>Evolutionary Bioinformatics</i> , 2009, 5, EBO.S3416.	1.2	1
164	<I>Geoglossomycetes</I> cl. nov., <I>Geoglossales</I> ord. nov. and taxa above class rank in the <I>Ascomycota</I> Tree of Life. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2009, 22, 129-138.	4.4	55
165	The Phylogenetic Informativeness of Nucleotide and Amino Acid Sequences for Reconstructing the Vertebrate Tree. <i>Journal of Molecular Evolution</i> , 2008, 67, 437-447.	1.8	61
166	Sleuthing the difference a nucleotide can make. <i>Molecular Ecology</i> , 2008, 17, 2793-2795.	3.9	1
167	HCLS 2.0/3.0: Health care and life sciences data mashup using Web 2.0/3.0. <i>Journal of Biomedical Informatics</i> , 2008, 41, 694-705.	4.3	78
168	Bringing Web 2.0 to bioinformatics. <i>Briefings in Bioinformatics</i> , 2008, 10, 1-10.	6.5	66
169	RNA extraction, probe preparation, and competitive hybridization for transcriptional profiling using <i>Neurospora crassa</i> long-oligomer DNA microarrays. <i>Fungal Genetics Reports</i> , 2008, 55, 18-28.	0.6	14
170	Enabling a Community to Dissect an Organism: Overview of the <i>Neurospora</i> Functional Genomics Project. <i>Advances in Genetics</i> , 2007, 57, 49-96.	1.8	191
171	Profiling Phylogenetic Informativeness. <i>Systematic Biology</i> , 2007, 56, 222-231.	5.6	305
172	Quantifying variation in gene expression. <i>Molecular Ecology</i> , 2007, 16, 2613-2616.	3.9	37
173	Eukaryotic microbes, species recognition and the geographic limits of species: examples from the kingdom Fungi. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 1947-1963.	4.0	291
174	Phase-specific gene expression underlying morphological adaptations of the dimorphic human pathogenic fungus, <i>Coccidioides posadasii</i> . <i>Fungal Genetics and Biology</i> , 2006, 43, 545-559.	2.1	26
175	Population structure and gene evolution in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2006, 6, 702-715.	2.3	138
176	Ecological and evolutionary genomics of <i>Saccharomyces cerevisiae</i> . <i>Molecular Ecology</i> , 2006, 15, 575-591.	3.9	94
177	Horizontal gene transfer, genome innovation and evolution. <i>Nature Reviews Microbiology</i> , 2005, 3, 679-687.	28.6	856
178	A Bayesian method for analysing spotted microarray data. <i>Briefings in Bioinformatics</i> , 2005, 6, 318-330.	6.5	17
179	Long-oligomer microarray profiling in <i>Neurospora crassa</i> reveals the transcriptional program underlying biochemical and physiological events of conidial germination. <i>Nucleic Acids Research</i> , 2005, 33, 6469-6485.	14.5	95
180	Concerted Evolution in the Repeats of an Immunomodulating Cell Surface Protein, SOWgp, of the Human Pathogenic Fungi <i>Coccidioides immitis</i> and <i>C. posadasii</i> . <i>Genetics</i> , 2005, 171, 109-117.	2.9	30

#	ARTICLE	IF	CITATIONS
181	Designing Experiments Using Spotted Microarrays to Detect Gene Regulation Differences Within and Among Species. <i>Methods in Enzymology</i> , 2005, 395, 597-617.	1.0	10
182	Gene expression profiling in evolutionary genetics. , 2004, , 74-93.		0
183	Monitoring and modeling horizontal gene transfer. <i>Nature Biotechnology</i> , 2004, 22, 1110-1114.	17.5	113
184	Mitochondrial genome size variation in New World and Old World populations of <i>Drosophila melanogaster</i> . <i>Heredity</i> , 2004, 93, 98-103.	2.6	19
185	Resolution of large and small differences in gene expression using models for the Bayesian analysis of gene expression levels and spotted DNA microarrays. <i>BMC Bioinformatics</i> , 2004, 5, 54.	2.6	53
186	Multifactorial experimental design and the transitivity of ratios with spotted DNA microarrays. <i>BMC Genomics</i> , 2003, 4, 41.	2.8	70
187	Population Genetic Variation in Genome-Wide Gene Expression. <i>Molecular Biology and Evolution</i> , 2003, 20, 955-963.	8.9	185
188	Horizontal Acquisition of Divergent Chromosomal DNA in Bacteria: Effects of Mutator Phenotypes. <i>Genetics</i> , 2003, 164, 13-21.	2.9	38
189	Pathway Processor: A Tool for Integrating Whole-Genome Expression Results into Metabolic Networks. <i>Genome Research</i> , 2002, 12, 1121-1126.	5.5	94
190	Bayesian analysis of gene expression levels: statistical quantification of relative mRNA level across multiple strains or treatments. <i>Genome Biology</i> , 2002, 3, research0071.1.	9.6	142
191	The kinetics of transposable element autoregulation. , 2000, 108, 229-237.		11
192	Solvent Accessibility and Purifying Selection Within Proteins of <i>Escherichia coli</i> and <i>Salmonella enterica</i> . <i>Molecular Biology and Evolution</i> , 2000, 17, 301-308.	8.9	99
193	Manifold anomalies in gene expression in a vineyard isolate of <i>Saccharomyces cerevisiae</i> revealed by DNA microarray analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 12369-12374.	7.1	164