

Toni Gabaldà³n

List of Publications by Year in descending order

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Version: 2024-02-01

260
papers

31,741
citations

7069

78
h-index

6113

159
g-index

316
all docs

316
docs citations

316
times ranked

38507
citing authors

#	ARTICLE	IF	CITATIONS
1	trimAl: a tool for automated alignment trimming in large-scale phylogenetic analyses. <i>Bioinformatics</i> , 2009, 25, 1972-1973.	1.8	7,974
2	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	6.0	1,583
3	Genome Sequence of the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>PLoS Biology</i> , 2010, 8, e1000313.	2.6	913
4	The genome of melon (<i>Cucumis melo</i> L.). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11872-11877.	3.3	654
5	Rapid transcriptional plasticity of duplicated gene clusters enables a clonally reproducing aphid to colonise diverse plant species. <i>Genome Biology</i> , 2017, 18, 27.	3.8	624
6	The genome of the recently domesticated crop plant sugar beet (<i>Beta vulgaris</i>). <i>Nature</i> , 2014, 505, 546-549.	13.7	569
7	eggNOG v4.0: nested orthology inference across 3686 organisms. <i>Nucleic Acids Research</i> , 2014, 42, D231-D239.	6.5	526
8	Functional and evolutionary implications of gene orthology. <i>Nature Reviews Genetics</i> , 2013, 14, 360-366.	7.7	516
9	Synonymous Mutations Frequently Act as Driver Mutations in Human Cancers. <i>Cell</i> , 2014, 156, 1324-1335.	13.5	482
10	Redundans: an assembly pipeline for highly heterozygous genomes. <i>Nucleic Acids Research</i> , 2016, 44, e113-e113.	6.5	429
11	Immunity and other defenses in pea aphids, <i>Acyrtosiphon pisum</i> . <i>Genome Biology</i> , 2010, 11, R21.	13.9	389
12	ETE: a python Environment for Tree Exploration. <i>BMC Bioinformatics</i> , 2010, 11, 24.	1.2	366
13	Beyond the Whole-Genome Duplication: Phylogenetic Evidence for an Ancient Interspecies Hybridization in the Baker's Yeast Lineage. <i>PLoS Biology</i> , 2015, 13, e1002220.	2.6	321
14	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	3.8	308
15	Genome structure and metabolic features in the red seaweed <i>Chondrus crispus</i> shed light on evolution of the Archaeplastida. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5247-5252.	3.3	307
16	Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014, 346, 1254449.	6.0	300
17	PhylomeDB v4: zooming into the plurality of evolutionary histories of a genome. <i>Nucleic Acids Research</i> , 2014, 42, D897-D902.	6.5	264
18	An anaerobic mitochondrion that produces hydrogen. <i>Nature</i> , 2005, 434, 74-79.	13.7	242

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19	The Human Oral Microbiome in Health and Disease: From Sequences to Ecosystems. <i>Microorganisms</i> , 2020, 8, 308.	1.6	231
20	Tracing the Evolution of a Large Protein Complex in the Eukaryotes, NADH:Ubiquinone Oxidoreductase (Complex I). <i>Journal of Molecular Biology</i> , 2005, 348, 857-870.	2.0	228
21	High Variability of Mitochondrial Gene Order among Fungi. <i>Genome Biology and Evolution</i> , 2014, 6, 451-465.	1.1	223
22	The First Myriapod Genome Sequence Reveals Conservative Arthropod Gene Content and Genome Organisation in the Centipede <i>Strigamia maritima</i> . <i>PLoS Biology</i> , 2014, 12, e1002005.	2.6	221
23	Acquisition of prokaryotic genes by fungal genomes. <i>Trends in Genetics</i> , 2010, 26, 5-8.	2.9	219
24	Adaptation of <i>S. cerevisiae</i> to Fermented Food Environments Reveals Remarkable Genome Plasticity and the Footprints of Domestication. <i>Molecular Biology and Evolution</i> , 2018, 35, 1712-1727.	3.5	214
25	Microbiome and colorectal cancer: Roles in carcinogenesis and clinical potential. <i>Molecular Aspects of Medicine</i> , 2019, 69, 93-106.	2.7	212
26	Genome sequence of the necrotrophic fungus <i>Penicillium digitatum</i> , the main postharvest pathogen of citrus. <i>BMC Genomics</i> , 2012, 13, 646.	1.2	205
27	Late acquisition of mitochondria by a host with chimaeric prokaryotic ancestry. <i>Nature</i> , 2016, 531, 101-104.	13.7	204
28	Genome sequence of the olive tree, <i>Olea europaea</i> . <i>GigaScience</i> , 2016, 5, 29.	3.3	201
29	Standardized benchmarking in the quest for orthologs. <i>Nature Methods</i> , 2016, 13, 425-430.	9.0	198
30	Molecular signatures of plastic phenotypes in two eusocial insect species with simple societies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13970-13975.	3.3	192
31	Fungal evolution: diversity, taxonomy and phylogeny of the Fungi. <i>Biological Reviews</i> , 2019, 94, 2101-2137.	4.7	191
32	Large-scale assignment of orthology: back to phylogenetics?. <i>Genome Biology</i> , 2008, 9, 235.	13.9	187
33	Genome, Transcriptome, and Functional Analyses of <i>Penicillium expansum</i> Provide New Insights Into Secondary Metabolism and Pathogenicity. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 232-248.	1.4	183
34	Phylemon 2.0: a suite of web-tools for molecular evolution, phylogenetics, phylogenomics and hypotheses testing. <i>Nucleic Acids Research</i> , 2011, 39, W470-W474.	6.5	182
35	Phylogenomics supports microsporidia as the earliest diverging clade of sequenced fungi. <i>BMC Biology</i> , 2012, 10, 47.	1.7	182
36	<i>Candida parapsilosis</i> : from Genes to the Bedside. <i>Clinical Microbiology Reviews</i> , 2019, 32, .	5.7	182

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37	Fungal evolution: major ecological adaptations and evolutionary transitions. <i>Biological Reviews</i> , 2019, 94, 1443-1476.	4.7	181
38	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. <i>Current Biology</i> , 2016, 26, 1577-1584.	1.8	175
39	Comparative genomics of emerging pathogens in the <i>Candida glabrata</i> clade. <i>BMC Genomics</i> , 2013, 14, 623.	1.2	174
40	Genome and transcriptome analysis of the Mesoamerican common bean and the role of gene duplications in establishing tissue and temporal specialization of genes. <i>Genome Biology</i> , 2016, 17, 32.	3.8	166
41	Evolutionary Emergence of Drug Resistance in <i>Candida</i> Opportunistic Pathogens. <i>Genes</i> , 2018, 9, 461.	1.0	161
42	Peroxisome diversity and evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 765-773.	1.8	158
43	Reconstruction of the Proto-Mitochondrial Metabolism. <i>Science</i> , 2003, 301, 609-609.	6.0	155
44	Systematic Phenotyping of a Large-Scale <i>Candida glabrata</i> Deletion Collection Reveals Novel Antifungal Tolerance Genes. <i>PLoS Pathogens</i> , 2014, 10, e1004211.	2.1	155
45	A comprehensive genome variation map of melon identifies multiple domestication events and loci influencing agronomic traits. <i>Nature Genetics</i> , 2019, 51, 1607-1615.	9.4	153
46	Origin and evolution of the peroxisomal proteome. <i>Biology Direct</i> , 2006, 1, 8.	1.9	152
47	The human phylome. <i>Genome Biology</i> , 2007, 8, R109.	3.8	150
48	Whole genome sequencing of turbot (<i>Scophthalmus maximus</i> ; Pleuronectiformes): a fish adapted to demersal life. <i>DNA Research</i> , 2016, 23, 181-192.	1.5	150
49	The <i>Solanum commersonii</i> Genome Sequence Provides Insights into Adaptation to Stress Conditions and Genome Evolution of Wild Potato Relatives. <i>Plant Cell</i> , 2015, 27, 954-968.	3.1	149
50	From <i>Saccharomyces cerevisiae</i> to <i>Candida glabrata</i> in a few easy steps: important adaptations for an opportunistic pathogen. <i>FEMS Microbiology Letters</i> , 2011, 314, 1-9.	0.7	144
51	Genome-wide signatures of complex introgression and adaptive evolution in the big cats. <i>Science Advances</i> , 2017, 3, e1700299.	4.7	142
52	Genomic history of the origin and domestication of common bean unveils its closest sister species. <i>Genome Biology</i> , 2017, 18, 60.	3.8	142
53	Eukaryotic cold shock domain proteins: highly versatile regulators of gene expression. <i>BioEssays</i> , 2010, 32, 109-118.	1.2	141
54	Transcriptome analyses of primitively eusocial wasps reveal novel insights into the evolution of sociality and the origin of alternative phenotypes. <i>Genome Biology</i> , 2013, 14, R20.	13.9	139

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55	The Genomic Aftermath of Hybridization in the Opportunistic Pathogen <i>Candida metapsilosis</i> . <i>PLoS Genetics</i> , 2015, 11, e1005626.	1.5	139
56	Genome Comparison of <i>Candida orthopsilosis</i> Clinical Strains Reveals the Existence of Hybrids between Two Distinct Subspecies. <i>Genome Biology and Evolution</i> , 2014, 6, 1069-1078.	1.1	138
57	PhylomeDB v3.0: an expanding repository of genome-wide collections of trees, alignments and phylogeny-based orthology and paralogy predictions. <i>Nucleic Acids Research</i> , 2011, 39, D556-D560.	6.5	134
58	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. <i>Genome Biology</i> , 2016, 17, 251.	3.8	131
59	Gene flow contributes to diversification of the major fungal pathogen <i>Candida albicans</i> . <i>Nature Communications</i> , 2018, 9, 2253.	5.8	131
60	Genetically encodable bioluminescent system from fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12728-12732.	3.3	130
61	Drug-Resistant Fungi: An Emerging Challenge Threatening Our Limited Antifungal Armamentarium. <i>Antibiotics</i> , 2020, 9, 877.	1.5	125
62	The birth of a deadly yeast: tracing the evolutionary emergence of virulence traits in <i>Candida glabrata</i> . <i>FEMS Yeast Research</i> , 2016, 16, fov110.	1.1	123
63	Shaping the mitochondrial proteome. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2004, 1659, 212-220.	0.5	122
64	Ancient Dispersal of the Human Fungal Pathogen <i>Cryptococcus gattii</i> from the Amazon Rainforest. <i>PLoS ONE</i> , 2013, 8, e71148.	1.1	122
65	Gene gain and loss across the metazoan tree of life. <i>Nature Ecology and Evolution</i> , 2020, 4, 524-533.	3.4	116
66	MetaPhOrs: orthology and paralogy predictions from multiple phylogenetic evidence using a consistency-based confidence score. <i>Nucleic Acids Research</i> , 2011, 39, e32-e32.	6.5	114
67	Patterns of Genomic Variation in the Opportunistic Pathogen <i>Candida glabrata</i> Suggest the Existence of Mating and a Secondary Association with Humans. <i>Current Biology</i> , 2018, 28, 15-27.e7.	1.8	114
68	Big data and other challenges in the quest for orthologs. <i>Bioinformatics</i> , 2014, 30, 2993-2998.	1.8	109
69	Massive gene presence-absence variation shapes an open pan-genome in the Mediterranean mussel. <i>Genome Biology</i> , 2020, 21, 275.	3.8	105
70	Hybridization and emergence of virulence in opportunistic human yeast pathogens. <i>Yeast</i> , 2018, 35, 5-20.	0.8	104
71	PeroxisomeDB 2.0: an integrative view of the global peroxisomal metabolome. <i>Nucleic Acids Research</i> , 2010, 38, D800-D805.	6.5	103
72	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

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73	Evolutionary genomics of yeast pathogens in the Saccharomycotina. FEMS Yeast Research, 2016, 16, fow064.	1.1	102
74	From Endosymbiont to Host-Controlled Organelle: The Hijacking of Mitochondrial Protein Synthesis and Metabolism. PLoS Computational Biology, 2007, 3, e219.	1.5	101
75	Origin and evolution of metabolic sub-cellular compartmentalization in eukaryotes. Biochimie, 2015, 119, 262-268.	1.3	101
76	Transposons played a major role in the diversification between the closely related almond and peach genomes: results from the almond genome sequence. Plant Journal, 2020, 101, 455-472.	2.8	94
77	spongeScan: A web for detecting microRNA binding elements in lncRNA sequences. Nucleic Acids Research, 2016, 44, W176-W180.	6.5	92
78	Prediction of protein function and pathways in the genome era. Cellular and Molecular Life Sciences, 2004, 61, 930-944.	2.4	90
79	PhylomeDB: a database for genome-wide collections of gene phylogenies. Nucleic Acids Research, 2007, 36, D491-D496.	6.5	90
80	A Midzone-Based Ruler Adjusts Chromosome Compaction to Anaphase Spindle Length. Science, 2011, 332, 465-468.	6.0	87
81	Citizen science charts two major ecotypes in the oral microbiome of adolescents and reveals links with habits and drinking water composition. Microbiome, 2018, 6, 218.	4.9	86
82	The Genome and Development-Dependent Transcriptomes of Pyronema confluens: A Window into Fungal Evolution. PLoS Genetics, 2013, 9, e1003820.	1.5	85
83	The Quiet and Underappreciated Rise of Drug-Resistant Invasive Fungal Pathogens. Journal of Fungi (Basel, Switzerland), 2020, 6, 138.	1.5	84
84	Fine-scale evolution: genomic, phenotypic and ecological differentiation in two coexisting <i>Salinibacter ruber</i> strains. ISME Journal, 2010, 4, 882-895.	4.4	81
85	Gene Expansion Shapes Genome Architecture in the Human Pathogen <i>Lichtheimia corymbifera</i> : An Evolutionary Genomics Analysis in the Ancient Terrestrial Mucorales (Mucoromycotina). PLoS Genetics, 2014, 10, e1004496.	1.5	80
86	The Genome of the Generalist Plant Pathogen <i>Fusarium avenaceum</i> Is Enriched with Genes Involved in Redox, Signaling and Secondary Metabolism. PLoS ONE, 2014, 9, e112703.	1.1	78
87	The Tree versus the Forest: The Fungal Tree of Life and the Topological Diversity within the Yeast Phylome. PLoS ONE, 2009, 4, e4357.	1.1	77
88	Recent trends in molecular diagnostics of yeast infections: from PCR to NGS. FEMS Microbiology Reviews, 2019, 43, 517-547.	3.9	77
89	Regulation of <i>Candida glabrata</i> oxidative stress resistance is adapted to host environment. FEBS Letters, 2011, 585, 319-327.	1.3	74
90	Skin microbiome modulation induced by probiotic solutions. Microbiome, 2019, 7, 95.	4.9	74

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91	Combining data from genomes, Y2H and 3D structure indicates that BolA is a reductase interacting with a glutaredoxin. <i>FEBS Letters</i> , 2005, 579, 591-596.	1.3	73
92	Phylogenomics of the oxidative phosphorylation in fungi reveals extensive gene duplication followed by functional divergence. <i>BMC Evolutionary Biology</i> , 2009, 9, 295.	3.2	73
93	Fungal evolution: cellular, genomic and metabolic complexity. <i>Biological Reviews</i> , 2020, 95, 1198-1232.	4.7	71
94	Genome sequencing and secondary metabolism of the postharvest pathogen <i>Penicillium griseofulvum</i> . <i>BMC Genomics</i> , 2016, 17, 19.	1.2	70
95	YibK is the 2-oxo-methyltransferase TrmL that modifies the wobble nucleotide in <i>Escherichia coli</i> tRNA ^{Leu} isoacceptors. <i>Rna</i> , 2010, 16, 2131-2143.	1.6	67
96	Evidence for short-time divergence and long-time conservation of tissue-specific expression after gene duplication. <i>Briefings in Bioinformatics</i> , 2011, 12, 442-448.	3.2	67
97	PeroxisomeDB: a database for the peroxisomal proteome, functional genomics and disease. <i>Nucleic Acids Research</i> , 2007, 35, D815-D822.	6.5	65
98	Assigning duplication events to relative temporal scales in genome-wide studies. <i>Bioinformatics</i> , 2011, 27, 38-45.	1.8	65
99	Long Non-Coding RNAs As Potential Novel Prognostic Biomarkers in Colorectal Cancer. <i>Frontiers in Genetics</i> , 2016, 7, 54.	1.1	64
100	Whole-Genome Sequencing of the Opportunistic Yeast Pathogen <i>Candida inconspicua</i> Uncovers Its Hybrid Origin. <i>Frontiers in Genetics</i> , 2019, 10, 383.	1.1	63
101	Unexpected Genomic Variability in Clinical and Environmental Strains of the Pathogenic Yeast <i>Candida parapsilosis</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 2382-2392.	1.1	62
102	The kinomes of apicomplexan parasites. <i>Microbes and Infection</i> , 2012, 14, 796-810.	1.0	61
103	Timing the origin of eukaryotic cellular complexity with ancient duplications. <i>Nature Ecology and Evolution</i> , 2021, 5, 92-100.	3.4	61
104	Impact of Homologous Recombination on the Evolution of Prokaryotic Core Genomes. <i>MBio</i> , 2019, 10, .	1.8	60
105	<i>Pochonia chlamydosporia</i> Induces Plant-Dependent Systemic Resistance to <i>Meloidogyne incognita</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 945.	1.7	59
106	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus. <i>BMC Genomics</i> , 2015, 16, 461.	1.2	58
107	Biological Processes Modulating Longevity across Primates: A Phylogenetic Genome-Phenome Analysis. <i>Molecular Biology and Evolution</i> , 2018, 35, 1990-2004.	3.5	58
108	The complete genome of <i>Blastobotrys (Arxula) adenivorans</i> LS3 - a yeast of biotechnological interest. <i>Biotechnology for Biofuels</i> , 2014, 7, 66.	6.2	57

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109	Origin, diversification and substrate specificity in the family of <scp>NCS</scp>1/<scp>FUR</scp> transporters. <i>Molecular Microbiology</i> , 2015, 96, 927-950.	1.2	56
110	Inferring gene function from evolutionary change in signatures of translation efficiency. <i>Genome Biology</i> , 2014, 15, R44.	13.9	53
111	From community approaches to single-cell genomics: the discovery of ubiquitous hyperhalophilic <i>Bacteroidetes</i> generalists. <i>ISME Journal</i> , 2015, 9, 16-31.	4.4	51
112	High-Throughput Proteomics Reveals the Unicellular Roots of Animal Phosphosignaling and Cell Differentiation. <i>Developmental Cell</i> , 2016, 39, 186-197.	3.1	51
113	Differential gene retention as an evolutionary mechanism to generate biodiversity and adaptation in yeasts. <i>Scientific Reports</i> , 2015, 5, 11571.	1.6	50
114	Genomes shed light on the secret life of <i>Candida glabrata</i> : not so asexual, not so commensal. <i>Current Genetics</i> , 2019, 65, 93-98.	0.8	49
115	<i>Candida</i> pathogens induce protective mitochondria-associated type I interferon signalling and a damage-driven response in vaginal epithelial cells. <i>Nature Microbiology</i> , 2021, 6, 643-657.	5.9	49
116	Phylemon: a suite of web tools for molecular evolution, phylogenetics and phylogenomics. <i>Nucleic Acids Research</i> , 2007, 35, W38-W42.	6.5	47
117	2Å— genomes - depth does matter. <i>Genome Biology</i> , 2010, 11, R16.	13.9	47
118	Peroxisomes in parasitic protists. <i>Molecular and Biochemical Parasitology</i> , 2016, 209, 35-45.	0.5	47
119	Narrow mutational signatures drive acquisition of multidrug resistance in the fungal pathogen <i>Candida glabrata</i> . <i>Current Biology</i> , 2021, 31, 5314-5326.e10.	1.8	47
120	TACC3-TSC2 maintains nuclear envelope structure and controls cell division. <i>Cell Cycle</i> , 2010, 9, 1143-1155.	1.3	46
121	TreeKO: a duplication-aware algorithm for the comparison of phylogenetic trees. <i>Nucleic Acids Research</i> , 2011, 39, e66-e66.	6.5	46
122	Evolution of selenophosphate synthetases: emergence and relocation of function through independent duplications and recurrent subfunctionalization. <i>Genome Research</i> , 2015, 25, 1256-1267.	2.4	46
123	Hybridization and the origin of new yeast lineages. <i>FEMS Yeast Research</i> , 2020, 20, .	1.1	46
124	Genomic evidence for a hybrid origin of the yeast opportunistic pathogen <i>Candida albicans</i> . <i>BMC Biology</i> , 2020, 18, 48.	1.7	46
125	A phylogenomics approach for selecting robust sets of phylogenetic markers. <i>Nucleic Acids Research</i> , 2014, 42, e54-e54.	6.5	45
126	Secondary structure impacts patterns of selection in human lncRNAs. <i>BMC Biology</i> , 2016, 14, 60.	1.7	43

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127	Comparative transcriptomics of early dipteran development. <i>BMC Genomics</i> , 2013, 14, 123.	1.2	41
128	Utilization of selenocysteine in early-branching fungal phyla. <i>Nature Microbiology</i> , 2019, 4, 759-765.	5.9	41
129	Commercial Formulates of <i>Trichoderma</i> Induce Systemic Plant Resistance to <i>Meloidogyne incognita</i> in Tomato and the Effect Is Additive to That of the Mi-1.2 Resistance Gene. <i>Frontiers in Microbiology</i> , 2019, 10, 3042.	1.5	41
130	Interactions between Closely Related Bacterial Strains Are Revealed by Deep Transcriptome Sequencing. <i>Applied and Environmental Microbiology</i> , 2015, 81, 8445-8456.	1.4	40
131	Genome Comparisons of <i>Candida glabrata</i> Serial Clinical Isolates Reveal Patterns of Genetic Variation in Infecting Clonal Populations. <i>Frontiers in Microbiology</i> , 2019, 10, 112.	1.5	40
132	The genome sequence of the grape phylloxera provides insights into the evolution, adaptation, and invasion routes of an iconic pest. <i>BMC Biology</i> , 2020, 18, 90.	1.7	40
133	The transposable element-rich genome of the cereal pest <i>Sitophilus oryzae</i> . <i>BMC Biology</i> , 2021, 19, 241.	1.7	40
134	Structural analyses of a hypothetical minimal metabolism. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2007, 362, 1751-1762.	1.8	39
135	Complete DNA Sequence of <i>Kuraishia capsulata</i> Illustrates Novel Genomic Features among Budding Yeasts (Saccharomycotina). <i>Genome Biology and Evolution</i> , 2013, 5, 2524-2539.	1.1	39
136	<i>Lokiarchaeota</i> Marks the Transition between the Archaeal and Eukaryotic Selenocysteine Encoding Systems. <i>Molecular Biology and Evolution</i> , 2016, 33, 2441-2453.	3.5	39
137	Genomic evidence for recurrent genetic admixture during the domestication of Mediterranean olive trees (<i>Olea europaea</i> L.). <i>BMC Biology</i> , 2020, 18, 148.	1.7	39
138	The Case of the Missing Ancient Fungal Polyploids. <i>American Naturalist</i> , 2016, 188, 602-614.	1.0	38
139	Contrasting Genomic Diversity in Two Closely Related Postharvest Pathogens: <i>Penicillium digitatum</i> and <i>Penicillium expansum</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 218-227.	1.1	37
140	<i>Bacillus firmus</i> Strain I-1582, a Nematode Antagonist by Itself and Through the Plant. <i>Frontiers in Plant Science</i> , 2020, 11, 796.	1.7	37
141	The evolving species concepts used for yeasts: from phenotypes and genomes to speciation networks. <i>Fungal Diversity</i> , 2021, 109, 27-55.	4.7	37
142	Relative timing of mitochondrial endosymbiosis and the "pre-mitochondrial symbioses" hypothesis. <i>IUBMB Life</i> , 2018, 70, 1188-1196.	1.5	36
143	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018, 34, 323-329.	1.8	36
144	Evolutionary and functional patterns of shared gene neighbourhood in fungi. <i>Nature Microbiology</i> , 2019, 4, 2383-2392.	5.9	35

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145	DeathBase: a database on structure, evolution and function of proteins involved in apoptosis and other forms of cell death. <i>Cell Death and Differentiation</i> , 2010, 17, 735-736.	5.0	34
146	Impact of the Mitochondrial Genetic Background in Complex III Deficiency. <i>PLoS ONE</i> , 2010, 5, e12801.	1.1	34
147	CROSSMAPPER: estimating cross-mapping rates and optimizing experimental design in multi-species sequencing studies. <i>Bioinformatics</i> , 2020, 36, 925-927.	1.8	34
148	Coronavirus Disease 2019 (COVID-19): Emerging and Future Challenges for Dental and Oral Medicine. <i>Journal of Dental Research</i> , 2020, 99, 1113-1113.	2.5	33
149	Parental origin of the allotetraploid tobacco <i>Nicotiana benthamiana</i> . <i>Plant Journal</i> , 2020, 102, 541-554.	2.8	31
150	Trends in yeast diversity discovery. <i>Fungal Diversity</i> , 2022, 114, 491-537.	4.7	31
151	Misidentification of genome assemblies in public databases: The case of <i>Naumovozyma dairenensis</i> and proposal of a protocol to correct misidentifications. <i>Yeast</i> , 2018, 35, 425-429.	0.8	30
152	Phylogenomics of the olive tree (<i>Olea europaea</i>) reveals the relative contribution of ancient allo- and autopolyploidization events. <i>BMC Biology</i> , 2018, 16, 15.	1.7	30
153	PhylomeDB V5: an expanding repository for genome-wide catalogues of annotated gene phylogenies. <i>Nucleic Acids Research</i> , 2022, 50, D1062-D1068.	6.5	30
154	Pathogenic mutations in the 5' untranslated region of BCS1L mRNA in mitochondrial complex III deficiency. <i>Mitochondrion</i> , 2009, 9, 299-305.	1.6	29
155	Characterization of ecologically diverse viruses infecting co-occurring strains of cosmopolitan hyperhalophilic <i>Bacteroidetes</i> . <i>ISME Journal</i> , 2018, 12, 424-437.	4.4	29
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