

# Antonis Rokas

## List of Publications by Year in descending order

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244  
papers

22,155  
citations

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22783  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 2012, 336, 1715-1719.	12.6	1,424
2	Genome-scale approaches to resolving incongruence in molecular phylogenies. <i>Nature</i> , 2003, 425, 798-804.	27.8	1,366
3	The genome of the choanoflagellate <i>Monosiga brevicollis</i> and the origin of metazoans. <i>Nature</i> , 2008, 451, 783-788.	27.8	1,006
4	Rare genomic changes as a tool for phylogenetics. <i>Trends in Ecology and Evolution</i> , 2000, 15, 454-459.	8.7	616
5	Inferring ancient divergences requires genes with strong phylogenetic signals. <i>Nature</i> , 2013, 497, 327-331.	27.8	541
6	Dynamics of <i>Pseudomonas aeruginosa</i> genome evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3100-3105.	7.1	492
7	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. <i>Science</i> , 2015, 347, 1258-1262.	12.6	492
8	Repeated morphological evolution through cis-regulatory changes in a pleiotropic gene. <i>Nature</i> , 2006, 440, 1050-1053.	27.8	475
9	Tempo and Mode of Genome Evolution in the Budding Yeast Subphylum. <i>Cell</i> , 2018, 175, 1533-1545.e20.	28.9	445
10	Bayesian Estimation of Concordance among Gene Trees. <i>Molecular Biology and Evolution</i> , 2006, 24, 412-426.	8.9	420
11	Contentious relationships in phylogenomic studies can be driven by a handful of genes. <i>Nature Ecology and Evolution</i> , 2017, 1, 126.	7.8	365
12	Animal Evolution and the Molecular Signature of Radiations Compressed in Time. <i>Science</i> , 2005, 310, 1933-1938.	12.6	357
13	More Genes or More Taxa? The Relative Contribution of Gene Number and Taxon Number to Phylogenetic Accuracy. <i>Molecular Biology and Evolution</i> , 2005, 22, 1337-1344.	8.9	349
14	The Awesome Power of Yeast Evolutionary Genetics: New Genome Sequences and Strain Resources for the <i>Saccharomyces sensu stricto</i> Genus. <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 11-25.	1.8	348
15	Comparative genomics of biotechnologically important yeasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9882-9887.	7.1	302
16	Comparing Bootstrap and Posterior Probability Values in the Four-Taxon Case. <i>Systematic Biology</i> , 2003, 52, 477-487.	5.6	277
17	The Origins of Multicellularity and the Early History of the Genetic Toolkit For Animal Development. <i>Annual Review of Genetics</i> , 2008, 42, 235-251.	7.6	268
18	Novel Information Theory-Based Measures for Quantifying Incongruence among Phylogenetic Trees. <i>Molecular Biology and Evolution</i> , 2014, 31, 1261-1271.	8.9	259

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19	Horizontal Transfer of a Large and Highly Toxic Secondary Metabolic Gene Cluster between Fungi. <i>Current Biology</i> , 2011, 21, 134-139.	3.9	253
20	Bushes in the Tree of Life. <i>PLoS Biology</i> , 2006, 4, e352.	5.6	251
21	Regulation of Body Pigmentation by the Abdominal-B Hox Protein and Its Gain and Loss in <i>Drosophila</i> Evolution. <i>Cell</i> , 2006, 125, 1387-1399.	28.9	240
22	ClipKIT: A multiple sequence alignment trimming software for accurate phylogenomic inference. <i>PLoS Biology</i> , 2020, 18, e3001007.	5.6	237
23	Animal mitochondrial DNA recombination revisited. <i>Trends in Ecology and Evolution</i> , 2003, 18, 411-417.	8.7	228
24	A Global Coexpression Network Approach for Connecting Genes to Specialized Metabolic Pathways in Plants. <i>Plant Cell</i> , 2017, 29, 944-959.	6.6	225
25	Phylogenetic and Transcriptomic Analysis of Chemosensory Receptors in a Pair of Divergent Ant Species Reveals Sex-Specific Signatures of Odor Coding. <i>PLoS Genetics</i> , 2012, 8, e1002930.	3.5	192
26	Reconstructing the Backbone of the Saccharomycotina Yeast Phylogeny Using Genome-Scale Data. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3927-3939.	1.8	187
27	Drivers of genetic diversity in secondary metabolic gene clusters within a fungal species. <i>PLoS Biology</i> , 2017, 15, e2003583.	5.6	187
28	The Evolution of Fungal Metabolic Pathways. <i>PLoS Genetics</i> , 2014, 10, e1004816.	3.5	183
29	Parallel inactivation of multiple GAL pathway genes and ecological diversification in yeasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 14144-14149.	7.1	182
30	Transcriptome profiling of chemosensory appendages in the malaria vector <i>Anopheles gambiae</i> reveals tissue- and sex-specific signatures of odor coding. <i>BMC Genomics</i> , 2011, 12, 271.	2.8	181
31	The Evolutionary Imprint of Domestication on Genome Variation and Function of the Filamentous Fungus <i>Aspergillus oryzae</i> . <i>Current Biology</i> , 2012, 22, 1403-1409.	3.9	177
32	A genome-scale phylogeny of the kingdom Fungi. <i>Current Biology</i> , 2021, 31, 1653-1665.e5.	3.9	170
33	Non-optimal codon usage is a mechanism to achieve circadian clock conditionality. <i>Nature</i> , 2013, 495, 116-120.	27.8	167
34	Toward a Fully Resolved Fungal Tree of Life. <i>Annual Review of Microbiology</i> , 2020, 74, 291-313.	7.3	156
35	The birth, evolution and death of metabolic gene clusters in fungi. <i>Nature Reviews Microbiology</i> , 2018, 16, 731-744.	28.6	155
36	Remarkably ancient balanced polymorphisms in a multi-locus gene network. <i>Nature</i> , 2010, 464, 54-58.	27.8	147

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37	Evaluating Fast Maximum Likelihood-Based Phylogenetic Programs Using Empirical Phylogenomic Data Sets. <i>Molecular Biology and Evolution</i> , 2018, 35, 486-503.	8.9	147
38	Multiple <i>GAL</i> pathway gene clusters evolved independently and by different mechanisms in fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10136-10141.	7.1	144
39	Blood meal-induced changes to antennal transcriptome profiles reveal shifts in odor sensitivities in <i>Anopheles gambiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 8260-8265.	7.1	143
40	Chemoreceptor Evolution in Hymenoptera and Its Implications for the Evolution of Eusociality. <i>Genome Biology and Evolution</i> , 2015, 7, 2407-2416.	2.5	141
41	Benchmarking Next-Generation Transcriptome Sequencing for Functional and Evolutionary Genomics. <i>Molecular Biology and Evolution</i> , 2009, 26, 2731-2744.	8.9	140
42	Collagen IV and basement membrane at the evolutionary dawn of metazoan tissues. <i>ELife</i> , 2017, 6, .	6.0	139
43	Out of Anatolia: longitudinal gradients in genetic diversity support an eastern origin for a circum-Mediterranean oak gallwasp <i>Andricus quercustoxae</i> . <i>Molecular Ecology</i> , 2003, 12, 2153-2174.	3.9	136
44	Fungal metabolic gene clusters—caravans traveling across genomes and environments. <i>Frontiers in Microbiology</i> , 2015, 6, 161.	3.5	136
45	The influence of evolutionary history on human health and disease. <i>Nature Reviews Genetics</i> , 2021, 22, 269-283.	16.3	133
46	Risk factors and outcome of pulmonary aspergillosis in critically ill coronavirus disease 2019 patients—a multinational observational study by the European Confederation of Medical Mycology. <i>Clinical Microbiology and Infection</i> , 2022, 28, 580-587.	6.0	133
47	Recurrent Tissue-Specific mtDNA Mutations Are Common in Humans. <i>PLoS Genetics</i> , 2013, 9, e1003929.	3.5	130
48	Harnessing genomics for evolutionary insights. <i>Trends in Ecology and Evolution</i> , 2009, 24, 192-200.	8.7	124
49	Conflicting phylogenetic signals at the base of the metazoan tree. <i>Evolution &amp; Development</i> , 2003, 5, 346-359.	2.0	116
50	Extensive loss of cell-cycle and DNA repair genes in an ancient lineage of bipolar budding yeasts. <i>PLoS Biology</i> , 2019, 17, e3000255.	5.6	116
51	Evidence for a High Frequency of Simultaneous Double-Nucleotide Substitutions. <i>Science</i> , 2000, 287, 1283-1286.	12.6	111
52	Gene Essentiality Analyzed by <i>In Vivo</i> Transposon Mutagenesis and Machine Learning in a Stable Haploid Isolate of <i>Candida albicans</i> . <i>MBio</i> , 2018, 9, .	4.1	110
53	Horizontal Transfer and Death of a Fungal Secondary Metabolic Gene Cluster. <i>Genome Biology and Evolution</i> , 2012, 4, 289-293.	2.5	108
54	The triple helix of collagens—“an ancient protein structure that enabled animal multicellularity and tissue evolution. <i>Journal of Cell Science</i> , 2018, 131, .	2.0	108

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55	EVOLUTIONARY SHIFTS BETWEEN HOST OAK SECTIONS AND HOST-PLANT ORGANS IN ANDRICUS GALLWASPS. <i>Evolution; International Journal of Organic Evolution</i> , 2002, 56, 1821-1830.	2.3	107
56	Global Transcriptome Changes Underlying Colony Growth in the Opportunistic Human Pathogen <i>Aspergillus fumigatus</i> . <i>Eukaryotic Cell</i> , 2012, 11, 68-78.	3.4	107
57	A Robust Phylogenomic Time Tree for Biotechnologically and Medically Important Fungi in the Genera <i>Aspergillus</i> and <i>Penicillium</i> . <i>MBio</i> , 2019, 10, .	4.1	106
58	Genomics and the making of yeast biodiversity. <i>Current Opinion in Genetics and Development</i> , 2015, 35, 100-109.	3.3	105
59	Leveraging skewed transcript abundance by RNA-Seq to increase the genomic depth of the tree of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1476-1481.	7.1	101
60	Embracing Uncertainty in Reconstructing Early Animal Evolution. <i>Current Biology</i> , 2017, 27, R1081-R1088.	3.9	101
61	A Maximum-Likelihood Analysis of Eight Phylogenetic Markers in Gallwasps (Hymenoptera: Cynipidae): Implications for Insect Phylogenetic Studies. <i>Molecular Phylogenetics and Evolution</i> , 2002, 22, 206-219.	2.7	98
62	Frequent and Widespread Parallel Evolution of Protein Sequences. <i>Molecular Biology and Evolution</i> , 2008, 25, 1943-1953.	8.9	98
63	Antennal transcriptome profiles of anopheline mosquitoes reveal human host olfactory specialization in <i>Anopheles gambiae</i> . <i>BMC Genomics</i> , 2013, 14, 749.	2.8	94
64	Biosynthetic gene clusters and the evolution of fungal chemodiversity. <i>Natural Product Reports</i> , 2020, 37, 868-878.	10.3	93
65	Rooting the Animal Tree of Life. <i>Molecular Biology and Evolution</i> , 2021, 38, 4322-4333.	8.9	93
66	In Silico Characterization and Molecular Evolutionary Analysis of a Novel Superfamily of Fungal Effector Proteins. <i>Molecular Biology and Evolution</i> , 2012, 29, 3371-3384.	8.9	90
67	Complete Bacteriophage Transfer in a Bacterial Endosymbiont ( <i>Wolbachia</i> ) Determined by Targeted Genome Capture. <i>Genome Biology and Evolution</i> , 2011, 3, 209-218.	2.5	89
68	Understanding patterns of genetic diversity in the oak gallwasp <i>Biorhiza pallida</i> : demographic history or a <i>Wolbachia</i> selective sweep?. <i>Heredity</i> , 2001, 87, 294-304.	2.6	86
69	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 October 2009–30 November 2009. <i>Molecular Ecology Resources</i> , 2010, 10, 404-408.	4.8	84
70	Evaluating Ortholog Prediction Algorithms in a Yeast Model Clade. <i>PLoS ONE</i> , 2011, 6, e18755.	2.5	84
71	Transcriptome-wide analysis of small RNA expression in early zebrafish development. <i>Rna</i> , 2012, 18, 915-929.	3.5	84
72	Genome-scale phylogeny and contrasting modes of genome evolution in the fungal phylum Ascomycota. <i>Science Advances</i> , 2020, 6, .	10.3	84

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73	What can comparative genomics tell us about species concepts in the genus <i>Aspergillus</i> ?. <i>Studies in Mycology</i> , 2007, 59, 11-17.	7.2	83
74	Physical linkage of metabolic genes in fungi is an adaptation against the accumulation of toxic intermediate compounds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11481-11486.	7.1	82
75	Evolution of the human pathogenic lifestyle in fungi. <i>Nature Microbiology</i> , 2022, 7, 607-619.	13.3	79
76	Extensive Copy Number Variation in Fermentation-Related Genes Among <i>Saccharomyces cerevisiae</i> Wine Strains. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1475-1485.	1.8	77
77	Functional and evolutionary characterization of a secondary metabolite gene cluster in budding yeasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 11030-11035.	7.1	75
78	Eukaryotic Acquisition of a Bacterial Operon. <i>Cell</i> , 2019, 176, 1356-1366.e10.	28.9	74
79	Lifecycle closure, lineage sorting, and hybridization revealed in a phylogenetic analysis of European oak gallwasps (Hymenoptera: Cynipidae: Cynipini) using mitochondrial sequence data. <i>Molecular Phylogenetics and Evolution</i> , 2003, 26, 36-45.	2.7	73
80	Computing the Internode Certainty and Related Measures from Partial Gene Trees. <i>Molecular Biology and Evolution</i> , 2016, 33, 1606-1617.	8.9	73
81	The function and evolution of the <i>Aspergillus</i> genome. <i>Trends in Microbiology</i> , 2013, 21, 14-22.	7.7	72
82	Examining the Evolution of the Regulatory Circuit Controlling Secondary Metabolism and Development in the Fungal Genus <i>Aspergillus</i> . <i>PLoS Genetics</i> , 2015, 11, e1005096.	3.5	70
83	A Genome-Scale Investigation of How Sequence, Function, and Tree-Based Gene Properties Influence Phylogenetic Inference. <i>Genome Biology and Evolution</i> , 2016, 8, 2565-2580.	2.5	70
84	Horizontally acquired genes in early-diverging pathogenic fungi enable the use of host nucleosides and nucleotides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 4116-4121.	7.1	70
85	Evolutionary instability of CUG-Leu in the genetic code of budding yeasts. <i>Nature Communications</i> , 2018, 9, 1887.	12.8	70
86	PhyKIT: a broadly applicable UNIX shell toolkit for processing and analyzing phylogenomic data. <i>Bioinformatics</i> , 2021, 37, 2325-2331.	4.1	69
87	The molecular origins of multicellular transitions. <i>Current Opinion in Genetics and Development</i> , 2008, 18, 472-478.	3.3	68
88	Evolution of a heavy metal homeostasis/resistance island reflects increasing copper stress in Enterobacteria. <i>Genome Biology and Evolution</i> , 2016, 8, evw031.	2.5	68
89	Systematic Dissection of the Evolutionarily Conserved WetA Developmental Regulator across a Genus of Filamentous Fungi. <i>MBio</i> , 2018, 9, .	4.1	68
90	Variation and selection on codon usage bias across an entire subphylum. <i>PLoS Genetics</i> , 2019, 15, e1008304.	3.5	68

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91	Evidence for loss and reacquisition of alcoholic fermentation in a fructophilic yeast lineage. <i>ELife</i> , 2018, 7, .	6.0	67
92	Evidence for genetic differentiation and variable recombination rates among Dutch populations of the opportunistic human pathogen <i>Aspergillus fumigatus</i> . <i>Molecular Ecology</i> , 2012, 21, 57-70.	3.9	65
93	Gestational tissue transcriptomics in term and preterm human pregnancies: a systematic review and meta-analysis. <i>BMC Medical Genomics</i> , 2015, 8, 27.	1.5	65
94	Differential success in northwards range expansion between ecotypes of the marble gallwasp <i>Andricus kollari</i> : a tale of two lifecycles. <i>Molecular Ecology</i> , 2008, 10, 761-778.	3.9	63
95	The diversity and evolution of circadian clock proteins in fungi. <i>Mycologia</i> , 2010, 102, 269-278.	1.9	63
96	Copy Number Variation in Fungi and Its Implications for Wine Yeast Genetic Diversity and Adaptation. <i>Frontiers in Microbiology</i> , 2018, 9, 288.	3.5	63
97	The Molecular Evolution of the p120-Catenin Subfamily and Its Functional Associations. <i>PLoS ONE</i> , 2010, 5, e15747.	2.5	61
98	The phylogeographical clade trade: tracing the impact of human-mediated dispersal on the colonization of northern Europe by the oak gallwasp <i>Andricus kollari</i> . <i>Molecular Ecology</i> , 2007, 16, 2768-2781.	3.9	60
99	An LaeA- and BrlA-Dependent Cellular Network Governs Tissue-Specific Secondary Metabolism in the Human Pathogen <i>Aspergillus fumigatus</i> . <i>MSphere</i> , 2018, 3, .	2.9	58
100	Regulation of Secondary Metabolism by the Velvet Complex Is Temperature-Responsive in <i>Aspergillus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 4023-4033.	1.8	58
101	Fragmentation of an aflatoxin-like gene cluster in a forest pathogen. <i>New Phytologist</i> , 2013, 198, 525-535.	7.3	55
102	Evidence for widespread cryptic sexual generations in apparently purely asexual <i>Andricus</i> gallwasps. <i>Molecular Ecology</i> , 2008, 17, 652-665.	3.9	54
103	Wolbachia as a speciation agent. <i>Trends in Ecology and Evolution</i> , 2000, 15, 44-45.	8.7	53
104	Functional Divergence for Every Paralog. <i>Molecular Biology and Evolution</i> , 2014, 31, 984-992.	8.9	53
105	Nutritional Heterogeneity Among <i>Aspergillus fumigatus</i> Strains Has Consequences for Virulence in a Strain- and Host-Dependent Manner. <i>Frontiers in Microbiology</i> , 2019, 10, 854.	3.5	52
106	Intron insertion as a phylogenetic character: the engrailed homeobox of Strepsiptera does not indicate affinity with Diptera. <i>Insect Molecular Biology</i> , 1999, 8, 527-530.	2.0	51
107	PhyloFisher: A phylogenomic package for resolving eukaryotic relationships. <i>PLoS Biology</i> , 2021, 19, e3001365.	5.6	51
108	Variation Among Biosynthetic Gene Clusters, Secondary Metabolite Profiles, and Cards of Virulence Across <i>Aspergillus</i> Species. <i>Genetics</i> , 2020, 216, 481-497.	2.9	50

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109	WetA bridges cellular and chemical development in <i>Aspergillus flavus</i> . PLoS ONE, 2017, 12, e0179571.	2.5	48
110	The incidence and diversity of <i>Wolbachia</i> in gallwasps (Hymenoptera; Cynipidae) on oak. Molecular Ecology, 2002, 11, 1815-1829.	3.9	47
111	Investigation of <i>Aspergillus fumigatus</i> biofilm formation by various "omics" approaches. Frontiers in Microbiology, 2013, 4, 13.	3.5	47
112	Comprehensive RNA profiling of villous trophoblast and decidua basalis in pregnancies complicated by preterm birth following intra-amniotic infection. Placenta, 2016, 44, 23-33.	1.5	47
113	Dynamic Evolution of Nitric Oxide Detoxifying Flavohemoglobins, a Family of Single-Protein Metabolic Modules in Bacteria and Eukaryotes. Molecular Biology and Evolution, 2016, 33, 1979-1987.	8.9	46
114	The Fumagillin Gene Cluster, an Example of Hundreds of Genes under veA Control in <i>Aspergillus fumigatus</i> . PLoS ONE, 2013, 8, e77147.	2.5	45
115	Fungal Isocyanide Synthases and Xanthocillin Biosynthesis in <i>Aspergillus fumigatus</i> . MBio, 2018, 9, .	4.1	44
116	Genomic and Phenotypic Heterogeneity of Clinical Isolates of the Human Pathogens <i>Aspergillus fumigatus</i> , <i>Aspergillus lentulus</i> , and <i>Aspergillus fumigatus</i> affinis. Frontiers in Genetics, 2020, 11, 459.	2.3	44
117	Phylogenetic Analysis of Protein Sequence Data Using the Randomized Accelerated Maximum Likelihood (RAXML) Program. Current Protocols in Molecular Biology, 2011, 96, Unit19.11.	2.9	43
118	Rapid Phenotypic and Metabolomic Domestication of Wild <i>Penicillium</i> Molds on Cheese. MBio, 2019, 10, .	4.1	43
119	Characterizing the Pathogenic, Genomic, and Chemical Traits of <i>Aspergillus fischeri</i> , a Close Relative of the Major Human Fungal Pathogen <i>Aspergillus fumigatus</i> . MSphere, 2019, 4, .	2.9	42
120	Evolving moldy murderers: <i>Aspergillus section Fumigati</i> as a model for studying the repeated evolution of fungal pathogenicity. PLoS Pathogens, 2020, 16, e1008315.	4.7	40
121	Longitudinal range expansion and cryptic eastern species in the western Palearctic oak gallwasp, <i>Andricus coriarius</i> . Molecular Ecology, 2007, 16, 2103-2114.	3.9	39
122	Repeated loss of an anciently horizontally transferred gene cluster in <i>Botrytis</i> . Mycologia, 2013, 105, 1126-1134.	1.9	39
123	In Silico Whole Genome Sequencer and Analyzer (iWGS): a Computational Pipeline to Guide the Design and Analysis of de novo Genome Sequencing Studies. G3: Genes, Genomes, Genetics, 2016, 6, 3655-3662.	1.8	39
124	Pathogenic Allodiploid Hybrids of <i>Aspergillus</i> Fungi. Current Biology, 2020, 30, 2495-2507.e7.	3.9	39
125	The effect of domestication on the fungal proteome. Trends in Genetics, 2009, 25, 60-63.	6.7	38
126	Transcriptome of the adult female malaria mosquito vector <i>Anopheles albimanus</i> . BMC Genomics, 2012, 13, 207.	2.8	38



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127	Quartet-Based Computations of Internode Certainty Provide Robust Measures of Phylogenetic Incongruence. <i>Systematic Biology</i> , 2020, 69, 308-324.	5.6	38
128	Ecology Drives the Distribution of Specialized Tyrosine Metabolism Modules in Fungi. <i>Genome Biology and Evolution</i> , 2014, 6, 121-132.	2.5	37
129	Factors driving metabolic diversity in the budding yeast subphylum. <i>BMC Biology</i> , 2018, 16, 26.	3.8	36
130	Whole exome sequencing reveals HSPA1L as a genetic risk factor for spontaneous preterm birth. <i>PLoS Genetics</i> , 2018, 14, e1007394.	3.5	35
131	Mapping the Fungal Battlefield: Using in situ Chemistry and Deletion Mutants to Monitor Interspecific Chemical Interactions Between Fungi. <i>Frontiers in Microbiology</i> , 2019, 10, 285.	3.5	35
132	Multiple Reinventions of Mating-type Switching during Budding Yeast Evolution. <i>Current Biology</i> , 2019, 29, 2555-2562.e8.	3.9	33
133	Clustering of Two Genes Putatively Involved in Cyanate Detoxification Evolved Recently and Independently in Multiple Fungal Lineages. <i>Genome Biology and Evolution</i> , 2015, 7, 789-800.	2.5	32
134	An investigation of irreproducibility in maximum likelihood phylogenetic inference. <i>Nature Communications</i> , 2020, 11, 6096.	12.8	32
135	Gliotoxin, a Known Virulence Factor in the Major Human Pathogen <i>Aspergillus fumigatus</i> , Is Also Biosynthesized by Its Nonpathogenic Relative <i>Aspergillus fischeri</i> . <i>MBio</i> , 2020, 11, .	4.1	32
136	Diversity of Secondary Metabolism in <i>Aspergillus nidulans</i> Clinical Isolates. <i>MSphere</i> , 2020, 5, .	2.9	32
137	Functional Characterization of Clinical Isolates of the Opportunistic Fungal Pathogen <i>Aspergillus nidulans</i> . <i>MSphere</i> , 2020, 5, .	2.9	32
138	Divergent and Conserved Elements Comprise the Chemoreceptive Repertoire of the Nonblood-Feeding Mosquito <i>Toxorhynchites amboinensis</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 2883-2896.	2.5	31
139	MybA, a transcription factor involved in conidiation and conidial viability of the human pathogen <i>Aspergillus fumigatus</i> . <i>Molecular Microbiology</i> , 2017, 105, 880-900.	2.5	31
140	Unearthing fungal chemodiversity and prospects for drug discovery. <i>Current Opinion in Microbiology</i> , 2019, 51, 22-29.	5.1	31
141	Genomic and Phenotypic Analysis of COVID-19-Associated Pulmonary Aspergillosis Isolates of <i>Aspergillus fumigatus</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0001021.	3.0	31
142	Into the wild: new yeast genomes from natural environments and new tools for their analysis. <i>FEMS Yeast Research</i> , 2020, 20, .	2.3	29
143	Transcriptomic, Protein-DNA Interaction, and Metabolomic Studies of VosA, VelB, and WetA in <i>Aspergillus nidulans</i> Asexual Spores. <i>MBio</i> , 2021, 12, .	4.1	29
144	Dissecting Incongruence between Concatenation- and Quartet-Based Approaches in Phylogenomic Data. <i>Systematic Biology</i> , 2021, 70, 997-1014.	5.6	28

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145	The <i>ASP3</i> locus in <i>Saccharomyces cerevisiae</i> originated by horizontal gene transfer from <i>Wickerhamomyces</i> . FEMS Yeast Research, 2012, 12, 859-863.	2.3	27
146	Is preterm birth a human-specific syndrome?. Evolution, Medicine and Public Health, 2015, 2015, 136-148.	2.5	27
147	The <i>Aspergillus fumigatus</i> transcription factor RglT is important for gliotoxin biosynthesis and self-protection, and virulence. PLoS Pathogens, 2020, 16, e1008645.	4.7	27
148	Prevention, diagnosis and treatment of high-throughput sequencing data pathologies. Molecular Ecology, 2014, 23, 1679-1700.	3.9	24
149	Genomic features and evolution of the conditionally dispensable chromosome in the tangerine pathotype of <i>Alternaria alternata</i> . Molecular Plant Pathology, 2019, 20, 1425-1438.	4.2	23
150	A Bioinformatics Approach for Integrated Transcriptomic and Proteomic Comparative Analyses of Model and Non-sequenced Anopheline Vectors of Human Malaria Parasites. Molecular and Cellular Proteomics, 2013, 12, 120-131.	3.8	21
151	Transcriptional Rewiring: The Proof Is in the Eating. Current Biology, 2007, 17, R626-R628.	3.9	20
152	Comparative and Functional Characterization of Intragenic Tandem Repeats in 10 <i>Aspergillus</i> Genomes. Molecular Biology and Evolution, 2008, 26, 591-602.	8.9	20
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