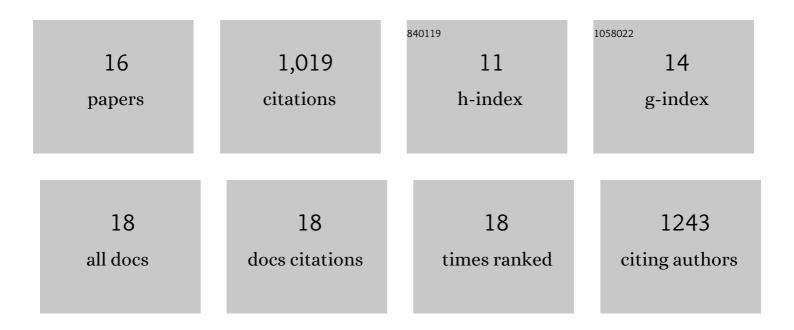
Chen-Tao Yang

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8831079/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Evolutionary and biomedical insights from a marmoset diploid genome assembly. Nature, 2021, 594, 227-233.	13.7	42
2	Ancient and modern genomes unravel the evolutionary history of the rhinoceros family. Cell, 2021, 184, 4874-4885.e16.	13.5	49
3	Callithrix jacchus (the common marmoset). Trends in Genetics, 2021, 37, 948-949.	2.9	0
4	Comparable Number of Genes Having Experienced Positive Selection among Great Ape Species. Animals, 2021, 11, 3264.	1.0	0
5	The phylogeny of leaf beetles (Chrysomelidae) inferred from mitochondrial genomes. Systematic Entomology, 2020, 45, 188-204.	1.7	56
6	Efficient COI barcoding using high throughput single-end 400 bp sequencing. BMC Genomics, 2020, 21, 862.	1.2	19
7	A draft genome assembly of spotted hyena, Crocuta crocuta. Scientific Data, 2020, 7, 126.	2.4	6
8	Diverse coral reef invertebrates exhibit patterns of phylosymbiosis. ISME Journal, 2020, 14, 2211-2222.	4.4	43
9	Genomic Analyses Provide Insights Into the Evolutionary History and Genetic Diversity of Auricularia Species. Frontiers in Microbiology, 2019, 10, 2255.	1.5	12
10	MitoZ: a toolkit for animal mitochondrial genome assembly, annotation and visualization. Nucleic Acids Research, 2019, 47, e63-e63.	6.5	593
11	Genome Sequencing of Cladobotryum protrusum Provides Insights into the Evolution and Pathogenic Mechanisms of the Cobweb Disease Pathogen on Cultivated Mushroom. Genes, 2019, 10, 124.	1.0	25
12	Characterization of viral RNA splicing using whole-transcriptome datasets from host species. Scientific Reports, 2018, 8, 3273.	1.6	10
13	Comparative Transcriptome Analysis Identified Candidate Genes Related to Bailinggu Mushroom Formation and Genetic Markers for Genetic Analyses and Breeding. Scientific Reports, 2017, 7, 9266.	1.6	50
14	Filling reference gaps via assembling DNA barcodes using high-throughput sequencing—moving toward barcoding the world. GigaScience, 2017, 6, 1-8.	3.3	18
15	Development of Novel Polymorphic EST-SSR Markers in Bailinggu (Pleurotus tuoliensis) for Crossbreeding. Genes, 2017, 8, 325.	1.0	27
16	De Novo Sequencing and Transcriptome Analysis of Pleurotus eryngii subsp. tuoliensis (Bailinggu) Mycelia in Response to Cold Stimulation. Molecules, 2016, 21, 560.	1.7	48