

Bin Chen

List of Publications by Year in descending order

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Version: 2024-02-01

75
papers

2,879
citations

257450

24
h-index

175258

52
g-index

78
all docs

78
docs citations

78
times ranked

3709
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | First report of complete mitochondrial genome in the subfamily Alleculinae and mitochondrial genome-based phylogenetics in Tenebrionidae (Coleoptera: Tenebrionoidea). <i>Insect Science</i> , 2022, 29, 1226-1238. | 3.0 | 8 |
| 2 | Complete mitochondrial genome of <i>Parnassius glacialis</i> (Lepidoptera: Papilionidae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 478-479. | 0.4 | 0 |
| 3 | Repellency and insecticidal activity of seven Mugwort (<i>Artemisia argyi</i>) essential oils against the malaria vector <i>Anopheles sinensis</i> . <i>Scientific Reports</i> , 2022, 12, 5337. | 3.3 | 19 |
| 4 | A revision of the genus <i>Jucancistrocerus</i> Blüthgen, 1938 from China, with review of three related genera (Hymenoptera: Vespidae: Eumeninae). <i>Zootaxa</i> , 2022, 5105, 401-420. | 0.5 | 2 |
| 5 | Genome-wide identification and expression profiling of odorant receptor genes in the malaria vector <i>Anopheles sinensis</i> . <i>Parasites and Vectors</i> , 2022, 15, 143. | 2.5 | 4 |
| 6 | CRISPR/Cas9 mediates efficient site-specific mutagenesis of the odorant receptor co-receptor (<i>Orco</i>) in the malaria vector <i>Anopheles sinensis</i> . <i>Pest Management Science</i> , 2022, 78, 3294-3304. | 3.4 | 9 |
| 7 | Mitochondrial composition of and diffusion limiting factors of three social wasp genera <i>Polistes</i> , <i>Ropalidia</i> , and <i>parapolybia</i> (Hymenoptera: Vespidae). <i>Bmc Ecology and Evolution</i> , 2022, 22, 63. | 1.6 | 2 |
| 8 | Glutathione S-transferase (GST) genes and their function associated with pyrethroid resistance in the malaria vector <i>Anopheles sinensis</i> . <i>Pest Management Science</i> , 2022, 78, 4127-4139. | 3.4 | 13 |
| 9 | Complete mitochondrial genomes of <i>Papilio nephelus chaon</i> and <i>Papilio epycides</i> (Lepidoptera: Papilionidae: Papilioninae) and phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 1203-1205. | 0.4 | 0 |
| 10 | piggyBac-mediated germline transformation of the malaria mosquito <i>Anopheles sinensis</i> (Diptera: Culicidae). <i>Insect Science</i> , 2021, 28, 1202-1206. | 3.0 | 9 |
| 11 | Electroporation-mediated nucleic acid delivery during non-embryonic stages for gene-function analysis in <i>Anopheles sinensis</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2021, 128, 103500. | 2.7 | 4 |
| 12 | First mtgenome sequences from three genera and phylogenetic relationships of the family Apidae based on mtgenome sequences (Hymenoptera: Apoidea). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1157-1159. | 0.4 | 1 |
| 13 | ASDB: A comprehensive omics database for <i>Anopheles sinensis</i> . <i>Genomics</i> , 2021, 113, 976-982. | 2.9 | 2 |
| 14 | Three new species of the subgenus <i>Jaynesia</i> Allen, 1969 of the genus <i>Tiphia</i> Fabricius, 1775 (Hymenoptera: Tiphiidae: Tiphiinae) from China, with a key to all known species. <i>Zootaxa</i> , 2021, 4970, 313-324. | 0.5 | 3 |
| 15 | A review of the genus <i>Bothynogria</i> Borchmann, 1915 with descriptions of one new species and two new record species from China (Coleoptera: Tenebrionidae: Lagriinae: Lagriini: Lagriina). <i>Journal of Asia-Pacific Entomology</i> , 2021, 24, 716-723. | 0.9 | 1 |
| 16 | Complete mitogenomes of <i>Anopheles peditaeniatus</i> and <i>Anopheles nitidus</i> and phylogenetic relationships within the genus <i>Anopheles</i> inferred from mitogenomes. <i>Parasites and Vectors</i> , 2021, 14, 452. | 2.5 | 8 |
| 17 | Two newly recorded genera <i>Malayepipona</i> Giordani Soika and <i>Megaodynerus</i> Gusenleitner, with eight new species from China (Hymenoptera, Vespidae, Eumeninae). <i>Zootaxa</i> , 2021, 5060, 371-391. | 0.5 | 1 |
| 18 | The complete mitogenome of the <i>Paranticropsis xenocles</i> (Lepidoptera: Papilionidae: Papilioninae) and phylogenetic implications. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3346-3347. | 0.4 | 0 |

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|----|---|-----|-----------|
| 19 | Mitochondrial genes associated with pyrethroid resistance revealed by mitochondrial genome and transcriptome analyses in the malaria vector <i>Anopheles sinensis</i> (Diptera: Culicidae). <i>Pest Management Science</i> , 2020, 76, 769-778. | 3.4 | 7 |
| 20 | Excess melanin precursors rescue defective cuticular traits in stony mutant silkworms probably by upregulating four genes encoding RR1-type larval cuticular proteins. <i>Insect Biochemistry and Molecular Biology</i> , 2020, 119, 103315. | 2.7 | 7 |
| 21 | Identification and molecular characterization of <i>Wolbachia</i> strains in natural populations of <i>Aedes albopictus</i> in China. <i>Parasites and Vectors</i> , 2020, 13, 28. | 2.5 | 30 |
| 22 | Taxonomy of the genus <i>Epsilon</i> from China, with a new species and an updated key to the Oriental species (Hymenoptera, Vespidae, Eumeninae). <i>ZooKeys</i> , 2020, 910, 131-142. | 1.1 | 2 |
| 23 | The complete mt genomes of <i>Lutzia halifaxia</i> , <i>Lt. fuscus</i> and <i>Culex pallidothorax</i> (Diptera: Culicidae) and comparative analysis of 16 <i>Culex</i> and <i>Lutzia</i> mt genome sequences. <i>Parasites and Vectors</i> , 2019, 12, 368. | 2.5 | 15 |
| 24 | The first divergence time estimation of the subfamily Stenogastrinae (Hymenoptera: Vespidae) based on mitochondrial phylogenomics. <i>International Journal of Biological Macromolecules</i> , 2019, 137, 767-773. | 7.5 | 13 |
| 25 | Complete mitochondrial genomes of <i>Anopheles aconitus</i> and <i>Anopheles splendidus</i> and phylogenetics analysis of known mtgenomes in the subgenus <i>Cellia</i> (Diptera: Culicidae: Tj ETQq1 1 0.784314 rgBT /Overlock 10 | | |
| 26 | ATP-Binding Cassette (ABC) Transporter Genes Involved in Pyrethroid Resistance in the Malaria Vector <i>Anopheles sinensis</i> : Genome-Wide Identification, Characteristics, Phylogenetics, and Expression Profile. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1409. | 4.1 | 33 |
| 27 | UDP-glycosyltransferase genes and their association and mutations associated with pyrethroid resistance in <i>Anopheles sinensis</i> (Diptera: Culicidae). <i>Malaria Journal</i> , 2019, 18, 62. | 2.3 | 46 |
| 28 | Modification of contact avoidance behaviour associated with pyrethroid resistance in <i>Anopheles sinensis</i> (Diptera: Culicidae). <i>Malaria Journal</i> , 2019, 18, 131. | 2.3 | 9 |
| 29 | HSP superfamily of genes in the malaria vector <i>Anopheles sinensis</i> : diversity, phylogenetics and association with pyrethroid resistance. <i>Malaria Journal</i> , 2019, 18, 132. | 2.3 | 17 |
| 30 | Comparative analyses of simple sequence repeats (SSRs) in 23 mosquito species genomes: Identification, characterization and distribution (Diptera: Culicidae). <i>Insect Science</i> , 2019, 26, 607-619. | 3.0 | 26 |
| 31 | Genome-wide and expression profiling analyses suggest the main cytochrome P450 genes related to pyrethroid resistance in the malaria vector, <i>Anopheles sinensis</i> (Diptera Culicidae). <i>Pest Management Science</i> , 2018, 74, 1810-1820. | 3.4 | 27 |
| 32 | Sialotranscriptome sequencing and analysis of <i>Anopheles sinensis</i> and comparison with <i>Psorophora albipes</i> sialotranscriptome (Diptera: Culicidae). <i>Insect Science</i> , 2018, 25, 368-378. | 3.0 | 1 |
| 33 | Genome-wide identification, characterization and evolution of cuticular protein genes in the malaria vector <i>Anopheles sinensis</i> (Diptera: Culicidae). <i>Insect Science</i> , 2018, 25, 739-750. | 3.0 | 13 |
| 34 | Identification of carboxylesterase genes associated with pyrethroid resistance in the malaria vector <i>Anopheles sinensis</i> (Diptera: Culicidae). <i>Pest Management Science</i> , 2018, 74, 159-169. | 3.4 | 26 |
| 35 | Descriptions of four new species of <i>Pararrhynchium</i> de Saussure (Hymenoptera: Vespidae: Tj ETQq1 1 0.784314 rgBT /Overlock 10 2018, 52, 175-189. | 0.3 | 2 |
| 36 | Global Transcriptome Sequencing Reveals Molecular Profiles of Summer Diapause Induction Stage of Onion Maggot, <i>Delia antiqua</i> (Diptera: Anthomyiidae). <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 207-217. | 1.8 | 38 |

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|----|--|-----|-----------|
| 37 | Complete mitogenome of <i>Anopheles sinensis</i> and mitochondrial insertion segments in the nuclear genomes of 19 mosquito species. <i>PLoS ONE</i> , 2018, 13, e0204667. | 2.5 | 10 |
| 38 | Genome-wide identification, characterization and classification of ionotropic glutamate receptor genes (iGluRs) in the malaria vector <i>Anopheles sinensis</i> (Diptera: Culicidae). <i>Parasites and Vectors</i> , 2018, 11, 34. | 2.5 | 14 |
| 39 | Subcellular stoichiogenomics reveal cell evolution and electrostatic interaction mechanisms in cytoskeleton. <i>BMC Genomics</i> , 2018, 19, 469. | 2.8 | 8 |
| 40 | Comparative genomics of chemosensory protein genes (CSPs) in twenty-two mosquito species (Diptera: Tj ETQq0,0,0 rgBT /Overlock 1 | 2.5 | 25 |
| 41 | The complete mitochondrial genome of <i>Orancistrocerus aterrimus aterrimus</i> and comparative analysis in the family Vespidae (Hymenoptera, Vespidae, Eumeninae). <i>ZooKeys</i> , 2018, 790, 127-144. | 1.1 | 6 |
| 42 | Complete mitochondrial genomes of <i>Anopheles stephensi</i> and <i>An. dirus</i> and comparative evolutionary mitochondriomics of 50 mosquitoes. <i>Scientific Reports</i> , 2017, 7, 7666. | 3.3 | 47 |
| 43 | Wingless is a positive regulator of eyespot color patterns in <i>Bicyclus anynana</i> butterflies. <i>Developmental Biology</i> , 2017, 429, 177-185. | 2.0 | 53 |
| 44 | Sequencing and analysis of the complete mitochondrial genome of <i>Culex gelidus</i> (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 | 0.4 | 2 |
| 45 | Suppression of Laccase 2 severely impairs cuticle tanning and pathogen resistance during the pupal metamorphosis of <i>Anopheles sinensis</i> (Diptera: Culicidae). <i>Parasites and Vectors</i> , 2017, 10, 171. | 2.5 | 38 |
| 46 | The mitochondrial genomes of <i>Culex tritaeniorhynchus</i> and <i>Culex pipiens pallens</i> (Diptera: Culicidae) and comparison analysis with two other <i>Culex</i> species. <i>Parasites and Vectors</i> , 2016, 9, 406. | 2.5 | 22 |
| 47 | Genome-wide identification and characterization of odorant-binding protein (OBP) genes in the malaria vector <i>Anopheles sinensis</i> (Diptera: Culicidae). <i>Insect Science</i> , 2016, 23, 366-376. | 3.0 | 30 |
| 48 | The complete mitochondrial genome of <i>Anopheles minimus</i> (Diptera: Culicidae) and the phylogenetics of known <i>Anopheles</i> mitogenomes. <i>Insect Science</i> , 2016, 23, 353-365. | 3.0 | 21 |
| 49 | Insight into the possible mechanism of the summer diapause of <i>Delia antiqua</i> (Diptera: Anthomyiidae) through digital gene expression analysis. <i>Insect Science</i> , 2016, 23, 438-451. | 3.0 | 50 |
| 50 | Leap forward with insect genomics. <i>Insect Science</i> , 2016, 23, 332-334. | 3.0 | 0 |
| 51 | Tyrosine Hydroxylase is crucial for maintaining pupal tanning and immunity in <i>Anopheles sinensis</i> . <i>Scientific Reports</i> , 2016, 6, 29835. | 3.3 | 34 |
| 52 | <i>Distal-less</i> homeobox genes of insects and spiders: genomic organization, function, regulation and evolution. <i>Insect Science</i> , 2016, 23, 335-352. | 3.0 | 9 |
| 53 | Sequencing and analysis of the complete mitochondrial genome in <i>Anopheles culicifacies</i> species B (Diptera: Culicidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2909-2910. | 0.7 | 11 |
| 54 | A taxonomic account of the genus <i>Stenodynerus</i> from China, with descriptions of five new species (Hymenoptera, Vespidae, Eumeninae). <i>ZooKeys</i> , 2016, 595, 17-48. | 1.1 | 5 |

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|----|---|-----|-----------|
| 55 | Simultaneous quantitative analysis of multi-compounds by a single marker in Radix Astragali by using serum HPLC-MS feature. Pakistan Journal of Pharmaceutical Sciences, 2016, 29, 1243-9. | 0.2 | 1 |
| 56 | Evaluation of Aucklandia lappa Decne extracts as antiulcer activity in animals. Pakistan Journal of Pharmaceutical Sciences, 2016, 29, 1695-1701. | 0.2 | 1 |
| 57 | The Complete Mitochondrial Genome of Delia antiqua and Its Implications in Dipteran Phylogenetics. PLoS ONE, 2015, 10, e0139736. | 2.5 | 17 |
| 58 | Gene cloning, characterization and expression and enzymatic activities related to trehalose metabolism during diapause of the onion maggot Delia antiqua (Diptera: Anthomyiidae). Gene, 2015, 565, 106-115. | 2.2 | 28 |
| 59 | Notes on the genus Xenoceroogia (Coleoptera, Tenebrionidae, Lagriini) from China. ZooKeys, 2014, 451, 93-108. | 1.1 | 4 |
| 60 | The taxonomic accounts of the genus Symmorphus Wesmael (Hymenoptera, Vespidae, Eumeninae) from China, with descriptions of three new species. ZooKeys, 2014, 389, 9-26. | 1.1 | 7 |
| 61 | The de novo Transcriptome and Its Analysis in the Worldwide Vegetable Pest, Delia antiqua (Diptera: Tj ETQq1 1 0.784314 rgBT /Ove | 1.8 | 16 |
| 62 | A Method for Inducible Gene Over-Expression and Down-Regulation in Emerging Model Species Using Pogostick. Methods in Molecular Biology, 2014, 1101, 249-266. | 0.9 | 0 |
| 63 | De novo transcriptome sequencing and sequence analysis of the malaria vector Anopheles sinensis (Diptera: Culicidae). Parasites and Vectors, 2014, 7, 314. | 2.5 | 29 |
| 64 | Macroevolutionary trends of atomic composition and related functional group proportion in eukaryotic and prokaryotic proteins. Gene, 2014, 534, 163-168. | 2.2 | 7 |
| 65 | <i>Distal</i> Regulates Eyespot Patterns and Melanization in <i>Bicyclus</i> Butterflies. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2013, 320, 321-331. | 1.3 | 74 |
| 66 | The Anopheles community and the role of Anopheles minimus on malaria transmission on the China-Myanmar border. Parasites and Vectors, 2013, 6, 264. | 2.5 | 37 |
| 67 | Relationship between Knockdown Resistance, Metabolic Detoxification and Organismal Resistance to Pyrethroids in Anopheles sinensis. PLoS ONE, 2013, 8, e55475. | 2.5 | 61 |
| 68 | Population genetics of the malaria vector Anopheles aconitus in China and Southeast Asia. Infection, Genetics and Evolution, 2012, 12, 1958-1967. | 2.3 | 6 |
| 69 | Permanent Genetic Resources added to Molecular Ecology Resources Database 1 April 2011-31 May 2011. Molecular Ecology Resources, 2011, 11, 935-936. | 4.8 | 8 |
| 70 | Guidelines for the nomenclature of the human heat shock proteins. Cell Stress and Chaperones, 2009, 14, 105-111. | 2.9 | 1,105 |
| 71 | Comparative genomics and evolution of the HSP90 family of genes across all kingdoms of organisms. BMC Genomics, 2006, 7, 156. | 2.8 | 271 |
| 72 | Cloning and Characterization of the HSP70 Gene, and Its Expression in Response to Diapauses and Thermal Stress in the Onion Maggot, Delia antiqua. BMB Reports, 2006, 39, 749-758. | 2.4 | 36 |

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|----|--|-----|-----------|
| 73 | DaTrypsin, a novel clip-domain serine proteinase gene up-regulated during winter and summer diapauses of the onion maggot, <i>Delia antiqua</i> . <i>Gene</i> , 2005, 347, 115-123. | 2.2 | 39 |
| 74 | The HSP90 family of genes in the human genome: Insights into their divergence and evolution. <i>Genomics</i> , 2005, 86, 627-637. | 2.9 | 317 |
| 75 | Molecular phylogenetics of the Oriental members of the <i>Myzomyia</i> Series of <i>Anopheles</i> subgenus <i>Cellia</i> (Diptera: Culicidae) inferred from nuclear and mitochondrial DNA sequences. <i>Systematic Entomology</i> , 2003, 28, 57-69. | 3.9 | 31 |