

# 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	Lignin degradation in wood-feeding insects. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 12932-12937.	7.1	279
2	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. Genome Biology, 2016, 17, 227.	8.8	244
3	Synonymization of key pest species within the <i>Bactrocera dorsalis</i> species complex ( <i>Drosophila</i> : <i>Tephritidae</i> ): taxonomic changes based on a review of 20 years of integrative morphological, molecular, cytogenetic, behavioural and chemoeological data. Systematic Entomology, 2015, 40, 456-471.	3.9	175
4	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. Genome Biology, 2016, 17, 192.	8.8	130
5	Metagenomic Profiling Reveals Lignocellulose Degrading System in a Microbial Community Associated with a Wood-Feeding Beetle. PLoS ONE, 2013, 8, e73827.	2.5	125
6	Effects of laccase on lignin depolymerization and enzymatic hydrolysis of ensiled corn stover. Bioresource Technology, 2012, 117, 186-192.	9.6	97
7	Functional genomics and microbiome profiling of the Asian longhorned beetle ( <i>Anoplophora</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 1000 beetles. BMC Genomics, 2014, 15, 1096.	2.8	93
8	Truncated transcripts of nicotinic acetylcholine subunit gene <i>Bd1±6</i> are associated with spinosad resistance in <i>Bactrocera dorsalis</i> . Insect Biochemistry and Molecular Biology, 2012, 42, 806-815.	2.7	79
9	Host plant species determines symbiotic bacterial community mediating suppression of plant defenses. Scientific Reports, 2017, 7, 39690.	3.3	76
10	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
11	Midgut transcriptome profiling of <i>Anoplophora glabripennis</i> , a lignocellulose degrading cerambycid beetle. BMC Genomics, 2013, 14, 850.	2.8	65
12	Effect of Host Tree Species on Cellulase Activity and Bacterial Community Composition in the Gut of Larval Asian Longhorned Beetle. Environmental Entomology, 2009, 38, 686-699.	1.4	64
13	Genome Sequence of a Cellulose-Producing Bacterium, <i>Gluconacetobacter hansenii</i> ATCC 23769. Journal of Bacteriology, 2010, 192, 4256-4257.	2.2	50
14	Sequencing and De Novo Assembly of the Western Tarnished Plant Bug ( <i>Lygus hesperus</i> ) Transcriptome. PLoS ONE, 2013, 8, e55105.	2.5	49
15	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> . Insect Science, 2010, 17, 253-264.	3.0	48
16	Transcriptome-Based Identification of ABC Transporters in the Western Tarnished Plant Bug <i>Lygus hesperus</i> . PLoS ONE, 2014, 9, e113046.	2.5	48
17	Variation in DNA Methylation Is Not Consistently Reflected by Sociality in Hymenoptera. Genome Biology and Evolution, 2017, 9, 1687-1698.	2.5	46
18	Rapid Viral Symbiogenesis via Changes in Parasitoid Wasp Genome Architecture. Molecular Biology and Evolution, 2018, 35, 2463-2474.	8.9	44

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19	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
20	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
21	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
22	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
23	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
24	A high-quality genome assembly from a single, field-collected spotted lanternfly ( <i>Lycorma delicatula</i> ) using the PacBio Sequel II system. <i>GigaScience</i> , 2019, 8, .	6.4	35
25	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
26	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
27	A Computer Model of Insect Traps in a Landscape. <i>Scientific Reports</i> , 2014, 4, 7015.	3.3	33
28	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
29	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
30	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> . <i>Insect Molecular Biology</i> , 2019, 28, 277-289.	2.0	32
31	The USDA-ARS Ag100Pest Initiative: High-Quality Genome Assemblies for Agricultural Pest Arthropod Research. <i>Insects</i> , 2021, 12, 626.	2.2	31
32	HiMAP: Robust phylogenomics from highly multiplexed amplicon sequencing. <i>Molecular Ecology Resources</i> , 2018, 18, 1000-1019.	4.8	30
33	Draft Genome of the Rice Coral <i>Montipora capitata</i> Obtained from Linked-Read Sequencing. <i>Genome Biology and Evolution</i> , 2019, 11, 2045-2054.	2.5	30
34	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
35	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
36	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

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37	White pupae phenotype of tephritids is caused by parallel mutations of a MFS transporter. <i>Nature Communications</i> , 2021, 12, 491.	12.8	25
38	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
39	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
40	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
41	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
42	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) <i>Tj ETQq0 0 0 rgBTi/0verlock210 Tf 50 5</i>		
43	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
44	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
45	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
46	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
47	Targeted amplicon sequencing of 40 nuclear genes supports a single introduction and rapid radiation of Hawaiian <i>Metrosideros</i> (Myrtaceae). <i>Plant Systematics and Evolution</i> , 2019, 305, 961-974.	0.9	15
48	Taro Genome Assembly and Linkage Map Reveal QTLs for Resistance to Taro Leaf Blight. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2763-2775.	1.8	15
49	Draft Genome Sequence of <i>Erwinia tracheiphila</i> , an Economically Important Bacterial Pathogen of Cucurbits. <i>Genome Announcements</i> , 2015, 3, .	0.8	14
50	Population genomic and phenotype diversity of invasive <i>Drosophila suzukii</i> in Hawaii. <i>Biological Invasions</i> , 2020, 22, 1753-1770.	2.4	14
51	An Expanded &lt;l&gt;&lt;/l&gt;&lt;/l&gt;&lt;/l&gt;&lt;/l&gt; (Myrtaceae) to Include &lt;l&gt;&lt;/l&gt;&lt;/l&gt;&lt;/l&gt; and &lt;l&gt;&lt;/l&gt;&lt;/l&gt;&lt;/l&gt; Based on Nuclear Genes. <i>Systematic Botany</i> , 2015, 40, 782-790.	0.5	13
52	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
53	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
54	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

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55	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
56	Range-wide population genomics of the Mexican fruit fly: Toward development of pathway analysis tools. <i>Evolutionary Applications</i> , 2019, 12, 1641-1660.	3.1	12
57	Implementing Low-Cost, High Accuracy DNA Barcoding From Single Molecule Sequencing to Screen Larval Tephritid Fruit Flies Intercepted at Ports of Entry. <i>Annals of the Entomological Society of America</i> , 2020, 113, 288-297.	2.5	12
58	MicroRNAs in the oriental fruit fly, <i>Bactrocera dorsalis</i> : extending <i>Drosophilid</i> miRNA conservation to the Tephritidae. <i>BMC Genomics</i> , 2015, 16, 740.	2.8	11
59	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
60	Genomics confirms surprising ecological divergence and isolation in an endangered butterfly. <i>Biodiversity and Conservation</i> , 2020, 29, 1897-1921.	2.6	11
61	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
62	Characterization of <i>Dendrolimus houi</i> Lajonquiere (Lepidoptera: Lasiocampidae) Transcriptome across All Life Stages. <i>Insects</i> , 2019, 10, 442.	2.2	10
63	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
64	A New Diagnostic Resource for <i>Ceratitidis capitata</i> Strain Identification Based on QTL Mapping. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3637-3647.	1.8	8
65	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
66	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
67	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
68	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
69	The Genetic Diversity of <i>Bactrocera dorsalis</i> (Diptera: Tephritidae) in China and Neighboring Countries: A Review From Published Studies. <i>Journal of Economic Entomology</i> , 2019, 112, 2001-2006.	1.8	6
70	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
71	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
72	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

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73	DIETARY LUFENURON REDUCES EGG HATCH AND INFLUENCES PROTEIN EXPRESSION IN THE FRUIT FLY <i>Bactrocera latifrons</i> (HENDEL). Archives of Insect Biochemistry and Physiology, 2014, 86, 193-208.	1.5	4
74	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
75	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
76	Proteomic interactions between the parasitoid <i>Diachasmimorpha longicaudata</i> and the oriental fruit fly, <i>Bactrocera dorsalis</i> during host parasitism. Journal of Asia-Pacific Entomology, 2018, 21, 335-344.	0.9	3
77	Divergent Switchgrass Cultivars Modify Cereal Aphid Transcriptomes. Journal of Economic Entomology, 2019, 112, 1887-1901.	1.8	3
78	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
79	<i>mvmapper</i> : Interactive spatial mapping of genetic structures. Molecular Ecology Resources, 2018, 18, 362-367.	4.8	2
80	Comparative Proteomic Profiling between Each of Two Consecutive Developmental Stages of the Solanum Fruit Fly, <i>Bactrocera latifrons</i> (Hendel). International Journal of Molecular Sciences, 2018, 19, 1996.	4.1	2
81	Comparative proteomic profiling within each developmental stage of the solanum fruit fly, <i>Bactrocera latifrons</i> Hendel. Journal of Asia-Pacific Entomology, 2018, 21, 1186-1197.	0.9	1