

Scott M Geib

List of Publications by Year in descending order

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81
papers

2,896
citations

186265

28
h-index

197818

49
g-index

85
all docs

85
docs citations

85
times ranked

4007
citing authors

#	ARTICLE	IF	CITATIONS
1	HiFiAdapterFilt, a memory efficient read processing pipeline, prevents occurrence of adapter sequence in PacBio HiFi reads and their negative impacts on genome assembly. BMC Genomics, 2022, 23, 157.	2.8	71
2	White pupae phenotype of tephritids is caused by parallel mutations of a MFS transporter. Nature Communications, 2021, 12, 491.	12.8	25
3	The USDA-ARS Ag100Pest Initiative: High-Quality Genome Assemblies for Agricultural Pest Arthropod Research. Insects, 2021, 12, 626.	2.2	31
4	Genomic-wide sequencing reveals remarkable connection between widely disjunct populations of the internationally threatened bog buck moth. Insect Conservation and Diversity, 2020, 13, 495-500.	3.0	4
5	Implementing Low-Cost, High Accuracy DNA Barcoding From Single Molecule Sequencing to Screen Larval Tephritid Fruit Flies Intercepted at Ports of Entry. Annals of the Entomological Society of America, 2020, 113, 288-297.	2.5	12
6	Taro Genome Assembly and Linkage Map Reveal QTLs for Resistance to Taro Leaf Blight. G3: Genes, Genomes, Genetics, 2020, 10, 2763-2775.	1.8	15
7	Genomics confirms surprising ecological divergence and isolation in an endangered butterfly. Biodiversity and Conservation, 2020, 29, 1897-1921.	2.6	11
8	Population genomic and phenotype diversity of invasive <i>Drosophila suzukii</i> in Hawaii. Biological Invasions, 2020, 22, 1753-1770.	2.4	14
9	Phylogenomics reveals conservation challenges and opportunities for cryptic endangered species in a rapidly disappearing desert ecosystem. Biodiversity and Conservation, 2020, 29, 2185-2200.	2.6	3
10	Draft Genome of the Rice Coral <i>Montipora capitata</i> Obtained from Linked-Read Sequencing. Genome Biology and Evolution, 2019, 11, 2045-2054.	2.5	30
11	A high-quality genome assembly from a single, field-collected spotted lanternfly (<i>Lycorma delicatula</i>) using the PacBio Sequel II system. GigaScience, 2019, 8, .	6.4	35
12	The Genetic Diversity of <i>Bactrocera dorsalis</i> (Diptera: Tephritidae) in China and Neighboring Countries: A Review From Published Studies. Journal of Economic Entomology, 2019, 112, 2001-2006.	1.8	6
13	Range-wide population genomics of the Mexican fruit fly: Toward development of pathway analysis tools. Evolutionary Applications, 2019, 12, 1641-1660.	3.1	12
14	Targeted amplicon sequencing of 40 nuclear genes supports a single introduction and rapid radiation of Hawaiian <i>Metrosideros</i> (Myrtaceae). Plant Systematics and Evolution, 2019, 305, 961-974.	0.9	15
15	Divergent Switchgrass Cultivars Modify Cereal Aphid Transcriptomes. Journal of Economic Entomology, 2019, 112, 1887-1901.	1.8	3
16	Characterization of <i>Dendrolimus houi</i> Lajonquiere (Lepidoptera: Lasiocampidae) Transcriptome across All Life Stages. Insects, 2019, 10, 442.	2.2	10
17	The ABCs of CRISPR in Tephritidae: developing methods for inducing heritable mutations in the genera <i>Anastrepha</i> , <i>Bactrocera</i> and <i>Ceratitis</i> . Insect Molecular Biology, 2019, 28, 277-289.	2.0	32
18	PCR-Based Gut Content Analysis to Detect Predation of <i>Eriococcus ironsidei</i> (Hemiptera: Eriococcidae) by Coccinellidae Species in Macadamia Nut Orchards in Hawaii. Journal of Economic Entomology, 2018, 111, 885-891.	1.8	3

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19	Genome Annotation Generator: a simple tool for generating and correcting WGS annotation tables for NCBI submission. <i>GigaScience</i> , 2018, 7, 1-5.	6.4	41
20	HiMAP: Robust phylogenomics from highly multiplexed amplicon sequencing. <i>Molecular Ecology Resources</i> , 2018, 18, 1000-1019.	4.8	30
21	Molecular characterization of interspecific competition of <i>Diachasmimorpha longicaudata</i> (Ashmead) and <i>Fopius arisanus</i> (Sonan) parasitizing the oriental fruit fly, <i>Bactrocera dorsalis</i> (Hendel). <i>Biological Control</i> , 2018, 118, 10-15.	3.0	5
22	Incongruence between molecules and morphology: A seven-gene phylogeny of Dacini fruit flies paves the way for reclassification (Diptera: Tephritidae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 121, 139-149.	2.7	42
23	Comparative rearing parameters for bisexual and genetic sexing strains of <i>Zeugodacus cucurbitae</i> and <i>Bactrocera dorsalis</i> (Diptera: Tephritidae) on an artificial diet. <i>Journal of Asia-Pacific Entomology</i> , 2018, 21, 283-287.	0.9	7
24	<scp>mvmapper</scp>: Interactive spatial mapping of genetic structures. <i>Molecular Ecology Resources</i> , 2018, 18, 362-367.	4.8	2
25	Proteomic interactions between the parasitoid <i>Diachasmimorpha longicaudata</i> and the oriental fruit fly, <i>Bactrocera dorsalis</i> during host parasitism. <i>Journal of Asia-Pacific Entomology</i> , 2018, 21, 335-344.	0.9	3
26	Population genomics and comparisons of selective signatures in two invasions of melon fly, <i>Bactrocera cucurbitae</i> (Diptera: Tephritidae). <i>Biological Invasions</i> , 2018, 20, 1211-1228.	2.4	19
27	Transpacific coalescent pathways of coconut rhinoceros beetle biotypes: Resistance to biological control catalyses resurgence of an old pest. <i>Molecular Ecology</i> , 2018, 27, 4459-4474.	3.9	26
28	Phylogenomics supports incongruence between ecological specialization and taxonomy in a charismatic clade of buck moths. <i>Molecular Ecology</i> , 2018, 27, 4417-4429.	3.9	13
29	Tracking the Origins of Fly Invasions; Using Mitochondrial Haplotype Diversity to Identify Potential Source Populations in Two Genetically Intertwined Fruit Fly Species (<i>Bactrocera carambolae</i> and) Tj ETQq1 1 0.784314 rgBT / Overlock		
30	Comparative proteomic profiling within each developmental stage of the solanum fruit fly, <i>Bactrocera latifrons</i> Hendel. <i>Journal of Asia-Pacific Entomology</i> , 2018, 21, 1186-1197.	0.9	1
31	Molecular Characterization of the 2016 New World Screwworm (Diptera: Calliphoridae) Outbreak in the Florida Keys. <i>Journal of Medical Entomology</i> , 2018, 55, 938-946.	1.8	7
32	Host-plant induced changes in microbial community structure and midgut gene expression in an invasive polyphage (<i>Anoplophora glabripennis</i>). <i>Scientific Reports</i> , 2018, 8, 9620.	3.3	22
33	Comparative Proteomic Profiling between Each of Two Consecutive Developmental Stages of the Solanum Fruit Fly, <i>Bactrocera latifrons</i> (Hendel). <i>International Journal of Molecular Sciences</i> , 2018, 19, 1996.	4.1	2
34	Rapid Viral Symbiogenesis via Changes in Parasitoid Wasp Genome Architecture. <i>Molecular Biology and Evolution</i> , 2018, 35, 2463-2474.	8.9	44
35	Host plant species determines symbiotic bacterial community mediating suppression of plant defenses. <i>Scientific Reports</i> , 2017, 7, 39690.	3.3	76
36	Organ-specific transcriptome profiling of metabolic and pigment biosynthesis pathways in the floral ornamental progenitor species <i>Anthurium amnicola</i> Dressler. <i>Scientific Reports</i> , 2017, 7, 1596.	3.3	13

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37	Whole Genome Sequencing of the Braconid Parasitoid Wasp <i>Fopius arisanus</i> , an Important Biocontrol Agent of Pest Tephritid Fruit Flies. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2407-2411.	1.8	33
38	A New Diagnostic Resource for <i>Ceratitis capitata</i> Strain Identification Based on QTL Mapping. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3637-3647.	1.8	8
39	A Chromosome-Scale Assembly of the <i>Bactrocera cucurbitae</i> Genome Provides Insight to the Genetic Basis of white pupae. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1927-1940.	1.8	33
40	Prediction of a peptidome for the western tarnished plant bug <i>Lygus hesperus</i> . <i>General and Comparative Endocrinology</i> , 2017, 243, 22-38.	1.8	13
41	Variation in DNA Methylation Is Not Consistently Reflected by Sociality in Hymenoptera. <i>Genome Biology and Evolution</i> , 2017, 9, 1687-1698.	2.5	46
42	De novo metatranscriptome assembly and coral gene expression profile of <i>Montipora capitata</i> with growth anomaly. <i>BMC Genomics</i> , 2017, 18, 710.	2.8	22
43	LARVAL X-RAY IRRADIATION INFLUENCES PROTEIN EXPRESSION IN PUPAE OF THE ORIENTAL FRUIT FLY, <i>BACTROCERA DORSALIS</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2016, 92, 192-209.	1.5	5
44	Genome Sequence of <i>Fusarium</i> Isolate MYA-4552 from the Midgut of <i>Anoplophora glabripennis</i> , an Invasive, Wood-Boring Beetle. <i>Genome Announcements</i> , 2016, 4, .	0.8	11
45	Identification of a carboxylesterase associated with resistance to naled in <i>Bactrocera dorsalis</i> (Hendel). <i>Pesticide Biochemistry and Physiology</i> , 2016, 131, 24-31.	3.6	8
46	The whole genome sequence of the Mediterranean fruit fly, <i>Ceratitis capitata</i> (Wiedemann), reveals insights into the biology and adaptive evolution of a highly invasive pest species. <i>Genome Biology</i> , 2016, 17, 192.	8.8	130
47	Predation by flat bark beetles (Coleoptera: Silvanidae and Laemophloeidae) on coffee berry borer (Coleoptera: Curculionidae) in Hawaii coffee. <i>Biological Control</i> , 2016, 101, 152-158.	3.0	24
48	Genome of the Asian longhorned beetle (<i>Anoplophora glabripennis</i>), a globally significant invasive species, reveals key functional and evolutionary innovations at the beetle-plant interface. <i>Genome Biology</i> , 2016, 17, 227.	8.8	244
49	Contrasting diets reveal metabolic plasticity in the tree-killing beetle, <i>Anoplophora glabripennis</i> (Cerambycidae: Lamiinae). <i>Scientific Reports</i> , 2016, 6, 33813.	3.3	21
50	De novo construction of an expanded transcriptome assembly for the western tarnished plant bug, <i>Lygus hesperus</i> . <i>GigaScience</i> , 2016, 5, 6.	6.4	26
51	Molecular Markers Detect Cryptic Predation on Coffee Berry Borer (Coleoptera: Curculionidae) by Silvanid and Laemophloeid Flat Bark Beetles (Coleoptera: Silvanidae, Laemophloeidae) in Coffee Beans. <i>Journal of Economic Entomology</i> , 2016, 109, 100-105.	1.8	12
52	MicroRNAs in the oriental fruit fly, <i>Bactrocera dorsalis</i> : extending <i>Drosophila</i> miRNA conservation to the Tephritidae. <i>BMC Genomics</i> , 2015, 16, 740.	2.8	11
53	An Expanded <i>Metrosideros</i> (Myrtaceae) to Include <i>Carpolepis</i> and <i>Tepualia</i> ; Based on Nuclear Genes. <i>Systematic Botany</i> , 2015, 40, 782-790.	0.5	13
54	A qPCR-based method for detecting parasitism of <i>Fopius arisanus</i> (Sonan) in oriental fruit flies, <i>Bactrocera dorsalis</i> (Hendel). <i>Pest Management Science</i> , 2015, 71, 1666-1674.	3.4	6

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55	Synonymization of key pest species within the <i>Bactrocera dorsalis</i> species complex (Diptera: Tephritidae): taxonomic changes based on a review of 20 years of integrative morphological, molecular, cytogenetic, behavioural and chemoecological data. <i>Systematic Entomology</i> , 2015, 40, 456-471.	3.9	175
56	Draft Genome Sequence of <i>Erwinia tracheiphila</i> , an Economically Important Bacterial Pathogen of Cucurbits. <i>Genome Announcements</i> , 2015, 3, .	0.8	14
57	Pupal X-ray irradiation influences protein expression in adults of the oriental fruit fly, <i>Bactrocera dorsalis</i> . <i>Journal of Insect Physiology</i> , 2015, 76, 7-16.	2.0	15
58	Reconstructing a comprehensive transcriptome assembly of a white-pupal translocated strain of the pest fruit fly <i>Bactrocera cucurbitae</i> . <i>GigaScience</i> , 2015, 4, 14.	6.4	18
59	Transcriptome of the egg parasitoid <i>Fopius arisanus</i> : an important biocontrol tool for Tephritid fruit fly suppression. <i>GigaScience</i> , 2015, 4, 36.	6.4	7
60	Functional genomics and microbiome profiling of the Asian longhorned beetle (<i>Anoplophora</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 547 beetles. <i>BMC Genomics</i> , 2014, 15, 1096.	2.8	93
61	Genetic Diversity of <i>Bactrocera dorsalis</i> (Diptera: Tephritidae) on the Hawaiian Islands: Implications for an Introduction Pathway Into California. <i>Journal of Economic Entomology</i> , 2014, 107, 1946-1958.	1.8	28
62	Characterizing the developmental transcriptome of the oriental fruit fly, <i>Bactrocera dorsalis</i> (Diptera: Tephritidae) through comparative genomic analysis with <i>Drosophila melanogaster</i> utilizing modENCODE datasets. <i>BMC Genomics</i> , 2014, 15, 942.	2.8	37
63	A genomic perspective to assessing quality of mass-reared SIT flies used in Mediterranean fruit fly (<i>Ceratitis capitata</i>) eradication in California. <i>BMC Genomics</i> , 2014, 15, 98.	2.8	33
64	DIETARY LUFENURON REDUCES EGG HATCH AND INFLUENCES PROTEIN EXPRESSION IN THE FRUIT FLY <i>Bactrocera latifrons</i> (HENDEL). <i>Archives of Insect Biochemistry and Physiology</i> , 2014, 86, 193-208.	1.5	4
65	Effect of host <i>Bactrocera dorsalis</i> sex on yield and quality of the parasitoid <i>Fopius arisanus</i> . <i>BioControl</i> , 2014, 59, 395-402.	2.0	5
66	A Computer Model of Insect Traps in a Landscape. <i>Scientific Reports</i> , 2014, 4, 7015.	3.3	33
67	Transcriptome-Based Identification of ABC Transporters in the Western Tarnished Plant Bug <i>Lygus hesperus</i> . <i>PLoS ONE</i> , 2014, 9, e113046.	2.5	48
68	Midgut transcriptome profiling of <i>Anoplophora glabripennis</i> , a lignocellulose degrading cerambycid beetle. <i>BMC Genomics</i> , 2013, 14, 850.	2.8	65
69	An Evaluation of the Species Status of <i>Bactrocera invadens</i> and the Systematics of the <i>Bactrocera dorsalis</i> (Diptera: Tephritidae) Complex. <i>Annals of the Entomological Society of America</i> , 2013, 106, 684-694.	2.5	41
70	Sequencing and De Novo Assembly of the Western Tarnished Plant Bug (<i>Lygus hesperus</i>) Transcriptome. <i>PLoS ONE</i> , 2013, 8, e55105.	2.5	49
71	Metagenomic Profiling Reveals Lignocellulose Degrading System in a Microbial Community Associated with a Wood-Feeding Beetle. <i>PLoS ONE</i> , 2013, 8, e73827.	2.5	125
72	Phylogenetic Analysis of <i>Fusarium solani</i> Associated with the Asian Longhorned Beetle, <i>Anoplophora glabripennis</i> . <i>Insects</i> , 2012, 3, 141-160.	2.2	20

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73	Truncated transcripts of nicotinic acetylcholine subunit gene <i>Bd1±6</i> are associated with spinosad resistance in <i>Bactrocera dorsalis</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2012, 42, 806-815.	2.7	79
74	Proteomic Analysis of <i>Fusarium solani</i> Isolated from the Asian Longhorned Beetle, <i>Anoplophora glabripennis</i> . <i>PLoS ONE</i> , 2012, 7, e32990.	2.5	33
75	Effects of laccase on lignin depolymerization and enzymatic hydrolysis of ensiled corn stover. <i>Bioresource Technology</i> , 2012, 117, 186-192.	9.6	97
76	An Optimized Protocol for Rearing <i>Fopius arisanus</i> , a Parasitoid of Tephritid Fruit Flies. <i>Journal of Visualized Experiments</i> , 2011, , .	0.3	10
77	Identification of proteins involved in lignocellulose degradation using in gel zymogram analysis combined with mass spectroscopy-based peptide analysis of gut proteins from larval Asian longhorned beetles, <i>Anoplophora glabripennis</i> . <i>Insect Science</i> , 2010, 17, 253-264.	3.0	48
78	Genome Sequence of a Cellulose-Producing Bacterium, <i>Gluconacetobacter hansenii</i> ATCC 23769. <i>Journal of Bacteriology</i> , 2010, 192, 4256-4257.	2.2	50
79	Microbial Community Profiling to Investigate Transmission of Bacteria Between Life Stages of the Wood-Boring Beetle, <i>Anoplophora glabripennis</i> . <i>Microbial Ecology</i> , 2009, 58, 199-211.	2.8	42
80	Effect of Host Tree Species on Cellulase Activity and Bacterial Community Composition in the Gut of Larval Asian Longhorned Beetle. <i>Environmental Entomology</i> , 2009, 38, 686-699.	1.4	64
81	Lignin degradation in wood-feeding insects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 12932-12937.	7.1	279