

Shu-Jun Wei

List of Publications by Year in descending order

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104
papers

2,708
citations

218381

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223531

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110
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1990
citing authors

#	ARTICLE	IF	CITATIONS
1	Lack of Genetic Structure Among Populations of Striped Flea Beetle <i>Phyllotreta striolata</i> (Coleoptera: Tj ETQq1 1 0,784314 rgBT /Over	1.1	6
2	Population genomic signatures of the oriental fruit moth related to the Pleistocene climates. <i>Communications Biology</i> , 2022, 5, 142.	2.0	6
3	Toxicity and Control Efficacy of an Organosilicone to the Two-Spotted Spider Mite <i>Tetranychus urticae</i> and Its Crop Hosts. <i>Insects</i> , 2022, 13, 341.	1.0	3
4	Chromosomal-level genome of a sheet- <i>web</i> spider provides insight into the composition and evolution of venom. <i>Molecular Ecology Resources</i> , 2022, 22, 2333-2348.	2.2	10
5	Increasing Frequency of G275E Mutation in the Nicotinic Acetylcholine Receptor $\alpha 6$ Subunit Conferring Spinetoram Resistance in Invading Populations of Western Flower Thrips in China. <i>Insects</i> , 2022, 13, 331.	1.0	9
6	Population differentiation and intraspecific genetic admixture in two <i>Eucryptorrhynchus</i> weevils (Coleoptera: Curculionidae) across northern China. <i>Ecology and Evolution</i> , 2022, 12, e8806.	0.8	0
7	Geographical and interspecific variation in susceptibility of three common thrips species to the insecticide, spinetoram. <i>Journal of Pest Science</i> , 2021, 94, 93-99.	1.9	27
8	Migration trajectories of the diamondback moth <i>Plutella xylostella</i> in China inferred from population genomic variation. <i>Pest Management Science</i> , 2021, 77, 1683-1693.	1.7	18
9	Chromosome-level genome assembly of the aphid parasitoid <i>Aphidius gifuensis</i> using Oxford Nanopore sequencing and Hi-C technology. <i>Molecular Ecology Resources</i> , 2021, 21, 941-954.	2.2	10
10	Chromosome-level genome of the peach fruit moth <i>Carposina sasakii</i> (Lepidoptera: Carposinidae) provides a resource for evolutionary studies on moths. <i>Molecular Ecology Resources</i> , 2021, 21, 834-848.	2.2	25
11	Association Between Susceptibility of Thrips <i>palmi</i> to Spinetoram and Frequency of G275E Mutation Provides Basis for Molecular Quantification of Field-Evolved Resistance. <i>Journal of Economic Entomology</i> , 2021, 114, 339-347.	0.8	6
12	Low levels of genetic differentiation with isolation by geography and environment in populations of <i>Drosophila melanogaster</i> from across China. <i>Heredity</i> , 2021, 126, 942-954.	1.2	5
13	Comparative mitogenomics and phylogenetics of the stinging wasps (Hymenoptera: Aculeata). <i>Molecular Phylogenetics and Evolution</i> , 2021, 159, 1071-1079.	1.2	13
14	Local climate adaptation and gene flow in the native range of two co-occurring fruit moths with contrasting invasiveness. <i>Molecular Ecology</i> , 2021, 30, 4204-4219.	2.0	12
15	Research and development of the longitudinal feedback system digital signal processing electronics in BEPCII. <i>Radiation Detection Technology and Methods</i> , 2021, 5, 213-219.	0.4	0
16	First development and characterization of 27 novel microsatellite markers in the dobsonfly <i>Neoneuromus ignobilis</i> (Megaloptera: Corydalidae) at genome-scale level. <i>Applied Entomology and Zoology</i> , 2020, 55, 149-158.	0.6	3
17	Effects of chlorantraniliprole and chromafenozide on mortality and feeding cessation of the fall webworm, <i>Hyphantria cunea</i> (Lepidoptera: Arctiidae). <i>Journal of Asia-Pacific Entomology</i> , 2020, 23, 1067-1072.	0.4	2
18	Similar Gut Bacterial Microbiota in Two Fruit-Feeding Moth Pests Collected from Different Host Species and Locations. <i>Insects</i> , 2020, 11, 840.	1.0	8

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19	Geographic patterns of <i>Lucanus</i> (Coleoptera: Lucanidae) species diversity and environmental determinants in China. <i>Ecology and Evolution</i> , 2020, 10, 13190-13197.	0.8	4
20	Chromosome-level assembly of the melon thrips genome yields insights into evolution of a sap-sucking lifestyle and pesticide resistance. <i>Molecular Ecology Resources</i> , 2020, 20, 1110-1125.	2.2	31
21	Variable resistance to spinetoram in populations of <i>Thrips palmi</i> across a small area unconnected to genetic similarity. <i>Evolutionary Applications</i> , 2020, 13, 2234-2245.	1.5	15
22	Increased density of endosymbiotic Buchnera related to pesticide resistance in yellow morph of melon aphid. <i>Journal of Pest Science</i> , 2020, 93, 1281-1294.	1.9	17
23	Rapid and strong population genetic differentiation and genomic signatures of climatic adaptation in an invasive mealybug. <i>Diversity and Distributions</i> , 2020, 26, 610-622.	1.9	15
24	Strong genetic differentiation among populations of <i>Cheirotonus gestroi</i> (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 547 Mapping, Sequencing, and Analysis, 2020, 31, 108-119.	0.7	3
25	Population analysis reveals genetic structure of an invasive agricultural thrips pest related to invasion of greenhouses and suitable climatic space. <i>Evolutionary Applications</i> , 2019, 12, 1868-1880.	1.5	21
26	Genome-wide developed microsatellites reveal a weak population differentiation in the hoverfly <i>Eupeodes corollae</i> (Diptera: Syrphidae) across China. <i>PLoS ONE</i> , 2019, 14, e0215888.	1.1	9
27	Design of RF front end of digital BPM for BEPCII. <i>Radiation Detection Technology and Methods</i> , 2019, 3, 1.	0.4	2
28	Field-evolved resistance and cross-resistance of the two-spotted spider mite, <i>Tetranychus urticae</i> , to bifentazate, cyenopyrafen and SYP-9625. <i>Experimental and Applied Acarology</i> , 2019, 77, 545-554.	0.7	17
29	Independently evolved and gene flow-accelerated pesticide resistance in two-spotted spider mites. <i>Ecology and Evolution</i> , 2019, 9, 2206-2219.	0.8	19
30	The genomes of two parasitic wasps that parasitize the diamondback moth. <i>BMC Genomics</i> , 2019, 20, 893.	1.2	17
31	Development of novel microsatellites for population genetic analysis of <i>Phenacoccus solenopsis</i> Tinsley (Hemiptera: Pseudococcidae) based on genomic analysis. <i>International Journal of Biological Macromolecules</i> , 2019, 121, 1135-1144.	3.6	7
32	Mitochondrial phylogenomics of the Hymenoptera. <i>Molecular Phylogenetics and Evolution</i> , 2019, 131, 8-18.	1.2	104
33	Gene arrangement and sequence of mitochondrial genomes yield insights into the phylogeny and evolution of bees and sphecid wasps (Hymenoptera: Apoidea). <i>Molecular Phylogenetics and Evolution</i> , 2018, 124, 1-9.	1.2	49
34	Laboratory selection for resistance to sulfoxaflor and fitness costs in the green peach aphid <i>Myzus persicae</i> . <i>Journal of Asia-Pacific Entomology</i> , 2018, 21, 408-412.	0.4	38
35	Extensive gene rearrangements in the mitochondrial genomes of two egg parasitoids, <i>Trichogramma japonicum</i> and <i>Trichogramma ostrinae</i> (Hymenoptera: Chalcidoidea: Trichogrammatidae). <i>Scientific Reports</i> , 2018, 8, 7034.	1.6	38
36	Efficacy of carbon dioxide treatments for the control of the two-spotted spider mite, <i>Tetranychus urticae</i> , and treatment impact on plant seedlings. <i>Experimental and Applied Acarology</i> , 2018, 75, 143-153.	0.7	3

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37	Preference and performance of the two-spotted spider mite <i>Tetranychus urticae</i> (Acari: Tetranychidae) on strawberry cultivars. <i>Experimental and Applied Acarology</i> , 2018, 76, 185-196.	0.7	16
38	Multiple refugia from penultimate glaciations in East Asia demonstrated by phylogeography and ecological modelling of an insect pest. <i>BMC Evolutionary Biology</i> , 2018, 18, 152.	3.2	26
39	Toxicity of seven insecticides to different developmental stages of the whitefly <i>Bemisia tabaci</i> MED (Hemiptera: Aleyrodidae) in multiple field populations of China. <i>Ecotoxicology</i> , 2018, 27, 742-751.	1.1	23
40	The first two mitochondrial genomes of the family Aphelinidae with novel gene orders and phylogenetic implications. <i>International Journal of Biological Macromolecules</i> , 2018, 118, 386-396.	3.6	23
41	Parasitic insect-derived miRNAs modulate host development. <i>Nature Communications</i> , 2018, 9, 2205.	5.8	77
42	Low genetic diversity but strong population structure reflects multiple introductions of western flower thrips (Thysanoptera: Thripidae) into China followed by human-mediated spread. <i>Evolutionary Applications</i> , 2017, 10, 391-401.	1.5	35
43	Mitochondrial genomes of the hoverflies <i>Episyrphus balteatus</i> and <i>Eupeodes corollae</i> (Diptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 30	1.6	29
44	Different genetic structures revealed resident populations of a specialist parasitoid wasp in contrast to its migratory host. <i>Ecology and Evolution</i> , 2017, 7, 5400-5409.	0.8	10
45	Effect of temperature on the development of <i>Echinothrips americanus</i> Morgan (Thysanoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 30	0.4	3
46	Next-generation sequencing of the mitochondrial genome of <i>Dolichovespula panda</i> (Hymenoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 30	0.4	3
47	Measurement of the ripple of magnet power supply and its effect to the beam energy. <i>Radiation Detection Technology and Methods</i> , 2017, 1, 1.	0.4	3
48	Novel microsatellite markers for the oriental fruit moth <i>Grapholita molesta</i> (Lepidoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 30	0.5	14
49	Patterns of genetic variation among geographic and host-plant associated populations of the peach fruit moth <i>Carposina sasakii</i> (Lepidoptera: Carposinidae). <i>BMC Evolutionary Biology</i> , 2017, 17, 265.	3.2	14
50	Development and Characterization of Novel Microsatellite Markers for the Peach Fruit Moth <i>Carposina sasakii</i> (Lepidoptera: Carposinidae) Using Next-Generation Sequencing. <i>International Journal of Molecular Sciences</i> , 2016, 17, 362.	1.8	19
51	Next-Generation Sequencing of Two Mitochondrial Genomes from Family Pompilidae (Hymenoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 30	1.8	19
52	Effects of spirotetramat on development and reproduction of <i>Myzuspersicae</i> (Hymenoptera: Aphelinidae). <i>Austral Entomology</i> , 2016, 55, 235-241.	0.8	10
53	Multiple Lines of Evidence from Mitochondrial Genomes Resolve Phylogenetic Relationships of Parasitic Wasps in Braconidae. <i>Genome Biology and Evolution</i> , 2016, 8, 2651-2662.	1.1	57
54	Comparative and phylogenetic analysis of the mitochondrial genomes in basal hymenopterans. <i>Scientific Reports</i> , 2016, 6, 20972.	1.6	56

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55	Rapid genetic structuring of populations of the invasive fall webworm in relation to spatial expansion and control campaigns. <i>Diversity and Distributions</i> , 2016, 22, 1276-1287.	1.9	35
56	Population genetic structure and post-LGM expansion of the plant bug <i>Nesidiocoris tenuis</i> (Hemiptera: Tj ETQq0 0.0rgBT /Overlock 10	1.6	16
57	Bulk development and stringent selection of microsatellite markers in the western flower thrips <i>Frankliniella occidentalis</i> . <i>Scientific Reports</i> , 2016, 6, 26512.	1.6	19
58	Field-evolved resistance to insecticides in the invasive western flower thrips <i>Frankliniella occidentalis</i> (Pergande) (Thysanoptera: Thripidae) in China. <i>Pest Management Science</i> , 2016, 72, 1440-1444.	1.7	56
59	The mitochondrial genome of the German wasp <i>Vespula germanica</i> (Fabricius, 1793) (Hymenoptera: Vespidae: Vespidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2917-2918.	0.7	12
60	The mitochondrial genome of the multicolored Asian lady beetle <i>Harmonia axyridis</i> (Pallas) and a phylogenetic analysis of the Polyphaga (Insecta: Coleoptera). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2725-2727.	0.7	6
61	The complete mitochondrial genome of the predatory bug <i>Orius sauteri</i> (Poppius) (Hemiptera: Tj ETQq1 1 0.784314 rgBT /Overlock 8	0.6	8
62	Complete mitochondrial genome of the <i>Grapholita dimorpha</i> Komai (Lepidoptera: Tortricidae). <i>Mitochondrial DNA</i> , 2016, 27, 775-776.	0.6	10
63	The mitochondrial genome of the <i>Vespa mandarinia</i> Smith (Hymenoptera: Vespidae: Vespinae) and a phylogenetic analysis of the Vespidae. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4414-4415.	0.7	18
64	The mitochondrial genome of the garden pea leafminer <i>Chromatomyia horticola</i> (Goureau, 1851) (Diptera: Agromyzidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2653-2655.	0.7	2
65	The mitochondrial genome of <i>Tenthredo tienmushana</i> (Takeuchi) and a related phylogenetic analysis of the sawflies (Insecta: Hymenoptera). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2860-2861.	0.7	12
66	The mitochondrial genome of <i>Polistes jokahamae</i> and a phylogenetic analysis of the Vespidae (Insecta: Hymenoptera). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2783-2784.	0.7	12
67	Rearrangement of <i>trnQ-trnM</i> in the mitochondrial genome of <i>Allantus luctifer</i> (Smith) (Hymenoptera: Tenthredinidae). <i>Mitochondrial DNA</i> , 2016, 27, 856-858.	0.6	19
68	The mitochondrial genome of the <i>Vespa bicolor</i> Fabricius (Hymenoptera: Vespidae: Vespinae). <i>Mitochondrial DNA</i> , 2016, 27, 875-876.	0.6	16
69	First Report of <i>Tomato yellow leaf curl virus</i> in <i>Viola prionantha</i> in China. <i>Plant Disease</i> , 2016, 100, 231-231.	0.7	3
70	Population genetic structure and approximate Bayesian computation analyses reveal the southern origin and northward dispersal of the oriental fruit moth <i>Grapholita molesta</i> (Lepidoptera: Tortricidae) in its native range. <i>Molecular Ecology</i> , 2015, 24, 4094-4111.	2.0	53
71	Sequencing and characterization of the <i>Monoclellampa pruni</i> (Hymenoptera: Tenthredinidae) mitochondrial genome. <i>Mitochondrial DNA</i> , 2015, 26, 157-158.	0.6	26
72	Characterization of the complete mitochondrial genome of the black cutworm <i>Agrotis ipsilon</i> (Lepidoptera: Noctuidae). <i>Mitochondrial DNA</i> , 2015, 26, 139-140.	0.6	21

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73	The mitochondrial genome of <i>Diadromus collaris</i> (Hymenoptera: Ichneumonidae). <i>Mitochondrial DNA</i> , 2015, 26, 303-304.	0.6	17
74	Complete mitochondrial genome of <i>Neochauliodes bowringi</i> (MacLachlan) (Megaloptera). <i>Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 7</i>	0.6	4
75	Characterization of novel microsatellite markers for <i>Hyphantria cunea</i> and implications for other Lepidoptera. <i>Bulletin of Entomological Research</i> , 2015, 105, 273-284.	0.5	9
76	Rearrangement of the <i>nad1</i> gene in <i>Pristaulacus compressus</i> (Spinola) (Hymenoptera: Evanioidea). <i>Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 6</i>	0.6	13
77	Mitochondrial phylogenomics and genetic relationships of closely related pine moth (Lasiocampidae). <i>Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50 7</i>	1.2	93
78	The complete mitochondrial genome of <i>Neopanorpa pulchra</i> (Mecoptera: Panorpidae). <i>Mitochondrial DNA</i> , 2015, 26, 305-306.	0.6	1
79	The first complete mitogenome for the superfamily Cossoidea of Lepidoptera: The seabuckthorn carpenter moth <i>Eogystia hippophaecolus</i> . <i>Mitochondrial DNA</i> , 2014, 25, 288-289.	0.6	9
80	Two mitochondrial genomes from the families Bethyridae and Mutillidae: Independent rearrangement of protein-coding genes and higher-level phylogeny of the Hymenoptera. <i>Molecular Phylogenetics and Evolution</i> , 2014, 77, 1-10.	1.2	57
81	The complete mitogenome of the turnip moth <i>Agrotis segetum</i> (Lepidoptera: Noctuidae). <i>Mitochondrial DNA</i> , 2014, 25, 345-347.	0.6	14
82	The complete mitochondrial genome of <i>Taeniogonalos taihorina</i> (Bischoff) (Hymenoptera). <i>Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 382 Td</i>	1.0	34
83	The complete mitochondrial genome of the codling moth <i>Cydia pomonella</i> (Lepidoptera: Tortricidae). <i>Mitochondrial DNA</i> , 2013, 24, 37-39.	0.6	19
84	<i>Pantoea beijingensis</i> sp. nov., isolated from the fruiting body of <i>Pleurotus eryngii</i> . <i>Antonie Van Leeuwenhoek</i> , 2013, 104, 1039-1047.	0.7	19
85	The complete mitochondrial genome of the beet armyworm <i>Spodoptera exigua</i> (Lepidoptera). <i>Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50 7</i>	0.6	27
86	Complete mitogenome of the <i>Argyrogramma agnata</i> (Lepidoptera: Noctuidae). <i>Mitochondrial DNA</i> , 2013, 24, 391-393.	0.6	17
87	Characterization of the Mitochondrial Genome of the Diamondback Moth <i>Plutella xylostella</i> (Lepidoptera: Plutellidae) and Phylogenetic Analysis of Advanced Moths and Butterflies. <i>DNA and Cell Biology</i> , 2013, 32, 173-187.	0.9	19
88	The complete mitochondrial genome of the summer fruit tortrix moth <i>Adoxophyes orana</i> (Lepidoptera). <i>Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 7</i>	0.6	16
89	The complete mitochondrial genome of the yellow peach moth <i>Dichocrocis punctiferalis</i> (Lepidoptera: Pyralidae). <i>Mitochondrial DNA</i> , 2013, 24, 105-107.	0.6	14
90	Genetic Structure and Demographic History Reveal Migration of the Diamondback Moth <i>Plutella xylostella</i> (Lepidoptera: Plutellidae) from the Southern to Northern Regions of China. <i>PLoS ONE</i> , 2013, 8, e59654.	1.1	89

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91	Hosts preference of <i>Echinothrips americanus</i> Morgan for different vegetables. <i>Acta Ecologica Sinica</i> , 2013, 33, 1607-1614.	0.0	1
92	Mitochondrial genome of the pine tip moth <i>Rhyacionia leptotubula</i> (Lepidoptera: Tortricidae). <i>Mitochondrial DNA</i> , 2012, 23, 376-378.	0.6	13
93	The complete mitochondrial genome of <i>Macrotermes barneyi</i> Light (Isoptera: Termitidae). <i>Mitochondrial DNA</i> , 2012, 23, 426-428.	0.6	15
94	Comparative analyses of the complete mitochondrial genomes of <i>Ascaris lumbricoides</i> and <i>Ascaris suum</i> from humans and pigs. <i>Gene</i> , 2012, 492, 110-116.	1.0	124
95	The complete mitochondrial genome of the oriental fruit moth <i>Grapholita molesta</i> (Busck) (Lepidoptera: Tortricidae). <i>Molecular Biology Reports</i> , 2012, 39, 2893-2900.	1.0	62
96	The Complete Mitochondrial Genome of <i>Galba perversa</i> (Gastropoda: Mollusca), an Intermediate Host Snail of <i>Fasciola</i> spp. <i>PLoS ONE</i> , 2012, 7, e42172.	1.1	33
97	Utility of Multi-Gene Loci for Forensic Species Diagnosis of Blowflies. <i>Journal of Insect Science</i> , 2011, 11, 1-12.	0.6	34
98	Deep sequencing of <i>Cotesia vestalis</i> bracovirus reveals the complexity of a polydnavirus genome. <i>Virology</i> , 2011, 414, 42-50.	1.1	70
99	<i>Yaotrips shii</i> gen. et sp. n. from western China (Thripidae: Thripinae). <i>Zootaxa</i> , 2011, 2900, 46.	0.2	3
100	The complete mitochondrial genome of <i>Evania appendigaster</i> (Hymenoptera: Evaniidae) has low A+T content and a long intergenic spacer between <i>atp8</i> and <i>atp6</i> . <i>Molecular Biology Reports</i> , 2010, 37, 1931-1942.	1.0	87
101	Comparative mitogenomics of Braconidae (Insecta: Hymenoptera) and the phylogenetic utility of mitochondrial genomes with special reference to Holometabolous insects. <i>BMC Genomics</i> , 2010, 11, 371.	1.2	153
102	New Views on Strand Asymmetry in Insect Mitochondrial Genomes. <i>PLoS ONE</i> , 2010, 5, e12708.	1.1	228
103	The complete mitochondrial genome of <i>Diadegma semiclausum</i> (Hymenoptera: Ichneumonidae) indicates extensive independent evolutionary events. <i>Genome</i> , 2009, 52, 308-319.	0.9	93
104	Phylogeography of the Oriental dobsonfly, <i>Neoneuromus ignobilis</i> (Navás), suggests Pleistocene allopatric isolation and glacial dispersal shaping its wide distribution. <i>Systematic Entomology</i> , 0, , .	1.7	3