

# Guanliang Meng

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5500697/publications.pdf>

Version: 2024-02-01

15  
papers

3,646  
citations

949033

11  
h-index

1113639

15  
g-index

22  
all docs

22  
docs citations

22  
times ranked

5799  
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylogeny and sex chromosome evolution of Palaeognathae. <i>Journal of Genetics and Genomics</i> , 2022, 49, 109-119.	1.7	10
2	Tracing the origin of honey products based on metagenomics and machine learning. <i>Food Chemistry</i> , 2022, 371, 131066.	4.2	15
3	Ancient and modern genomes unravel the evolutionary history of the rhinoceros family. <i>Cell</i> , 2021, 184, 4874-4885.e16.	13.5	49
4	Phylogenomic analysis sheds light on the evolutionary pathways towards acoustic communication in Orthoptera. <i>Nature Communications</i> , 2020, 11, 4939.	5.8	82
5	Efficient COI barcoding using high throughput single-end 400bp sequencing. <i>BMC Genomics</i> , 2020, 21, 862.	1.2	19
6	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	13.7	251
7	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
8	Comparison of the two up-to-date sequencing technologies for genome assembly: HiFi reads of Pacific Biosciences Sequel II system and ultralong reads of Oxford Nanopore. <i>GigaScience</i> , 2020, 9, .	3.3	90
9	Four myriapod relatives “ but who are sisters? No end to debates on relationships among the four major myriapod subgroups. <i>BMC Evolutionary Biology</i> , 2020, 20, 144.	3.2	13
10	Regional assemblages shaped by historical and contemporary factors: Evidence from a species-rich insect group. <i>Molecular Ecology</i> , 2020, 29, 2492-2510.	2.0	8
11	Phenotypic plasticity as a mechanism of cave colonization and adaptation. <i>ELife</i> , 2020, 9, .	2.8	48
12	MitoZ: a toolkit for animal mitochondrial genome assembly, annotation and visualization. <i>Nucleic Acids Research</i> , 2019, 47, e63-e63.	6.5	593
13	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
14	Phylogenomics resolves the timing and pattern of insect evolution. <i>Science</i> , 2014, 346, 763-767.	6.0	2,096
15	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