

Shanlin Liu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1494302/publications.pdf>

Version: 2024-02-01

50
papers

8,368
citations

168829

31
h-index

206121

51
g-index

54
all docs

54
docs citations

54
times ranked

10984
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	A super pan-genomic landscape of rice. <i>Cell Research</i> , 2022, 32, 878-896.	5.7	99
3	Viromics of extant insect orders unveil the evolution of the flavi-like superfamily. <i>Virus Evolution</i> , 2021, 7, veab030.	2.2	35
4	Genomic insights into the conservation status of the world's last remaining Sumatran rhinoceros populations. <i>Nature Communications</i> , 2021, 12, 2393.	5.8	39
5	Combining molecular datasets with strongly heterogeneous taxon coverage enlightens the peculiar biogeographic history of stoneflies (Insecta: Plecoptera). <i>Systematic Entomology</i> , 2021, 46, 952-967.	1.7	13
6	Ancient and modern genomes unravel the evolutionary history of the rhinoceros family. <i>Cell</i> , 2021, 184, 4874-4885.e16.	13.5	49
7	Evolutionary history and divergence times of Odonata (dragonflies and damselflies) revealed through transcriptomics. <i>iScience</i> , 2021, 24, 103324.	1.9	25
8	NextPolish: a fast and efficient genome polishing tool for long-read assembly. <i>Bioinformatics</i> , 2020, 36, 2253-2255.	1.8	554
9	Historical isolation facilitates species radiation by sexual selection: Insights from <i>Chorthippus</i> grasshoppers. <i>Molecular Ecology</i> , 2020, 29, 4985-5002.	2.0	18
10	Efficient COI barcoding using high throughput single-end 400bp sequencing. <i>BMC Genomics</i> , 2020, 21, 862.	1.2	19
11	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
12	Gene reuse facilitates rapid radiation and independent adaptation to diverse habitats in the Asian honeybee. <i>Science Advances</i> , 2020, 6, .	4.7	42
13	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
14	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
15	The evolutionary history of extinct and living lions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10927-10934.	3.3	70
16	An integrative phylogenomic approach to elucidate the evolutionary history and divergence times of Neuropterida (Insecta: Holometabola). <i>BMC Evolutionary Biology</i> , 2020, 20, 64.	3.2	48
17	Recent mitochondrial lineage extinction in the critically endangered Javan rhinoceros. <i>Zoological Journal of the Linnean Society</i> , 2020, 190, 372-383.	1.0	13
18	Phylogeny of Neotropical Seirinae (Collembola, Entomobryidae) based on mitochondrial genomes. <i>Zoologica Scripta</i> , 2020, 49, 329-339.	0.7	11

#	ARTICLE	IF	CITATIONS
19	The discovery of Neotropical Lepidosira (Collembola, Entomobryidae) and its systematic position. <i>Zoologica Scripta</i> , 2019, 48, 783-800.	0.7	6
20	Phylogenomics reveals the evolutionary timing and pattern of butterflies and moths. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 22657-22663.	3.3	291
21	Early Pleistocene enamel proteome from Dmanisi resolves <i>Stephanorhinus</i> phylogeny. <i>Nature</i> , 2019, 574, 103-107.	13.7	135
22	RAD-Seq data advance captive-based conservation of wild bactrian camels (<i>Camelus ferus</i>). <i>Conservation Genetics</i> , 2019, 20, 817-824.	0.8	4
23	MitoZ: a toolkit for animal mitochondrial genome assembly, annotation and visualization. <i>Nucleic Acids Research</i> , 2019, 47, e63-e63.	6.5	593
24	Phylogenomics of the superfamily Dytiscoidea (Coleoptera: Adephaga) with an evaluation of phylogenetic conflict and systematic error. <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 270-285.	1.2	36
25	An integrative phylogenomic approach illuminates the evolutionary history of cockroaches and termites (Blattodea). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182076.	1.2	143
26	The evolution and genomic basis of beetle diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24729-24737.	3.3	372
27	Re-assessing the diversity of negative strand RNA viruses in insects. <i>PLoS Pathogens</i> , 2019, 15, e1008224.	2.1	101
28	Evolutionary history of Polyneoptera and its implications for our understanding of early winged insects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 3024-3029.	3.3	150
29	New data, same story: phylogenomics does not support Syrphoidea (Diptera: Syrphidae, Pipunculidae). <i>Systematic Entomology</i> , 2018, 43, 447-459.	1.7	53
30	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
31	Transcriptome sequence-based phylogeny of chalcidoid wasps (Hymenoptera: Chalcidoidea) reveals a history of rapid radiations, convergence, and evolutionary success. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 286-296.	1.2	83
32	Identification of transcription factor genes involved in anthocyanin biosynthesis in carrot (<i>Daucus</i>). <i>Plant Physiology</i> , 2018, 178, 1011-1021.	1.2	38
33	Phylogenomics and the evolution of hemipteroid insects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12775-12780.	3.3	275
34	Evolutionary History of the Hymenoptera. <i>Current Biology</i> , 2017, 27, 1013-1018.	1.8	611
35	An expanded mammal mitogenome dataset from Southeast Asia. <i>GigaScience</i> , 2017, 6, 1-8.	3.3	27
36	Transcriptome and target DNA enrichment sequence data provide new insights into the phylogeny of vespid wasps (Hymenoptera: Aculeata: Vespidae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 116, 213-226.	1.2	87

#	ARTICLE	IF	CITATIONS
37	Positive and relaxed selection associated with flight evolution and loss in insect transcriptomes. <i>GigaScience</i> , 2017, 6, 1-14.	3.3	40
38	Orthograph: a versatile tool for mapping coding nucleotide sequences to clusters of orthologous genes. <i>BMC Bioinformatics</i> , 2017, 18, 111.	1.2	146
39	Comparative performance of the BGISEQ-500 vs Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing. <i>GigaScience</i> , 2017, 6, 1-13.	3.3	137
40	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
41	The molecular evolutionary dynamics of oxidative phosphorylation (OXPHOS) genes in Hymenoptera. <i>BMC Evolutionary Biology</i> , 2017, 17, 269.	3.2	40
42	Transcriptomic data from panarthropods shed new light on the evolution of insulator binding proteins in insects. <i>BMC Genomics</i> , 2016, 17, 861.	1.2	23
43	Evolution of neuropeptides in non-apterygote hexapods. <i>BMC Evolutionary Biology</i> , 2016, 16, 51.	3.2	63
44	Mitochondrial capture enriches mitoâ€DNA 100 fold, enabling PCRâ€free mitogenomics biodiversity analysis. <i>Molecular Ecology Resources</i> , 2016, 16, 470-479.	2.2	74
45	Highâ€throughput monitoring of wild bee diversity and abundance via mitogenomics. <i>Methods in Ecology and Evolution</i> , 2015, 6, 1034-1043.	2.2	119
46	Phylogenomics resolves the timing and pattern of insect evolution. <i>Science</i> , 2014, 346, 763-767.	6.0	2,096
47	Multiplex sequencing of pooled mitochondrial genomesâ€”a crucial step toward biodiversity analysis using mito-metagenomics. <i>Nucleic Acids Research</i> , 2014, 42, e166-e166.	6.5	230
48	SOAPdenovo-Trans: <i>de novo</i> transcriptome assembly with short RNA-Seq reads. <i>Bioinformatics</i> , 2014, 30, 1660-1666.	1.8	826
49	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
50	SOAP B arcade: 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