

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

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18
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docs citations

18
times ranked

1243
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolutionary and biomedical insights from a marmoset diploid genome assembly. <i>Nature</i> , 2021, 594, 227-233.	13.7	42
2	Ancient and modern genomes unravel the evolutionary history of the rhinoceros family. <i>Cell</i> , 2021, 184, 4874-4885.e16.	13.5	49
3	<i>Callithrix jacchus</i> (the common marmoset). <i>Trends in Genetics</i> , 2021, 37, 948-949.	2.9	0
4	Comparable Number of Genes Having Experienced Positive Selection among Great Ape Species. <i>Animals</i> , 2021, 11, 3264.	1.0	0
5	The phylogeny of leaf beetles (Chrysomelidae) inferred from mitochondrial genomes. <i>Systematic Entomology</i> , 2020, 45, 188-204.	1.7	56
6	Efficient COI barcoding using high throughput single-end 400â€%bp sequencing. <i>BMC Genomics</i> , 2020, 21, 862.	1.2	19
7	A draft genome assembly of spotted hyena, <i>Crocuta crocuta</i> . <i>Scientific Data</i> , 2020, 7, 126.	2.4	6
8	Diverse coral reef invertebrates exhibit patterns of phyllosymbiosis. <i>ISME Journal</i> , 2020, 14, 2211-2222.	4.4	43
9	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
10	MitoZ: a toolkit for animal mitochondrial genome assembly, annotation and visualization. <i>Nucleic Acids Research</i> , 2019, 47, e63-e63.	6.5	593
11	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
12	Characterization of viral RNA splicing using whole-transcriptome datasets from host species. <i>Scientific Reports</i> , 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. <i>Scientific Reports</i> , 2017, 7, 9266.	1.6	50
14	Filling reference gaps via assembling DNA barcodes using high-throughput sequencingâ€”moving toward barcoding the world. <i>GigaScience</i> , 2017, 6, 1-8.	3.3	18
15	Development of Novel Polymorphic EST-SSR Markers in Bailinggu (<i>Pleurotus tuoliensis</i>) for Crossbreeding. <i>Genes</i> , 2017, 8, 325.	1.0	27
16	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