

# Yuanning Li

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3451928/publications.pdf>

Version: 2024-02-01

25  
papers

1,128  
citations

586496

16  
h-index

651938

25  
g-index

40  
all docs

40  
docs citations

40  
times ranked

1279  
citing authors

#	ARTICLE	IF	CITATIONS
1	BioKIT: a versatile toolkit for processing and analyzing diverse types of sequence data. <i>Genetics</i> , 2022, 221, .	1.2	13
2	Contrasting Modes of Mitochondrial Genome Evolution in Sister Taxa of Wood-Eating Marine Bivalves (Teredinidae and Xylophagaidae). <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	2
3	PhyKIT: a broadly applicable UNIX shell toolkit for processing and analyzing phylogenomic data. <i>Bioinformatics</i> , 2021, 37, 2325-2331.	1.8	69
4	A genome-scale phylogeny of the kingdom Fungi. <i>Current Biology</i> , 2021, 31, 1653-1665.e5.	1.8	170
5	Longitudinal typing of molecular HIV clusters in a statewide epidemic. <i>Aids</i> , 2021, 35, 1711-1722.	1.0	4
6	Rooting the Animal Tree of Life. <i>Molecular Biology and Evolution</i> , 2021, 38, 4322-4333.	3.5	93
7	Genomic and Phenotypic Analysis of COVID-19-Associated Pulmonary Aspergillosis Isolates of <i>Aspergillus fumigatus</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0001021.	1.2	31
8	Empirical comparison of analytical approaches for identifying molecular HIV-1 clusters. <i>Scientific Reports</i> , 2020, 10, 18547.	1.6	11
9	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.	3.3	3
10	An investigation of irreproducibility in maximum likelihood phylogenetic inference. <i>Nature Communications</i> , 2020, 11, 6096.	5.8	32
11	Genome-scale phylogeny and contrasting modes of genome evolution in the fungal phylum Ascomycota. <i>Science Advances</i> , 2020, 6, .	4.7	84
12	Mitogenomics reveals phylogenetic relationships of Arcoida (Mollusca, Bivalvia) and multiple independent expansions and contractions in mitochondrial genome size. <i>Molecular Phylogenetics and Evolution</i> , 2020, 150, 106857.	1.2	32
13	The mitochondrial genome of the bone-eating worm <i>Osedax rubiplumus</i> (Annelida, Siboglinidae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2267-2268.	0.2	2
14	First report of <i>Osedax</i> in the Indian Ocean indicative of trans-oceanic dispersal through the Southern Ocean. <i>Marine Biodiversity</i> , 2020, 50, 1.	0.3	8
15	ClipKIT: A multiple sequence alignment trimming software for accurate phylogenomic inference. <i>PLoS Biology</i> , 2020, 18, e3001007.	2.6	237
16	Life in wood: preliminary phylogeny of deep-sea wood-boring bivalves (Xylophagaidae), with descriptions of three new genera and one new species. <i>Journal of Molluscan Studies</i> , 2019, 85, 232-243.	0.4	21
17	Genomic adaptations to chemosymbiosis in the deep-sea seep-dwelling tubeworm <i>Lamellibrachia luyesi</i> . <i>BMC Biology</i> , 2019, 17, 91.	1.7	33
18	Mitogenomics Reveals a Novel Genetic Code in Hemichordata. <i>Genome Biology and Evolution</i> , 2019, 11, 29-40.	1.1	20

#	ARTICLE	IF	CITATIONS
19	Conservation of mitochondrial genome arrangements in brittle stars (Echinodermata, Ophiuroidea). <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 115-120.	1.2	18
20	Genome sequence of walking catfish ( <i>Clarias batrachus</i> ) provides insights into terrestrial adaptation. <i>BMC Genomics</i> , 2018, 19, 952.	1.2	36
21	Endosymbiont genomes yield clues of tubeworm success. <i>ISME Journal</i> , 2018, 12, 2785-2795.	4.4	33
22	Multiple introns in a deep-sea Annelid (Decemunciger: Ampharetidae) mitochondrial genome. <i>Scientific Reports</i> , 2017, 7, 4295.	1.6	21
23	Phylogenomics of tubeworms (Siboglinidae, Annelida) and comparative performance of different reconstruction methods. <i>Zoologica Scripta</i> , 2017, 46, 200-213.	0.7	33
24	Evolution of Sulfur Binding by Hemoglobin in Siboglinidae (Annelida) with Special Reference to Bone-Eating Worms, <i>Osedax</i> . <i>Journal of Molecular Evolution</i> , 2016, 82, 219-229.	0.8	5
25	Mitogenomics reveals phylogeny and repeated motifs in control regions of the deep-sea family Siboglinidae (Annelida). <i>Molecular Phylogenetics and Evolution</i> , 2015, 85, 221-229.	1.2	62