Jeffrey P Townsend

List of Publications by Year in descending order

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193 papers 11,825 citations

48 h-index

44042

99 g-index

215 all docs

215 docs citations

215 times ranked

15401 citing authors

#	Article	IF	CITATIONS
1	A comprehensive phylogeny of birds (Aves) using targeted next-generation DNA sequencing. Nature, 2015, 526, 569-573.	13.7	1,341
2	A comprehensive phylogeny of birds (Aves) using targeted next-generation DNA sequencing. Nature, 2016, 534, S7-S8.	13.7	872
3	Horizontal gene transfer, genome innovation and evolution. Nature Reviews Microbiology, 2005, 3, 679-687.	13.6	856
4	The Ascomycota Tree of Life: A Phylum-wide Phylogeny Clarifies the Origin and Evolution of Fundamental Reproductive and Ecological Traits. Systematic Biology, 2009, 58, 224-239.	2.7	581
5	Profiling Phylogenetic Informativeness. Systematic Biology, 2007, 56, 222-231.	2.7	305
6	Eukaryotic microbes, species recognition and the geographic limits of species: examples from the kingdom Fungi. Philosophical Transactions of the Royal Society B: Biological Sciences, 2006, 361, 1947-1963.	1.8	291
7	Phylogenetic and phylogenomic overview of the Polyporales. Mycologia, 2013, 105, 1350-1373.	0.8	259
8	Strategies for containing Ebola in West Africa. Science, 2014, 346, 991-995.	6.0	244
9	Enabling a Community to Dissect an Organism: Overview of the Neurospora Functional Genomics Project. Advances in Genetics, 2007, 57, 49-96.	0.8	191
10	Population Genetic Variation in Genome-Wide Gene Expression. Molecular Biology and Evolution, 2003, 20, 955-963.	3.5	185
11	PhyDesign: an online application for profiling phylogenetic informativeness. BMC Evolutionary Biology, 2011, 11, 152.	3.2	174
12	The influence of altruism on influenza vaccination decisions. Journal of the Royal Society Interface, 2012, 9, 2234-2243.	1.5	168
13	Manifold anomalies in gene expression in a vineyard isolate of Saccharomyces cerevisiae revealed by DNA microarray analysis. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 12369-12374.	3.3	164
14	Optimal COVID-19 quarantine and testing strategies. Nature Communications, 2021, 12, 356.	5.8	164
15	Whole-exome sequencing and immune profiling of early-stage lung adenocarcinoma with fully annotated clinical follow-up. Annals of Oncology, 2017, 28, 75-82.	0.6	159
16	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.	3.3	157
17	The durability of immunity against reinfection by SARS-CoV-2: a comparative evolutionary study. Lancet Microbe, The, 2021, 2, e666-e675.	3.4	147
18	Bayesian analysis of gene expression levels: statistical quantification of relative mRNA level across multiple strains or treatments. Genome Biology, 2002, 3, research0071.1.	13.9	142

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19	A multigene phylogeny toward a new phylogenetic classification of Leotiomycetes. IMA Fungus, 2019, 10, 1.	1.7	140
20	Population structure and gene evolution in Saccharomyces cerevisiae. FEMS Yeast Research, 2006, 6, 702-715.	1.1	138
21	Evolving gene expression: from G to E to G×E. Trends in Ecology and Evolution, 2009, 24, 649-658.	4.2	134
22	Phylogenetic Signal and Noise: Predicting the Power of a Data Set to Resolve Phylogeny. Systematic Biology, 2012, 61, 835.	2.7	120
23	Monitoring and modeling horizontal gene transfer. Nature Biotechnology, 2004, 22, 1110-1114.	9.4	113
24	Factors affecting the reversal of antimicrobial-drug resistance. Lancet Infectious Diseases, The, 2009, 9, 357-364.	4.6	112
25	Solvent Accessibility and Purifying Selection Within Proteins of Escherichia coli and Salmonella enterica. Molecular Biology and Evolution, 2000, 17, 301-308.	3 . 5	99
26	Mutation profiles in early-stage lung squamous cell carcinoma with clinical follow-up and correlation with markers of immune function. Annals of Oncology, 2017, 28, 83-89.	0.6	97
27	Long-oligomer microarray profiling in Neurospora crassa reveals the transcriptional program underlying biochemical and physiological events of conidial germination. Nucleic Acids Research, 2005, 33, 6469-6485.	6.5	95
28	Pathway Processor: A Tool for Integrating Whole-Genome Expression Results into Metabolic Networks. Genome Research, 2002, 12, 1121-1126.	2.4	94
29	Ecological and evolutionary genomics of Saccharomyces cerevisiae. Molecular Ecology, 2006, 15, 575-591.	2.0	94
30	Taxon Sampling and the Optimal Rates of Evolution for Phylogenetic Inference. Systematic Biology, 2011, 60, 358-365.	2.7	87
31	Genome-Wide Characterization of Light-Regulated Genes in <i>Neurospora crassa</i> . G3: Genes, Genomes, Genetics, 2014, 4, 1731-1745.	0.8	82
32	APOBEC-induced mutations and their cancer effect size in head and neck squamous cell carcinoma. Oncogene, 2019, 38, 3475-3487.	2.6	81
33	Quantitative analyses and modelling to support achievement of the 2020 goals for nine neglected tropical diseases. Parasites and Vectors, 2015, 8, 630.	1.0	80
34	HCLS 2.0/3.0: Health care and life sciences data mashup using Web 2.0/3.0. Journal of Biomedical Informatics, 2008, 41, 694-705.	2.5	78
35	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.	0.9	78
36	Phylogenetic informativeness reconciles ray-finned fish molecular divergence times. BMC Evolutionary Biology, 2014, 14, 169.	3.2	77

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37	Effect Sizes of Somatic Mutations in Cancer. Journal of the National Cancer Institute, 2018, 110, 1171-1177.	3.0	71
38	Multifactorial experimental design and the transitivity of ratios with spotted DNA microarrays. BMC Genomics, 2003, 4, 41.	1.2	70
39	Optimal Selection of Gene and Ingroup Taxon Sampling for Resolving Phylogenetic Relationships. Systematic Biology, 2010, 59, 446-457.	2.7	70
40	Gene Expression Evolves under a House-of-Cards Model of Stabilizing Selection. Molecular Biology and Evolution, 2015, 32, 2130-2140.	3.5	70
41	Vaccination strategies against respiratory syncytial virus. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13239-13244.	3.3	70
42	RBE controls microRNA164 expression to effect floral organogenesis. Development (Cambridge), 2012, 139, 2161-2169.	1.2	69
43	Bringing Web 2.0 to bioinformatics. Briefings in Bioinformatics, 2008, 10, 1-10.	3.2	66
44	Global Gene Expression and Focused Knockout Analysis Reveals Genes Associated with Fungal Fruiting Body Development in Neurospora crassa. Eukaryotic Cell, 2014, 13, 154-169.	3.4	66
45	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.	3.3	63
46	The Phylogenetic Informativeness of Nucleotide and Amino Acid Sequences for Reconstructing the Vertebrate Tree. Journal of Molecular Evolution, 2008, 67, 437-447.	0.8	61
47	Epidemiological and Viral Genomic Sequence Analysis of the 2014 Ebola Outbreak Reveals Clustered Transmission. Clinical Infectious Diseases, 2015, 60, 1079-1082.	2.9	59
48	<i>Geoglossomycetes</i> cl. nov., <i>Geoglossales</i> ord. nov. and taxa above class rank in the <i>Ascomycota</i> Tree of Life. Persoonia: Molecular Phylogeny and Evolution of Fungi, 2009, 22, 129-138.	1.6	55
49	Resolution of large and small differences in gene expression using models for the Bayesian analysis of gene expression levels and spotted DNA microarrays. BMC Bioinformatics, 2004, 5, 54.	1.2	53
50	Codon Deviation Coefficient: a novel measure for estimating codon usage bias and its statistical significance. BMC Bioinformatics, 2012, 13, 43.	1.2	53
51	Germline variant burden in cancer genes correlates with age at diagnosis and somatic mutation burden. Nature Communications, 2020, 11, 2438.	5.8	52
52	Retrospective evidence for a biological cost of vancomycin resistance determinants in the absence of glycopeptide selective pressures. Journal of Antimicrobial Chemotherapy, 2011, 66, 608-610.	1.3	51
53	Optimal Rates for Phylogenetic Inference and Experimental Design in the Era of Genome-Scale Data Sets. Systematic Biology, 2019, 68, 145-156.	2.7	51
54	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.	3.2	51

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55	Quantifying Transmission of <i>Clostridium difficile </i> and outside Healthcare Settings. Emerging Infectious Diseases, 2016, 22, 608-616.	2.0	48
56	The durability of natural infection and vaccine-induced immunity against future infection by SARS-CoV-2. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	47
57	Potential for Rabies Control through Dog Vaccination in Wildlife-Abundant Communities of Tanzania. PLoS Neglected Tropical Diseases, 2012, 6, e1796.	1.3	46
58	The Impact of Enhanced Screening and Treatment on Hepatitis C in the United States. Clinical Infectious Diseases, 2016, 62, 298-304.	2.9	46
59	The ancestral levels of transcription and the evolution of sexual phenotypes in filamentous fungi. PLoS Genetics, 2017, 13, e1006867.	1.5	46
60	The peopling of the African continent and the diaspora into the new world. Current Opinion in Genetics and Development, 2014, 29, 120-132.	1.5	45
61	Detecting rare gene transfer events in bacterial populations. Frontiers in Microbiology, 2014, 4, 415.	1.5	43
62	Inferring the Origin of Metastases from Cancer Phylogenies. Cancer Research, 2015, 75, 4021-4025.	0.4	43
63	Cost-Effectiveness of Pertussis Vaccination During Pregnancy in the United States. American Journal of Epidemiology, 2016, 183, 1159-1170.	1.6	43
64	Light sensing by opsins and fungal ecology: NOPâ€1 modulates entry into sexual reproduction in response to environmental cues. Molecular Ecology, 2018, 27, 216-232.	2.0	43
65	Molecular Biology and Evolution of Cancer: From Discovery to Action. Molecular Biology and Evolution, 2020, 37, 320-326.	3.5	43
66	New insights on the sister lineage of percomorph fishes with an anchored hybrid enrichment dataset. Molecular Phylogenetics and Evolution, 2017, 110 , $27-38$.	1.2	40
67	Gene Expression Differences among Three Neurospora Species Reveal Genes Required for Sexual Reproduction in Neurospora crassa. PLoS ONE, 2014, 9, e110398.	1.1	39
68	PhyInformR: phylogenetic experimental design and phylogenomic data exploration in R. BMC Evolutionary Biology, 2016, 16, 262.	3.2	39
69	Genomic Comparison Among Global Isolates of L. interrogans Serovars Copenhageni and Icterohaemorrhagiae Identified Natural Genetic Variation Caused by an Indel. Frontiers in Cellular and Infection Microbiology, 2018, 8, 193.	1.8	39
70	Under-reporting and case fatality estimates for emerging epidemics. BMJ, The, 2015, 350, h1115-h1115.	3.0	38
71	Horizontal Acquisition of Divergent Chromosomal DNA in Bacteria: Effects of Mutator Phenotypes. Genetics, 2003, 164, 13-21.	1.2	38
72	Quantifying variation in gene expression. Molecular Ecology, 2007, 16, 2613-2616.	2.0	37

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73	Abundant Gene-by-Environment Interactions in Gene Expression Reaction Norms to Copper within Saccharomyces cerevisiae. Genome Biology and Evolution, 2012, 4, 1061-1079.	1.1	37
74	The Fast-Evolving <i>phy-2</i> Gene Modulates Sexual Development in Response to Light in the Model Fungus Neurospora crassa. MBio, 2016, 7, e02148.	1.8	37
75	Developmental Dynamics of Long Noncoding RNA Expression during Sexual Fruiting Body Formation in Fusarium graminearum. MBio, $2018,9,.$	1.8	37
76	Potential effectiveness of long-acting injectable pre-exposure prophylaxis for HIV prevention in men who have sex with men: a modelling study. Lancet HIV,the, 2018, 5, e498-e505.	2.1	37
77	CDKN2A Copy Number Loss Is an Independent Prognostic Factor in HPV-Negative Head and Neck Squamous Cell Carcinoma. Frontiers in Oncology, 2018, 8, 95.	1.3	36
78	Cost-effectiveness of a community-based intervention for reducing the transmission of $\langle i \rangle$ Schistosoma haematobium $\langle i \rangle$ and HIV in Africa. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7952-7957.	3.3	35
79	Modelling microbial infection to address global health challenges. Nature Microbiology, 2019, 4, 1612-1619.	5.9	34
80	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.	0.9	33
81	Potential Cost-Effectiveness of Schistosomiasis Treatment for Reducing HIV Transmission in Africa – The Case of Zimbabwean Women. PLoS Neglected Tropical Diseases, 2013, 7, e2346.	1.3	33
82	The filamentous fungal gene expression database (FFGED). Fungal Genetics and Biology, 2010, 47, 199-204.	0.9	32
83	Tasting Soil Fungal Diversity with Earth Tongues: Phylogenetic Test of SATé Alignments for Environmental ITS Data. PLoS ONE, 2011, 6, e19039.	1.1	32
84	Neural Gene Expression Profiles and Androgen Levels Underlie Alternative Reproductive Tactics in the Ocellated Wrasse, <i>Symphodus ocellatus</i> . Ethology, 2015, 121, 152-167.	0.5	32
85	Evolution of Reproductive Morphology in Leaf Endophytes. PLoS ONE, 2009, 4, e4246.	1.1	31
86	Sex-specific gene expression during asexual development of Neurospora crassa. Fungal Genetics and Biology, 2012, 49, 533-543.	0.9	31
87	Harnessing Case Isolation and Ring Vaccination to Control Ebola. PLoS Neglected Tropical Diseases, 2015, 9, e0003794.	1.3	31
88	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.	2.6	31
89	Concerted Evolution in the Repeats of an Immunomodulating Cell Surface Protein, SOWgp, of the Human Pathogenic Fungi Coccidioides immitis and C. posadasii. Genetics, 2005, 171, 109-117.	1.2	30
90	LOX: inferring Level Of eXpression from diverse methods of census sequencing. Bioinformatics, 2010, 26, 1918-1919.	1.8	30

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91	Reevaluation of Epidemiological Data Demonstrates That It Is Consistent With Cross-Immunity Among Human Papillomavirus Types. Journal of Infectious Diseases, 2012, 206, 1291-1298.	1.9	30
92	Probabilistic uncertainty analysis of epidemiological modeling to guide public health intervention policy. Epidemics, 2014, 6, 37-45.	1.5	29
93	Maximizing Power in Phylogenetics and Phylogenomics: A Perspective Illuminated by Fungal Big Data. Advances in Genetics, 2017, 100, 1-47.	0.8	28
94	Yeast response to LA virus indicates coadapted global gene expression during mycoviral infection. FEMS Yeast Research, 2013, 13, 162-179.	1.1	27
95	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.	2.9	27
96	Phase-specific gene expression underlying morphological adaptations of the dimorphic human pathogenic fungus, Coccidioides posadasii. Fungal Genetics and Biology, 2006, 43, 545-559.	0.9	26
97	Assessing the Probability of Detection of Horizontal Gene Transfer Events in Bacterial Populations. Frontiers in Microbiology, 2012, 3, 27.	1.5	26
98	Sex-linked transcriptional divergence in the hermaphrodite fungus Neurospora tetrasperma. Proceedings of the Royal Society B: Biological Sciences, 2013, 280, 20130862.	1.2	26
99	Neutral Theory and the Somatic Evolution of Cancer. Molecular Biology and Evolution, 2018, 35, 1308-1315.	3.5	26
100	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
101	Primary hepatic neuroendocrine carcinoma: report of two cases and literature review. BMC Clinical Pathology, 2018, 18, 3.	1.8	23
102	Unmatched Level of Molecular Convergence among Deeply Divergent Complex Multicellular Fungi. Molecular Biology and Evolution, 2020, 37, 2228-2240.	3.5	23
103	PhyloOncology: Understanding cancer through phylogenetic analysis. Biochimica Et Biophysica Acta: Reviews on Cancer, 2017, 1867, 101-108.	3.3	22
104	Using evolutionary genomics, transcriptomics, and systems biology to reveal gene networks underlying fungal development. Fungal Biology Reviews, 2018, 32, 249-264.	1.9	22
105	Integrating Community-Based Interventions to Reverse the Convergent TB/HIV Epidemics in Rural South Africa. PLoS ONE, 2015, 10, e0126267.	1.1	21
106	Determinants of Human African Trypanosomiasis Elimination via Paratransgenesis. PLoS Neglected Tropical Diseases, 2016, 10, e0004465.	1.3	21
107	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, .	1.8	21
108	Controlling Antimicrobial Resistance through Targeted, Vaccine-Induced Replacement of Strains. PLoS ONE, 2012, 7, e50688.	1.1	20

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109	Cellular Superspreaders: An Epidemiological Perspective on HIV Infection inside the Body. PLoS Pathogens, 2014, 10, e1004092.	2.1	20
110	Somatic evolutionary timings of driver mutations. BMC Cancer, 2018, 18, 85.	1.1	20
111	Quarantine and testing strategies to ameliorate transmission due to travel during the COVID-19 pandemic: a modelling study. Lancet Regional Health - Europe, The, 2022, 14, 100304.	3.0	20
112	Mitochondrial genome size variation in New World and Old World populations of Drosophila melanogaster. Heredity, 2004, 93, 98-103.	1.2	19
113	Phylogenetic informativeness profiling of 12 genes for 28 vertebrate taxa without divergence dates. Molecular Phylogenetics and Evolution, 2011, 60, 271-272.	1.2	19
114	A Test for Selection Employing Quantitative Trait Locus and Mutation Accumulation Data. Genetics, 2012, 190, 1533-1545.	1.2	19
115	Lvr, a Signaling System That Controls Global Gene Regulation and Virulence in Pathogenic Leptospira. Frontiers in Cellular and Infection Microbiology, 2018, 8, 45.	1.8	19
116	Solving the ecological puzzle of mycorrhizal associations using data from annotated collections and environmental samples â€" an example of saddle fungi. Environmental Microbiology Reports, 2015, 7, 658-667.	1.0	18
117	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.	3.3	18
118	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.	0.8	18
119	A Bayesian method for analysing spotted microarray data. Briefings in Bioinformatics, 2005, 6, 318-330.	3.2	17
120	Maximum-Likelihood Model Averaging To Profile Clustering of Site Types across Discrete Linear Sequences. PLoS Computational Biology, 2009, 5, e1000421.	1.5	17
121	Measuring Transcription Factor–Binding Site Turnover: A Maximum Likelihood Approach Using Phylogenies. Genome Biology and Evolution, 2009, 1, 85-98.	1.1	17
122	Evaluating Phylogenetic Informativeness as a Predictor of Phylogenetic Signal for Metazoan, Fungal, and Mammalian Phylogenomic Data Sets. BioMed Research International, 2013, 2013, 1-14.	0.9	17
123	Future Perspectives and Challenges of Fungal Systematics in the Age of Big Data. Fungal Biology, 2016, , 25-46.	0.3	16
124	Comparative Genomics and Transcriptomics During Sexual Development Gives Insight Into the Life History of the Cosmopolitan Fungus Fusarium neocosmosporiellum. Frontiers in Microbiology, 2019, 10, 1247.	1.5	15
125	Analysis of mutation, selection, and epistasis: an informed approach to cancer clinical trials. Oncotarget, 2018, 9, 22243-22253.	0.8	15
126	Multi-targeted priming for genome-wide gene expression assays. BMC Genomics, 2010, 11, 477.	1.2	14

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127	Identification of new molecular markers for assembling the eukaryotic tree of life. Molecular Phylogenetics and Evolution, 2010, 55, 1177-1182.	1.2	14
128	RNA extraction, probe preparation, and competitive hybridization for transcriptional profiling using Neurospora crassa long-oligomer DNA microarrays. Fungal Genetics Reports, 2008, 55, 18-28.	0.6	14
129	Attribution of Cancer Origins to Endogenous, Exogenous, and Preventable Mutational Processes. Molecular Biology and Evolution, 2022, 39, .	3.5	14
130	Optimal targeting of seasonal influenza vaccination toward younger ages is robust to parameter uncertainty. Vaccine, 2013, 31, 3079-3089.	1.7	13
131	Identifying modules of cooperating cancer drivers. Molecular Systems Biology, 2021, 17, e9810.	3.2	13
132	Comparative analyses of eighteen rapid antigen tests and RT-PCR for COVID-19 quarantine and surveillance-based isolation. Communications Medicine, 2022, 2, .	1.9	13
133	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
134	Environmental and sex-specific molecular signatures of glioma causation. Neuro-Oncology, 2022, 24, 29-36.	0.6	12
135	The kinetics of transposable element autoregulation. , 2000, 108, 229-237.		11
136	Northern species of earth tongue genus <i>Thuemenidium</i> revisited, considering morphology, ecology and molecular phylogeny. Mycologia, 2010, 102, 1089-1095.	0.8	11
137	The somatic molecular evolution of cancer: Mutation, selection, and epistasis. Progress in Biophysics and Molecular Biology, 2021, 165, 56-65.	1.4	11
138	Genomic and Gene-Expression Comparisons among Phage-Resistant Type-IV Pilus Mutants of Pseudomonas syringae pathovar phaseolicola. PLoS ONE, 2015, 10, e0144514.	1.1	11
139	Designing Experiments Using Spotted Microarrays to Detect Gene Regulation Differences Within and Among Species. Methods in Enzymology, 2005, 395, 597-617.	0.4	10
140	SIR2 and other genes are abundantly expressed in long-lived natural segregants for replicative aging of the budding yeast Saccharomyces cerevisiae. FEMS Yeast Research, 2011, 11, 345-355.	1.1	10
141	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.	0.8	10
142	AuthorReward: increasing community curation in biological knowledge wikis through automated authorship quantification. Bioinformatics, 2013, 29, 1837-1839.	1.8	10
143	Retrospective Analysis of the 2014–2015 Ebola Epidemic in Liberia. American Journal of Tropical Medicine and Hygiene, 2016, 94, 833-839.	0.6	10
144	Detection of Regional Variation in Selection Intensity within Protein-Coding Genes Using DNA Sequence Polymorphism and Divergence. Molecular Biology and Evolution, 2017, 34, 3006-3022.	3.5	10

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145	Premetastatic shifts of endogenous and exogenous mutational processes support consolidative therapy in EGFR-driven lung adenocarcinoma. Cancer Letters, 2022, 526, 346-351.	3.2	10
146	PathScore: a web tool for identifying altered pathways in cancer data. Bioinformatics, 2016, 32, 3688-3690.	1.8	9
147	Optimizing age of cytomegalovirus screening and vaccination to avert congenital disease in the US. Vaccine, 2016, 34, 225-229.	1.7	9
148	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.	0.9	9
149	The landscape of novel and complementary targets for immunotherapy: an analysis of gene expression in the tumor microenvironment. Oncotarget, 2019, 10, 4532-4545.	0.8	8
150	The impact of incorporating molecular evolutionary model into predictions of phylogenetic signal and noise. Frontiers in Ecology and Evolution, $2014, 2, \ldots$	1.1	7
151	Integrative Activity of Mating Loci, Environmentally Responsive Genes, and Secondary Metabolism Pathways during Sexual Development of Chaetomium globosum. MBio, 2019, 10, .	1.8	7
152	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.	3.3	6
153	Distributions of Mutational Effects and the Estimation of Directional Selection in Divergent Lineages of <i>Arabidopsis thaliana</i>	1.2	6
154	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, .	1.1	6
155	Wagging the long tail of drivers of prostate cancer. PLoS Genetics, 2019, 15, e1007820.	1.5	5
156	Epidemiological mechanisms of genetic resistance to kuru. Journal of the Royal Society Interface, 2013, 10, 20130331.	1.5	4
157	Radiation-Specific Clinical Data Should Be Included in Existing Large-Scale Genomic Datasets. International Journal of Radiation Oncology Biology Physics, 2017, 98, 8-10.	0.4	4
158	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;76:9–13. European Urology, 2020, 77, e24-e25.	0.9	4
159	Non-Coding Mutations in Urothelial Bladder Cancer: Biological and Clinical Relevance and Potential Utility as Biomarkers. Bladder Cancer, 2020, 6, 211-213.	0.2	4
160	The GUL-1 Protein Binds Multiple RNAs Involved in Cell Wall Remodeling and Affects the MAK-1 Pathway in Neurospora crassa. Frontiers in Fungal Biology, 2021, 2, .	0.9	4
161	Mechanistic basis of post-treatment control of SIV after anti- $\hat{l}\pm4\hat{l}^27$ antibody therapy. PLoS Computational Biology, 2021, 17, e1009031.	1.5	4
162	Modeling Approaches Toward Understanding Infectious Disease Transmission., 2019,, 227-243.		4

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163	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. Journal of Molecular Diagnostics, 2022, 24, 101-103.	1.2	4
164	Sequencing and Analysis of the Entire Genome of the Mycoparasitic Bioeffector Fungus Trichoderma asperelloides Strain T 203 (Hypocreales). Microbiology Resource Announcements, 2022, 11, e0099521.	0.3	4
165	Transcriptional Divergence Underpinning Sexual Development in the Fungal Class Sordariomycetes. MBio, 2022, 13, .	1.8	4
166	Response to: The relative utility of sequence divergence and phylogenetic informativeness profiling in phylogenetic study design. Molecular Phylogenetics and Evolution, 2013, 66, 436.	1.2	3
167	Cost-effectiveness of next-generation vaccines: The case of pertussis. Vaccine, 2016, 34, 3405-3411.	1.7	3
168	Heavy mutagenesis by tobacco leads to lung adenocarcinoma tumors with KRAS G12 mutations other than G12D, leading KRAS G12D tumors—on average—to exhibit a lower mutation burden. Lung Cancer, 2022, 166, 265-269.	0.9	3
169	A phylogenetic approach to study the evolution of somatic mutational processes in cancer. Communications Biology, 2022, 5, .	2.0	3
170	GEM-NET: Lessons in Multi-Institution Teamwork Using Collaboration Software. ACS Central Science, 2019, 5, 1159-1169.	5.3	2
171	EPID-26. SEX-SPECIFIC GLIOMA MOLECULAR SIGNATURES. Neuro-Oncology, 2019, 21, vi80-vi80.	0.6	2
172	Cancer Relevance of Human Genes. Journal of the National Cancer Institute, 2022, 114, 988-995.	3.0	2
173	Secondary Metabolism Gene Clusters Exhibit Increasingly Dynamic and Differential Expression during Asexual Growth, Conidiation, and Sexual Development in Neurospora crassa. MSystems, 2022, 7, .	1.7	2
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