

# Chen-Tao Yang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8831079/publications.pdf>

Version: 2024-02-01

16  
papers

1,019  
citations

840119

11  
h-index

1058022

14  
g-index

18  
all docs

18  
docs citations

18  
times ranked

1243  
citing authors

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