

# Fei Li

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6420138/publications.pdf>

Version: 2024-02-01

90  
papers

3,773  
citations

136940

32  
h-index

144002

57  
g-index

94  
all docs

94  
docs citations

94  
times ranked

3811  
citing authors

#	ARTICLE	IF	CITATIONS
1	Chromosome-level genome assembly of an agricultural pest, the rice leaffolder <i>Cnaphalocrocis exigua</i> (Crambidae, Lepidoptera). <i>Molecular Ecology Resources</i> , 2022, 22, 307-318.	4.8	7
2	Chromosome-level genome assembly of the mirid predator <i>Cyrtorhinus lividipennis</i> Reuter (Hemiptera: Miridae), an important natural enemy in the rice ecosystem. <i>Molecular Ecology Resources</i> , 2022, 22, 1086-1099.	4.8	7
3	InsectBase 2.0: a comprehensive gene resource for insects. <i>Nucleic Acids Research</i> , 2022, 50, D1040-D1045.	14.5	74
4	Using transcriptome Shannon entropy to evaluate the off-target effects and safety of insecticidal siRNAs. <i>Journal of Integrative Agriculture</i> , 2022, 21, 170-177.	3.5	2
5	Genome of the parasitoid wasp <i>Cotesia chilonis</i> sheds light on amino acid resource exploitation. <i>BMC Biology</i> , 2022, 20, .	3.8	6
6	Expression and functional characterization of odorant-binding protein genes in the endoparasitic wasp <i>Cotesia vestalis</i> . <i>Insect Science</i> , 2021, 28, 1354-1368.	3.0	16
7	Chromosomal-level genomes of three rice planthoppers provide new insights into sex chromosome evolution. <i>Molecular Ecology Resources</i> , 2021, 21, 226-237.	4.8	44
8	A chromosome-level genome assembly of rice leaffolder, <i>Cnaphalocrocis medinalis</i> . <i>Molecular Ecology Resources</i> , 2021, 21, 561-572.	4.8	15
9	Transgenic rice overexpressing insect endogenous microRNA csu260 is resistant to striped stem borer under field conditions. <i>Plant Biotechnology Journal</i> , 2021, 19, 421-423.	8.3	17
10	InSexBase: an annotated genomic resource of sex chromosomes and sex-biased genes in insects. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	3.0	3
11	A chromosome-level assembly of the harlequin ladybird <i>Harmonia axyridis</i> as a genomic resource to study beetle and invasion biology. <i>Molecular Ecology Resources</i> , 2021, 21, 1318-1332.	4.8	17
12	Large-Scale Annotation and Evolution Analysis of MiRNA in Insects. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	15
13	Genome of the pincer wasp <i>Gonatopus flavifemur</i> reveals unique venom evolution and a dual adaptation to parasitism and predation. <i>BMC Biology</i> , 2021, 19, 145.	3.8	15
14	Diet-derived transmission of MicroRNAs from host plant into honey bee Midgut. <i>BMC Genomics</i> , 2021, 22, 587.	2.8	4
15	Comparative Genomics Sheds Light on the Convergent Evolution of Miniaturized Wasps. <i>Molecular Biology and Evolution</i> , 2021, 38, 5539-5554.	8.9	11
16	Host-pathogen interaction between Asian citrus psyllid and entomopathogenic fungus ( <i>Cordyceps</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 population of the host. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2021, 248, 109112.	2.6	20
17	MM-6mAPred: identifying DNA N6-methyladenine sites based on Markov model. <i>Bioinformatics</i> , 2020, 36, 388-392.	4.1	55
18	miR+Pathway: the integration and visualization of miRNA and KEGG pathways. <i>Briefings in Bioinformatics</i> , 2020, 21, 699-708.	6.5	14

#	ARTICLE	IF	CITATIONS
19	A chromosome-level genome assembly reveals the genetic basis of cold tolerance in a notorious rice insect pest, <i>Chilo suppressalis</i> . <i>Molecular Ecology Resources</i> , 2020, 20, 268-282.	4.8	51
20	Impact of landfill garbage on insect ecology and human health. <i>Acta Tropica</i> , 2020, 211, 105630.	2.0	24
21	Genetic engineering and bacterial pathogenesis against the vectorial capacity of mosquitoes. <i>Microbial Pathogenesis</i> , 2020, 147, 104391.	2.9	1
22	A chromosome-level genome assembly provides new insights into paternal genome elimination in the cotton mealybug <i>Phenacoccus solenopsis</i> . <i>Molecular Ecology Resources</i> , 2020, 20, 1733-1747.	4.8	12
23	Identification and Analysis of MicroRNAs Associated with Wing Polyphenism in the Brown Planthopper, <i>Nilaparvata lugens</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 9754.	4.1	8
24	FastD: Fast detection of insecticide target site mutations and overexpressed detoxification genes in insect populations from RNA-seq data. <i>Ecology and Evolution</i> , 2020, 10, 14346-14358.	1.9	1
25	The genetic adaptations of fall armyworm <i>Spodoptera frugiperda</i> facilitated its rapid global dispersal and invasion. <i>Molecular Ecology Resources</i> , 2020, 20, 1050-1068.	4.8	88
26	A chromosome-level genome assembly of the parasitoid wasp <i>Pteromalus puparum</i> . <i>Molecular Ecology Resources</i> , 2020, 20, 1384-1402.	4.8	35
27	The Roles of DNA Methyltransferases 1 (DNMT1) in Regulating Sexual Dimorphism in the Cotton Mealybug, <i>Phenacoccus solenopsis</i> . <i>Insects</i> , 2020, 11, 121.	2.2	10
28	Discovering Cancer-Related miRNAs from miRNA-Target Interactions by Support Vector Machines. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 19, 1423-1433.	5.1	8
29	Transgenic microRNA-14 rice shows high resistance to rice stem borer. <i>Plant Biotechnology Journal</i> , 2019, 17, 461-471.	8.3	46
30	Progress and prospects of noncoding RNAs in insects. <i>Journal of Integrative Agriculture</i> , 2019, 18, 729-747.	3.5	21
31	A chromosome-level genome assembly of <i>Cydia pomonella</i> provides insights into chemical ecology and insecticide resistance. <i>Nature Communications</i> , 2019, 10, 4237.	12.8	102
32	miR-34 modulates wing polyphenism in planthopper. <i>PLoS Genetics</i> , 2019, 15, e1008235.	3.5	50
33	microRNA-14 as an efficient suppressor to switch off ecdysone production after ecdysis in insects. <i>RNA Biology</i> , 2019, 16, 1313-1325.	3.1	28
34	The genomes of two parasitic wasps that parasitize the diamondback moth. <i>BMC Genomics</i> , 2019, 20, 893.	2.8	17
35	LncRNAs are potentially involved in the immune interaction between small brown planthopper and rice stripe virus. <i>Journal of Integrative Agriculture</i> , 2019, 18, 2814-2822.	3.5	21
36	The vitellogenin receptor has an essential role in vertical transmission of rice stripe virus during oogenesis in the small brown plant hopper. <i>Pest Management Science</i> , 2019, 75, 1370-1382.	3.4	17

#	ARTICLE	IF	CITATIONS
37	Discovering the “Dark matters”™ in expression data of miRNA based on the miRNA-mRNA and miRNA-lncRNA networks. BMC Bioinformatics, 2018, 19, 379.	2.6	3
38	WaspBase: a genomic resource for the interactions among parasitic wasps, insect hosts and plants. Database: the Journal of Biological Databases and Curation, 2018, 2018, 1-9.	3.0	3
39	LncCeRBase: a database of experimentally validated human competing endogenous long non-coding RNAs. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	32
40	The genomic features of parasitism, Polyembryony and immune evasion in the endoparasitic wasp <i>Macrocentrus cingulum</i> . BMC Genomics, 2018, 19, 420.	2.8	53
41	Parasitic insect-derived miRNAs modulate host development. Nature Communications, 2018, 9, 2205.	12.8	77
42	Large-scale identification of differentially expressed genes during pupa development reveals solute carrier gene is essential for pupal pigmentation in <i>Chilo suppressalis</i> . Journal of Insect Physiology, 2017, 98, 117-125.	2.0	4
43	Multiple miRNAs jointly regulate the biosynthesis of ecdysteroid in the holometabolous insects, <i>Chilo suppressalis</i> . Rna, 2017, 23, 1817-1833.	3.5	35
44	Knockdown of two Cadherin genes confers resistance to Cry2A and Cry1C in <i>Chilo suppressalis</i> . Scientific Reports, 2017, 7, 5992.	3.3	18
45	Two <i>Bombyx mori</i> acetylcholinesterase genes influence motor control and development in different ways. Scientific Reports, 2017, 7, 4985.	3.3	8
46	ACE: an efficient and sensitive tool to detect insecticide resistance-associated mutations in insect acetylcholinesterase from RNA-Seq data. BMC Bioinformatics, 2017, 18, 330.	2.6	28
47	Large-scale analysis reveals that the genome features of simple sequence repeats are generally conserved at the family level in insects. BMC Genomics, 2017, 18, 848.	2.8	48
48	Genome Sizes of Nine Insect Species Determined by Flow Cytometry and k-mer Analysis. Frontiers in Physiology, 2016, 7, 569.	2.8	36
49	<i>Cotesia vestalis</i> teratocytes express a diversity of genes and exhibit novel immune functions in parasitism. Scientific Reports, 2016, 6, 26967.	3.3	20
50	Insights into the venom composition and evolution of an endoparasitoid wasp by combining proteomic and transcriptomic analyses. Scientific Reports, 2016, 6, 19604.	3.3	53
51	InsectBase: a resource for insect genomes and transcriptomes. Nucleic Acids Research, 2016, 44, D801-D807.	14.5	126
52	Genome-wide identification of long noncoding RNA genes and their potential association with fecundity and virulence in rice brown planthopper, <i>Nilaparvata lugens</i> . BMC Genomics, 2015, 16, 749.	2.8	82
53	Large number of putative chemoreception and pheromone biosynthesis genes revealed by analyzing transcriptome from ovipositor-pheromone glands of <i>Chilo suppressalis</i> . Scientific Reports, 2015, 5, 7888.	3.3	69
54	DNA methyltransferases have an essential role in female fecundity in Brown planthopper, <i>Nilaparvata lugens</i> . Biochemical and Biophysical Research Communications, 2015, 464, 83-88.	2.1	43

#	ARTICLE	IF	CITATIONS
55	KNOCKDOWN OF <i>CSPOOK</i> INDUCES DELAYED LARVAL MOLTING IN RICE STRIPED STEM BORER <i>Chilo suppressalis</i> . Archives of Insect Biochemistry and Physiology, 2015, 88, 179-191.	1.5	14
56	Chemosensory Gene Families in Adult Antennae of <i>Anomala corpulenta</i> Motschulsky (Coleoptera: Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	2.5	66
57	TRANSCRIPTOME AND TISSUE-SPECIFIC EXPRESSION ANALYSIS OF <i>OBP</i> AND <i>CSP</i> GENES IN THE DARK BLACK CHAFER. Archives of Insect Biochemistry and Physiology, 2014, 87, 177-200.	1.5	38
58	Prediction of piRNAs using transposon interaction and a support vector machine. BMC Bioinformatics, 2014, 15, 419.	2.6	72
59	ChiloDB: a genomic and transcriptome database for an important rice insect pest <i>Chilo suppressalis</i> . Database: the Journal of Biological Databases and Curation, 2014, 2014, bau065-bau065.	3.0	50
60	iPathCons and iPathDB: an improved insect pathway construction tool and the database. Database: the Journal of Biological Databases and Curation, 2014, 2014, .	3.0	14
61	OMIGA: Optimized Maker-Based Insect Genome Annotation. Molecular Genetics and Genomics, 2014, 289, 567-573.	2.1	24
62	Genome-wide analysis reveals the expansion of Cytochrome P450 genes associated with xenobiotic metabolism in rice striped stem borer, <i>Chilo suppressalis</i> . Biochemical and Biophysical Research Communications, 2014, 443, 756-760.	2.1	44
63	Evidence of horizontal transfer of non-autonomous Lep1 Helitrons facilitated by host-parasite interactions. Scientific Reports, 2014, 4, 5119.	3.3	21
64	The involvement of several enzymes in methanol detoxification in <i>Drosophila melanogaster</i> adults. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2013, 166, 7-14.	1.6	25
65	Amplifying long transcripts of ryanodine receptors of five agricultural pests by transcriptome analysis and gap filling. Genome, 2013, 56, 651-658.	2.0	7
66	Validation of Reference Genes for Quantitative Expression Analysis by Real-Time RT-PCR in Four Lepidopteran Insects. Journal of Insect Science, 2012, 12, 1-17.	1.5	142
67	Methods for Identifying Small RNA Genes. Advances in Insect Physiology, 2012, , 155-194.	2.7	0
68	Characterization of Three Novel SINE Families with Unusual Features in <i>Helicoverpa armigera</i> . PLoS ONE, 2012, 7, e31355.	2.5	16
69	Exploring the Midgut Transcriptome and Brush Border Membrane Vesicle Proteome of the Rice Stem Borer, <i>Chilo suppressalis</i> (Walker). PLoS ONE, 2012, 7, e38151.	2.5	30
70	<i>RNA</i> INTERFERENCE OF TWO ACETYLCHOLINESTERASE GENES IN <i>Plutella xylostella</i> REVEALS THEIR DIFFERENT FUNCTIONS. Archives of Insect Biochemistry and Physiology, 2012, 79, 75-86.	1.5	30
71	THE INVOLVEMENT OF CYTOCHROME P450 MONOOXYGENASES IN METHANOL ELIMINATION IN <i>Drosophila melanogaster</i> LARVAE. Archives of Insect Biochemistry and Physiology, 2012, 79, 264-275.	1.5	17
72	The full-length transcripts and promoter analysis of intergenic microRNAs in <i>Drosophila melanogaster</i> . Genomics, 2011, 97, 294-303.	2.9	21

#	ARTICLE	IF	CITATIONS
73	Discovering conserved insect microRNAs from expressed sequence tags. <i>Journal of Insect Physiology</i> , 2010, 56, 1763-1769.	2.0	21
74	Identification of two piwi genes and their expression profile in honeybee, <i>Apis mellifera</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2010, 74, 91-102.	1.5	19
75	Large-scale identification of odorant-binding proteins and chemosensory proteins from expressed sequence tags in insects. <i>BMC Genomics</i> , 2009, 10, 632.	2.8	213
76	Abundant conserved microRNA target sites in the 5' untranslated region and coding sequence. <i>Genetica</i> , 2009, 137, 159-164.	1.1	86
77	<i>Ace2</i> , rather than <i>ace1</i> , is the major acetylcholinesterase in the silkworm, <i>Bombyx mori</i> . <i>Insect Science</i> , 2009, 16, 297-303.	3.0	24
78	Independent transcription of miR-281 in the intron of ODA in <i>Drosophila melanogaster</i> . <i>Biochemical and Biophysical Research Communications</i> , 2009, 378, 883-889.	2.1	24
79	Weighted Subspace Distance and Its Applications to Object Recognition and Retrieval With Image Sets. <i>IEEE Signal Processing Letters</i> , 2009, 16, 227-230.	3.6	31
80	Insect-Specific microRNA Involved in the Development of the Silkworm <i>Bombyx mori</i> . <i>PLoS ONE</i> , 2009, 4, e4677.	2.5	98
81	Computational identification of 99 insect MicroRNAs using comparative genomics. <i>Tsinghua Science and Technology</i> , 2008, 13, 425-432.	6.1	2
82	Computational identification and evolutionary analysis of Piwi subfamily in 11 <i>Drosophila</i> species. <i>Insect Science</i> , 2008, 15, 537-544.	3.0	0
83	Finding noncoding RNA transcripts from low abundance expressed sequence tags. <i>Cell Research</i> , 2008, 18, 695-700.	12.0	14
84	Identification of MicroRNA Precursors with Support Vector Machine and String Kernel. <i>Genomics, Proteomics and Bioinformatics</i> , 2008, 6, 121-128.	6.9	17
85	Identification and characterization of Piwi subfamily in insects. <i>Biochemical and Biophysical Research Communications</i> , 2007, 362, 126-131.	2.1	20
86	Classification of real and pseudo microRNA precursors using local structure-sequence features and support vector machine. <i>BMC Bioinformatics</i> , 2005, 6, 310.	2.6	417
87	MicroRNA identification based on sequence and structure alignment. <i>Bioinformatics</i> , 2005, 21, 3610-3614.	4.1	270
88	Mutations in acetylcholinesterase associated with insecticide resistance in the cotton aphid, <i>Aphis gossypii</i> Glover. <i>Insect Biochemistry and Molecular Biology</i> , 2004, 34, 397-405.	2.7	118
89	Two different genes encoding acetylcholinesterase existing in cotton aphid ( <i>Aphis gossypii</i> ). <i>Genome</i> , 2002, 45, 1134-1141.	2.0	70
90	Purification and characterization of acetylcholinesterase from cotton aphid ( <i>Aphis gossypii</i> Glover). <i>Archives of Insect Biochemistry and Physiology</i> , 2002, 51, 37-45.	1.5	57