

Xing-Xing Shen

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

3,137
citations

236925

25
h-index

345221

36
g-index

60
all docs

60
docs citations

60
times ranked

3991
citing authors

#	ARTICLE	IF	CITATIONS
1	Tempo and Mode of Genome Evolution in the Budding Yeast Subphylum. <i>Cell</i> , 2018, 175, 1533-1545.e20.	28.9	445
2	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
3	ClipKIT: A multiple sequence alignment trimming software for accurate phylogenomic inference. <i>PLoS Biology</i> , 2020, 18, e3001007.	5.6	237
4	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
5	A genome-scale phylogeny of the kingdom Fungi. <i>Current Biology</i> , 2021, 31, 1653-1665.e5.	3.9	170
6	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
7	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
8	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
9	Rooting the Animal Tree of Life. <i>Molecular Biology and Evolution</i> , 2021, 38, 4322-4333.	8.9	93
10	Multiple Genome Alignments Facilitate Development of NPCL Markers: A Case Study of Tetrapod Phylogeny Focusing on the Position of Turtles. <i>Molecular Biology and Evolution</i> , 2011, 28, 3237-3252.	8.9	89
11	Prickly waterlily and rigid hornwort genomes shed light on early angiosperm evolution. <i>Nature Plants</i> , 2020, 6, 215-222.	9.3	88
12	Genome-scale phylogeny and contrasting modes of genome evolution in the fungal phylum Ascomycota. <i>Science Advances</i> , 2020, 6, .	10.3	84
13	A Versatile and Highly Efficient Toolkit Including 102 Nuclear Markers for Vertebrate Phylogenomics, Tested by Resolving the Higher Level Relationships of the Caudata. <i>Molecular Biology and Evolution</i> , 2013, 30, 2235-2248.	8.9	76
14	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
15	Eukaryotic Acquisition of a Bacterial Operon. <i>Cell</i> , 2019, 176, 1356-1366.e10.	28.9	74
16	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
17	Evolutionary instability of CUG-Leu in the genetic code of budding yeasts. <i>Nature Communications</i> , 2018, 9, 1887.	12.8	70
18	PhyKIT: a broadly applicable UNIX shell toolkit for processing and analyzing phylogenomic data. <i>Bioinformatics</i> , 2021, 37, 2325-2331.	4.1	69

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19	Evidence for loss and reacquisition of alcoholic fermentation in a fructophilic yeast lineage. <i>ELife</i> , 2018, 7, .	6.0	67
20	Enlarged Multilocus Data set Provides Surprisingly Younger Time of Origin for the Plethodontidae, the Largest Family of Salamanders. <i>Systematic Biology</i> , 2016, 65, 66-81.	5.6	64
21	PhyloFisher: A phylogenomic package for resolving eukaryotic relationships. <i>PLoS Biology</i> , 2021, 19, e3001365.	5.6	51
22	One Thousand Two Hundred Ninety Nuclear Genes from a Genome-Wide Survey Support Lungfishes as the Sister Group of Tetrapods. <i>Molecular Biology and Evolution</i> , 2013, 30, 1803-1807.	8.9	45
23	<i>Fusarium</i> fruiting body microbiome member <i>Pantoea agglomerans</i> inhibits fungal pathogenesis by targeting lipid rafts. <i>Nature Microbiology</i> , 2022, 7, 831-843.	13.3	44
24	Multiple Reinventions of Mating-type Switching during Budding Yeast Evolution. <i>Current Biology</i> , 2019, 29, 2555-2562.e8.	3.9	33
25	An investigation of irreproducibility in maximum likelihood phylogenetic inference. <i>Nature Communications</i> , 2020, 11, 6096.	12.8	32
26	The Development of Three Long Universal Nuclear Protein-Coding Locus Markers and Their Application to Osteichthyan Phylogenetics with Nested PCR. <i>PLoS ONE</i> , 2012, 7, e39256.	2.5	28
27	Dissecting Incongruence between Concatenation- and Quartet-Based Approaches in Phylogenomic Data. <i>Systematic Biology</i> , 2021, 70, 997-1014.	5.6	28
28	Genomic features and evolution of the conditionally dispensable chromosome in the tangerine pathotype of <i>Alternaria alternata</i> . <i>Molecular Plant Pathology</i> , 2019, 20, 1425-1438.	4.2	23
29	Repeated horizontal gene transfer of <i>GAL</i> actose metabolism genes violates Dollo's law of irreversible loss. <i>Genetics</i> , 2021, 217, .	2.9	18
30	Selective base excision repair of DNA damage by the non-base-flipping DNA glycosylase AlkC. <i>EMBO Journal</i> , 2018, 37, 63-74.	7.8	17
31	The Impact of Natural Selection on the Evolution and Function of Placentally Expressed Galectins. <i>Genome Biology and Evolution</i> , 2019, 11, 2574-2592.	2.5	16
32	Recurrent Loss of <i>abaA</i> , a Master Regulator of Asexual Development in Filamentous Fungi, Correlates with Changes in Genomic and Morphological Traits. <i>Genome Biology and Evolution</i> , 2020, 12, 1119-1130.	2.5	16
33	Examination of Gene Loss in the DNA Mismatch Repair Pathway and Its Mutational Consequences in a Fungal Phylum. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	10
34	Structural Biology of the HEAT-Like Repeat Family of DNA Glycosylases. <i>BioEssays</i> , 2018, 40, e1800133.	2.5	9
35	Defining upstream enhancing and inhibiting sequence patterns for plant peroxisome targeting signal type 1 using large-scale <i>in silico</i> and <i>in vivo</i> analyses. <i>Plant Journal</i> , 2022, 111, 567-582.	5.7	5
36	Feature frequency profile-based phylogenies are inaccurate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31580-31581.	7.1	3