

Jing Tao

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

410
citations

840776

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752698

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27
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326
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Species-specific primers for rapid detection of <i>Monoctonus saltuarius</i> , an effective vector of <i>Bursaphelenchus xylophilus</i> in China. <i>Journal of Applied Entomology</i> , 2022, 146, 636-647. | 1.8 | 7 |
| 2 | Genome-wide identification and expression analysis of the Hsp gene superfamily in Asian long-horned beetle (<i>Anoplophora glabripennis</i>). <i>International Journal of Biological Macromolecules</i> , 2022, 200, 583-592. | 7.5 | 9 |
| 3 | Identification of key genes associated with overwintering in <i>Anoplophora glabripennis</i> larva using gene co-expression network analysis. <i>Pest Management Science</i> , 2021, 77, 805-816. | 3.4 | 11 |
| 4 | Comparative transcriptome analysis of the newly discovered insect vector of the pine wood nematode in China, revealing putative genes related to host plant adaptation. <i>BMC Genomics</i> , 2021, 22, 189. | 2.8 | 14 |
| 5 | Expression analysis of genes related to cold tolerance in <i>Dendroctonus valens</i> . <i>PeerJ</i> , 2021, 9, e10864. | 2.0 | 9 |
| 6 | Seasonal Shifts in Cold Tolerance and the Composition of the Gut Microbiome of <i>Dendroctonus valens</i> LeConte Occur Concurrently. <i>Forests</i> , 2021, 12, 888. | 2.1 | 8 |
| 7 | Pheromone biosynthetic pathway and chemoreception proteins in sex pheromone gland of <i>Eogystia hippophaecolus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 35, 100702. | 1.0 | 1 |
| 8 | Reference Gene Selection for Expression Analyses by qRT-PCR in <i>Dendroctonus valens</i> . <i>Insects</i> , 2020, 11, 328. | 2.2 | 13 |
| 9 | Invasion History of <i>Sirex noctilio</i> Based on COI Sequence: The First Six Years in China. <i>Insects</i> , 2020, 11, 111. | 2.2 | 4 |
| 10 | Identification of putative Type-I sex pheromone biosynthesis-related genes expressed in the female pheromone gland of <i>Streltziella insularis</i> . <i>PLoS ONE</i> , 2020, 15, e0227666. | 2.5 | 4 |
| 11 | Characterization and expression profiling of odorant-binding proteins in <i>Anoplophora glabripennis</i> Motsch. <i>Gene</i> , 2019, 693, 25-36. | 2.2 | 16 |
| 12 | Antennal transcriptome analyses and olfactory protein identification in an important wood-boring moth pest, <i>Streltziella insularis</i> (Lepidoptera: Cossidae). <i>Scientific Reports</i> , 2019, 9, 17951. | 3.3 | 17 |
| 13 | Different Responses of Cytoplasmic and Endoplasmic Reticulum Hsp90 Genes from <i>Eogystia hippophaecola</i> (Lepidoptera: Cossidae) to Cold Stress. <i>Forests</i> , 2019, 10, 1039. | 2.1 | 3 |
| 14 | Sensilla on six olfactory organs of male <i>Eogystia hippophaecolus</i> (Lepidoptera: Cossidae). <i>Microscopy Research and Technique</i> , 2018, 81, 1059-1070. | 2.2 | 5 |
| 15 | Pheromone Binding Protein EhipPBP1 Is Highly Enriched in the Male Antennae of the Seabuckthorn Carpenterworm and Is Binding to Sex Pheromone Components. <i>Frontiers in Physiology</i> , 2018, 9, 447. | 2.8 | 8 |
| 16 | Development and characterization of polymorphic genomic-SSR markers in Asian long-horned beetle (<i>Anoplophora glabripennis</i>). <i>Bulletin of Entomological Research</i> , 2017, 107, 749-755. | 1.0 | 2 |
| 17 | Antennal transcriptome analysis and expression profiles of olfactory genes in <i>Anoplophora chinensis</i> . <i>Scientific Reports</i> , 2017, 7, 15470. | 3.3 | 58 |
| 18 | Differential transcriptome analysis reveals genes related to cold tolerance in seabuckthorn carpenter moth, <i>Eogystia hippophaecolus</i> . <i>PLoS ONE</i> , 2017, 12, e0187105. | 2.5 | 26 |

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|----|---|-----|-----------|
| 19 | Seasonal changes in supercooling capacity and major cryoprotectants of overwintering Asian longhorned beetle (<i>Anoplophora glabripennis</i>) larvae. Agricultural and Forest Entomology, 2016, 18, 302-312. | 1.3 | 32 |
| 20 | Antennal transcriptome analysis and expression profiles of odorant binding proteins in <i>Egystia hippophaecolus</i> (Lepidoptera: Cossidae). BMC Genomics, 2016, 17, 651. | 2.8 | 36 |
| 21 | Antennal transcriptome analysis of the Asian longhorned beetle <i>Anoplophora glabripennis</i> . Scientific Reports, 2016, 6, 26652. | 3.3 | 85 |
| 22 | Identification of <i>Sirex noctilio</i> (Hymenoptera: Siricidae) Using a Species-Specific Cytochrome C Oxidase Subunit I PCR Assay. Journal of Economic Entomology, 2016, 109, 1424-1430. | 1.8 | 21 |
| 23 | Genetic Structure in the Seabuckthorn Carpenter Moth (<i>Holcocerus hippophaecolus</i>) in China: The Role of Outbreak Events, Geographical and Host Factors. PLoS ONE, 2012, 7, e30544. | 2.5 | 5 |
| 24 | AFLP analysis of genetic variation of <i>Hyphantria cunea</i> (Drury) populations in Beijing and a nearby site. Forestry Studies in China, 2009, 11, 14-19. | 0.4 | 4 |
| 25 | Methodological comparison of DNA extraction from <i>Holcocerus hippophaecolus</i> (Lepidoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 0,4 11 | | |
| 26 | Characterization of the complete mitochondrial genome of <i>Dendroctonus valens</i> and elimination of nuclear mitochondrial pseudogene interference. Journal of Applied Entomology, 0, , . | 1.8 | 1 |