

# Ze Zhang

## List of Publications by Year in descending order

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56  
papers

68,942  
citations

236612

25  
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149479

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56  
docs citations

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times ranked

71719  
citing authors

#	ARTICLE	IF	CITATIONS
1	The miR-282-5p regulates larval moulting process by targeting chitinase 5 in <i>Bombyx mori</i> . <i>Insect Molecular Biology</i> , 2022, 31, 190-201.	1.0	9
2	piggyBac-based transgenic RNAi of serine protease 2 results in male sterility in <i>Hyphantria cunea</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2022, 143, 103726.	1.2	5
3	Identification of Genes Involved in Resistance to High Exogenous 20-Hydroxyecdysone in <i>Spodoptera litura</i> . <i>Insects</i> , 2022, 13, 297.	1.0	1
4	Genus-Wide Characterization of Bumblebee Genomes Provides Insights into Their Evolution and Variation in Ecological and Behavioral Traits. <i>Molecular Biology and Evolution</i> , 2021, 38, 486-501.	3.5	58
5	Genome Sequence of the Asian Honeybee in Pakistan Sheds Light on Its Phylogenetic Relationship with Other Honeybees. <i>Insects</i> , 2021, 12, 652.	1.0	1
6	Solitary Living Brings a Decreased Weight and an Increased Agility to the Domestic Silkworm, <i>Bombyx mori</i> . <i>Insects</i> , 2021, 12, 809.	1.0	3
7	Heat Shock Protein 70 Family in Response to Multiple Abiotic Stresses in the Silkworm. <i>Insects</i> , 2021, 12, 928.	1.0	11
8	Exploring the Terminal Pathway of Sex Pheromone Biosynthesis and Metabolism in the Silkworm. <i>Insects</i> , 2021, 12, 1062.	1.0	1
9	Identification of genes involved in sex pheromone biosynthesis and metabolic pathway in the Chinese oak silkworm, <i>Antheraea pernyi</i> . <i>International Journal of Biological Macromolecules</i> , 2020, 163, 1487-1497.	3.6	9
10	Identification and Characterization of Genes Involved in Ecdysteroid Esterification Pathway Contributing to the High 20-Hydroxyecdysone Resistance of <i>Helicoverpa armigera</i> . <i>Frontiers in Physiology</i> , 2020, 11, 508.	1.3	7
11	Genetic and genomic analysis for cocoon yield traits in silkworm. <i>Scientific Reports</i> , 2020, 10, 5682.	1.6	11
12	A Comparison of Co-expression Networks in Silk Gland Reveals the Causes of Silk Yield Increase During Silkworm Domestication. <i>Frontiers in Genetics</i> , 2020, 11, 225.	1.1	10
13	Subcellular localization of mutated $\beta$ -catenins with different incidences of cis-peptide bonds at the Xaa246-P247 site in HepG2 cells. <i>FASEB Journal</i> , 2019, 33, 6574-6583.	0.2	2
14	SGID: a comprehensive and interactive database of the silkworm. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	12
15	Functional characterization of the horizontally transferred 4,5-DOPA extradiol dioxygenase gene in the domestic silkworm, <i>Bombyx mori</i> . <i>Insect Molecular Biology</i> , 2019, 28, 409-419.	1.0	4
16	Comparative analysis of iTRAQ-based proteomes for cocoons between the domestic silkworm ( <i>Bombyx mori</i> ) and wild silkworm ( <i>Bombyx mori</i> ). <i>Journal of Proteomics</i> , 2019, 12, 32.	1.2	32
17	Genome-wide identification and evolution of TC1/Mariner in the silkworm ( <i>Bombyx mori</i> ) genome. <i>Genes and Genomics</i> , 2018, 40, 485-495.	0.5	8
18	Identification and comparison of long non-coding RNAs in the silk gland between domestic and wild silkworms. <i>Insect Science</i> , 2018, 25, 604-616.	1.5	37

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19	Ecdysone oxidase and 3-dehydroecdysone-3 $\beta$ -reductase contribute to the synthesis of ecdysone during early embryonic development of the silkworm. <i>International Journal of Biological Sciences</i> , 2018, 14, 1472-1482.	2.6	17
20	Evidence of peripheral olfactory impairment in the domestic silkworms: insight from the comparative transcriptome and population genetics. <i>BMC Genomics</i> , 2018, 19, 788.	1.2	14
21	Identification of two isoforms of Pop in the domestic silkworm, <i>Bombyx mori</i> : Cloning, characterization and expression analysis. <i>Gene</i> , 2018, 667, 101-111.	1.0	5
22	The dynamic landscape of gene regulation during <i>Bombyx mori</i> oogenesis. <i>BMC Genomics</i> , 2017, 18, 714.	1.2	11
23	Transcription factor E74A affects the ecdysone titer by regulating the expression of the EO gene in the silkworm, <i>Bombyx mori</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 551-558.	1.1	14
24	BmncRNAdb: a comprehensive database of non-coding RNAs in the silkworm, <i>Bombyx mori</i> . <i>BMC Bioinformatics</i> , 2016, 17, 370.	1.2	36
25	Ecdysone Titer Determined by 3DE-3 $\beta$ -Reductase Enhances the Immune Response in the Silkworm. <i>Journal of Immunology</i> , 2016, 196, 1646-1654.	0.4	35
26	Molecular cloning, expression and characterization of acylpeptide hydrolase in the silkworm, <i>Bombyx mori</i> . <i>Gene</i> , 2016, 580, 8-16.	1.0	1
27	Characterization of an epsilon-class glutathione S-transferase involved in tolerance in the silkworm larvae after long term exposure to insecticides. <i>Ecotoxicology and Environmental Safety</i> , 2015, 120, 20-26.	2.9	27
28	Comparative analysis of the silk gland transcriptomes between the domestic and wild silkworms. <i>BMC Genomics</i> , 2015, 16, 60.	1.2	84
29	Repeated horizontal transfers of four DNA transposons in invertebrates and bats. <i>Mobile DNA</i> , 2015, 6, 3.	1.3	33
30	Identification and evolution of the orphan genes in the domestic silkworm, <i>Bombyx mori</i> . <i>FEBS Letters</i> , 2015, 589, 2731-2738.	1.3	21
31	Genetic diversity and population structure of wild <i>Dipsacus asperoides</i> in China as indicated by ISSR markers. <i>Genetics and Molecular Research</i> , 2014, 13, 6340-6349.	0.3	3
32	Recurrent Horizontal Transfers of Chapaev Transposons in Diverse Invertebrate and Vertebrate Animals. <i>Genome Biology and Evolution</i> , 2014, 6, 1375-1386.	1.1	42
33	Demographic history and gene flow during silkworm domestication. <i>BMC Evolutionary Biology</i> , 2014, 14, 185.	3.2	33
34	An Adaptive Transposable Element Insertion in the Regulatory Region of the EO Gene in the Domesticated Silkworm, <i>Bombyx mori</i> . <i>Molecular Biology and Evolution</i> , 2014, 31, 3302-3313.	3.5	30
35	Copy number variations among silkworms. <i>BMC Genomics</i> , 2014, 15, 251.	1.2	10
36	Detection of copy number variants in the horse genome and examination of their association with recurrent laryngeal neuropathy. <i>Animal Genetics</i> , 2013, 44, 206-208.	0.6	34

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37	A novel <i>hAT</i> element in <i>Bombyx mori</i> and <i>Rhodnius prolixus</i> : its relationship with miniature inverted repeat transposable elements (MITEs) and horizontal transfer. <i>Insect Molecular Biology</i> , 2013, 22, 584-596.	1.0	15
38	Segmental duplications in the silkworm genome. <i>BMC Genomics</i> , 2013, 14, 521.	1.2	18
39	BmTEdb: a collective database of transposable elements in the silkworm genome. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat055.	1.4	34
40	The Origin and Evolution of Six Miniature Inverted-Repeat Transposable Elements in <i>Bombyx mori</i> and <i>Rhodnius prolixus</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 2020-2031.	1.1	20
41	Molecular cloning and characterization of peroxiredoxin 4 involved in protection against oxidative stress in the silkworm <i>Bombyx mori</i> . <i>Insect Molecular Biology</i> , 2012, 21, 581-592.	1.0	19
42	Expansion of the silkworm GMC oxidoreductase genes is associated with immunity. <i>Insect Biochemistry and Molecular Biology</i> , 2012, 42, 935-945.	1.2	29
43	Molecular Cloning and Characterization of <i>Ecdysone oxidase</i> and <i>3-dehydroecdysone-3<math>\beta</math>-reductase</i> Involved in the Ecdysone Inactivation Pathway of Silkworm, <i>Bombyx mori</i> . <i>International Journal of Biological Sciences</i> , 2012, 8, 125-138.	2.6	35
44	ANNOTATION AND EVOLUTION OF THE ANTIOXIDANT GENES IN THE SILKWORM, <i>Bombyx mori</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2012, 79, 87-103.	0.6	13
45	Phylogeny and evolutionary history of the silkworm. <i>Science China Life Sciences</i> , 2012, 55, 483-496.	2.3	71
46	Pathogen-origin horizontally transferred genes contribute to the evolution of Lepidopteran insects. <i>BMC Evolutionary Biology</i> , 2011, 11, 356.	3.2	39
47	Nucleotide Diversity and Selection Signature in the Domesticated Silkworm, <i>Bombyx mori</i> , and Wild Silkworm, <i>Bombyx mandarina</i> . <i>Journal of Insect Science</i> , 2011, 11, 1-16.	0.6	22
48	Effect of Organophosphate Phoxim Exposure on Certain Oxidative Stress Biomarkers in the Silkworm. <i>Journal of Economic Entomology</i> , 2011, 104, 101-106.	0.8	45
49	Evidence of Selection at Melanin Synthesis Pathway Loci during Silkworm Domestication. <i>Molecular Biology and Evolution</i> , 2011, 28, 1785-1799.	3.5	53
50	Burst expansion, distribution and diversification of MITEs in the silkworm genome. <i>BMC Genomics</i> , 2010, 11, 520.	1.2	31
51	Complete Resequencing of 40 Genomes Reveals Domestication Events and Genes in Silkworm ( <i>Bombyx mori</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 11 6.0 342	6.0	342
52	Annotation and expression of carboxylesterases in the silkworm, <i>Bombyx mori</i> . <i>BMC Genomics</i> , 2009, 10, 553.	1.2	131
53	Identification, genomic organization and expression pattern of glutathione S-transferase in the silkworm, <i>Bombyx mori</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 1158-1164.	1.2	134
54	Microarray-based gene expression profiles in multiple tissues of the domesticated silkworm, <i>Bombyx mori</i> . <i>Genome Biology</i> , 2007, 8, R162.	13.9	271

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55	WEGO: a web tool for plotting GO annotations. <i>Nucleic Acids Research</i> , 2006, 34, W293-W297.	6.5	2,529
56	Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. <i>Nucleic Acids Research</i> , 1997, 25, 3389-3402.	6.5	64,420