

Min Tang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5277698/publications.pdf>

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15
papers

3,057
citations

949033

11
h-index

1181555

14
g-index

16
all docs

16
docs citations

16
times ranked

5164
citing authors

#	ARTICLE	IF	CITATIONS
1	Tracing the origin of honey products based on metagenomics and machine learning. <i>Food Chemistry</i> , 2022, 371, 131066.	4.2	15
2	The phylogeny of leaf beetles (Chrysomelidae) inferred from mitochondrial genomes. <i>Systematic Entomology</i> , 2020, 45, 188-204.	1.7	56
3	Using full-length metabarcoding and DNA barcoding to infer community assembly for speciose taxonomic groups: a case study. <i>Evolutionary Ecology</i> , 2020, 34, 1063-1088.	0.5	2
4	First mitochondrial genomes of five hoverfly species of the genus <i>Eristalinus</i> (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622	0.9	11
5	Genome-skimming provides accurate quantification for pollen mixtures. <i>Molecular Ecology Resources</i> , 2019, 19, 1433-1446.	2.2	31
6	Performance of amplicon and shotgun sequencing for accurate biomass estimation in invertebrate community samples. <i>Molecular Ecology Resources</i> , 2018, 18, 1020-1034.	2.2	104
7	The genome of an underwater architect, the caddisfly <i>Stenopsyche tienmushanensis</i> Hwang (Insecta: Trichoptera). <i>GigaScience</i> , 2018, 7, .	3.3	41
8	Mitochondrial capture enriches mitochondrial DNA 100 fold, enabling PCR-free mitogenomics biodiversity analysis. <i>Molecular Ecology Resources</i> , 2016, 16, 470-479.	2.2	74
9	High-throughput monitoring of wild bee diversity and abundance via mitogenomics. <i>Methods in Ecology and Evolution</i> , 2015, 6, 1034-1043.	2.2	119
10	Phylogenomics resolves the timing and pattern of insect evolution. <i>Science</i> , 2014, 346, 763-767.	6.0	2,096
11	Multiplex sequencing of pooled mitochondrial genomes—a crucial step toward biodiversity analysis using mito-metagenomics. <i>Nucleic Acids Research</i> , 2014, 42, e166-e166.	6.5	230
12	Ultra-deep sequencing enables high-fidelity recovery of biodiversity for bulk arthropod samples without PCR amplification. <i>GigaScience</i> , 2013, 2, 4.	3.3	227
13	SOAP B arcode: revealing arthropod biodiversity through assembly of Illumina shotgun sequences of PCR amplicons. <i>Methods in Ecology and Evolution</i> , 2013, 4, 1142-1150.	2.2	45
14	Distinctive heat-shock response of bioleaching microorganism <i>Acidithiobacillus ferrooxidans</i> observed using genome-wide microarray. <i>Canadian Journal of Microbiology</i> , 2012, 58, 628-636.	0.8	4
15	Microbial Leaching of Copper from Tailings of Low Grade Sulphide Ores in Zambia. <i>Advanced Materials Research</i> , 0, 1130, 473-476.	0.3	2