

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	Guidelines for the nomenclature of the human heat shock proteins. <i>Cell Stress and Chaperones</i> , 2009, 14, 105-111.	2.9	1,105
2	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
3	Comparative genomics and evolution of the HSP90 family of genes across all kingdoms of organisms. <i>BMC Genomics</i> , 2006, 7, 156.	2.8	271
4	<i>Distal-less</i> Regulates Eyespot Patterns and Melanization in <i>Bicyclus</i> Butterflies. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2013, 320, 321-331.	1.3	74
5	Relationship between Knockdown Resistance, Metabolic Detoxification and Organismal Resistance to Pyrethroids in <i>Anopheles sinensis</i> . <i>PLoS ONE</i> , 2013, 8, e55475.	2.5	61
6	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
7	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
8	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
9	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
10	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
11	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
12	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
13	The <i>Anopheles</i> community and the role of <i>Anopheles minimus</i> on malaria transmission on the China-Myanmar border. <i>Parasites and Vectors</i> , 2013, 6, 264.	2.5	37
14	Cloning and Characterization of the HSP70 Gene, and Its Expression in Response to Diapauses and Thermal Stress in the Onion Maggot, <i>Delia antiqua</i> . <i>BMB Reports</i> , 2006, 39, 749-758.	2.4	36
15	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
16	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
17	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
18	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

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19	Identification and molecular characterization of Wolbachia strains in natural populations of <i>Aedes albopictus</i> in China. <i>Parasites and Vectors</i> , 2020, 13, 28.	2.5	30
20	De novo transcriptome sequencing and sequence analysis of the malaria vector <i>Anopheles sinensis</i> (Diptera: Culicidae). <i>Parasites and Vectors</i> , 2014, 7, 314.	2.5	29
21	Gene cloning, characterization and expression and enzymatic activities related to trehalose metabolism during diapause of the onion maggot <i>Delia antiqua</i> (Diptera: Anthomyiidae). <i>Gene</i> , 2015, 565, 106-115.	2.2	28
22	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
23	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
24	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
25	Comparative genomics of chemosensory protein genes (CSPs) in twenty-two mosquito species (Diptera: Tj ETQq1.1 0.784314 rgBT /Ove	2.5	25
26	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
27	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
28	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
29	The Complete Mitochondrial Genome of <i>Delia antiqua</i> and Its Implications in Dipteran Phylogenetics. <i>PLoS ONE</i> , 2015, 10, e0139736.	2.5	17
30	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
31	The de novo Transcriptome and Its Analysis in the Worldwide Vegetable Pest, <i>Delia antiqua</i> (Diptera: Tj ETQq1.1 0.784314 rgBT /Ove	1.8	16
32	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
33	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
34	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
35	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
36	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

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37	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
38	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
39	<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
40	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
41	<i>piggyBac</i> -mediated germline transformation of the malaria mosquito <i>Anopheles sinensis</i> (Diptera: Culicidae). <i>Insect Science</i> , 2021, 28, 1202-1206.	3.0	9
42	<i>CRISPR/Cas9</i> 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
43	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 April 2011-31 May 2011. <i>Molecular Ecology Resources</i> , 2011, 11, 935-936.	4.8	8
44	Subcellular stoichiogenomics reveal cell evolution and electrostatic interaction mechanisms in cytoskeleton. <i>BMC Genomics</i> , 2018, 19, 469.	2.8	8
45	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
46	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
47	The taxonomic accounts of the genus <i>Symmorphus</i> Wesmael (Hymenoptera, Vespidae, Eumeninae) from China, with descriptions of three new species. <i>ZooKeys</i> , 2014, 389, 9-26.	1.1	7
48	Macroevolutionary trends of atomic composition and related functional group proportion in eukaryotic and prokaryotic proteins. <i>Gene</i> , 2014, 534, 163-168.	2.2	7
49	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
50	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
51	Population genetics of the malaria vector <i>Anopheles aconitus</i> in China and Southeast Asia. <i>Infection, Genetics and Evolution</i> , 2012, 12, 1958-1967.	2.3	6
52	The complete mitochondrial genome of <i>Orancistrocerus aterrimus</i> and comparative analysis in the family Vespidae (Hymenoptera, Vespidae, Eumeninae). <i>ZooKeys</i> , 2018, 790, 127-144.	1.1	6
53	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
54	Notes on the genus <i>Xenoceroxia</i> (Coleoptera, Tenebrionidae, Lagriini) from China. <i>ZooKeys</i> , 2014, 451, 93-108.	1.1	4

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55	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
56	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
57	Three new species of the subgenus <i>Jaynesia</i> Allen, 1969 of the genus <i>Tiphia</i> Fabricius, 1775 (Hymenoptera: Tiphidae: Tiphinae) from China, with a key to all known species . <i>Zootaxa</i> , 2021, 4970, 313-324.	0.5	3
58	Sequencing and analysis of the complete mitochondrial genome of <i>Culex gelidus</i> (Diptera: Culexini). <i>Open Access Library Journal</i> , 2021, 10, 1-10.	0.4	2
59	Descriptions of four new species of <i>Pararrhynchium</i> de Saussure (Hymenoptera: Vespidae). <i>Zootaxa</i> , 2018, 52, 175-189.	0.3	2
60	ASDB: A comprehensive omics database for <i>Anopheles sinensis</i> . <i>Genomics</i> , 2021, 113, 976-982.	2.9	2
61	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
62	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
63	Mitochondrial composition 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
64	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
65	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
66	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
67	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
68	Simultaneous quantitative analysis of multi-compounds by a single marker in <i>Radix Astragali</i> by using serum HPLC-MS feature. <i>Pakistan Journal of Pharmaceutical Sciences</i> , 2016, 29, 1243-9.	0.2	1
69	Evaluation of <i>Aucklandia lappa</i> Decne extracts as antiulcer activity in animals. <i>Pakistan Journal of Pharmaceutical Sciences</i> , 2016, 29, 1695-1701.	0.2	1
70	A Method for Inducible Gene Over-Expression and Down-Regulation in Emerging Model Species Using Pogostick. <i>Methods in Molecular Biology</i> , 2014, 1101, 249-266.	0.9	0
71	Leap forward with insect genomics. <i>Insect Science</i> , 2016, 23, 332-334.	3.0	0
72	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). <i>Open Access Library Journal</i> , 2021, 10, 1-10.	0.4	2

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73	The complete mitogenome of the <i>Paranticopsis xenocles</i> (Lepidoptera: Papilionidae: Papilioninae) and phylogenetic implications. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3346-3347.	0.4	0
74	Complete mitochondrial genome of <i>Parnassius glacialis</i> (Lepidoptera: Papilionidae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 478-479.	0.4	0
75	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