

# Thomas K Walsh

## List of Publications by Year in descending order

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74  
papers

4,507  
citations

136950

32  
h-index

114465

63  
g-index

84  
all docs

84  
docs citations

84  
times ranked

4578  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome Sequence of the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>PLoS Biology</i> , 2010, 8, e1000313.	5.6	913
2	A Brave New World for an Old World Pest: <i>Helicoverpa armigera</i> (Lepidoptera: Noctuidae) in Brazil. <i>PLoS ONE</i> , 2013, 8, e80134.	2.5	271
3	Genomic innovations, transcriptional plasticity and gene loss underlying the evolution and divergence of two highly polyphagous and invasive <i>Helicoverpa</i> pest species. <i>BMC Biology</i> , 2017, 15, 63.	3.8	238
4	Comparative analysis of detoxification enzymes in <i>Acyrtosiphon pisum</i> and <i>Myzus persicae</i> . <i>Insect Molecular Biology</i> , 2010, 19, 155-164.	2.0	203
5	Insect Resistance to <i>Bacillus thuringiensis</i> Toxin Cry2Ab Is Conferred by Mutations in an ABC Transporter Subfamily A Protein. <i>PLoS Genetics</i> , 2015, 11, e1005534.	3.5	155
6	Multifaceted biological insights from a draft genome sequence of the tobacco hornworm moth, <i>Manduca sexta</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2016, 76, 118-147.	2.7	154
7	The Potential Distribution of Invading <i>Helicoverpa armigera</i> in North America: Is It Just a Matter of Time?. <i>PLoS ONE</i> , 2015, 10, e0119618.	2.5	136
8	A functional DNA methylation system in the pea aphid, <i>Acyrtosiphon pisum</i> . <i>Insect Molecular Biology</i> , 2010, 19, 215-228.	2.0	123
9	Molecular detection of benzimidazole resistance in <i>Haemonchus contortus</i> using real-time PCR and pyrosequencing. <i>Parasitology</i> , 2009, 136, 349-358.	1.5	120
10	Hybridization and gene flow in the mega-pest lineage of moth, <i>Helicoverpa</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 5034-5039.	7.1	113
11	Bioinformatic prediction, deep sequencing of microRNAs and expression analysis during phenotypic plasticity in the pea aphid, <i>Acyrtosiphon pisum</i> . <i>BMC Genomics</i> , 2010, 11, 281.	2.8	95
12	CRISPR/Cas9 mediated genome editing of <i>Helicoverpa armigera</i> with mutations of an ABC transporter gene HaABCA2 confers resistance to <i>Bacillus thuringiensis</i> Cry2A toxins. <i>Insect Biochemistry and Molecular Biology</i> , 2017, 87, 147-153.	2.7	95
13	Detection of sister-species in invasive populations of the fall armyworm <i>Spodoptera frugiperda</i> (Lepidoptera: Noctuidae) from Uganda. <i>PLoS ONE</i> , 2018, 13, e0194571.	2.5	82
14	Are feeding preferences and insecticide resistance associated with the size of detoxifying enzyme families in insect herbivores?. <i>Current Opinion in Insect Science</i> , 2016, 13, 70-76.	4.4	80
15	Detoxifying enzyme complements and host use phenotypes in 160 insect species. <i>Current Opinion in Insect Science</i> , 2019, 31, 131-138.	4.4	75
16	Population structure and gene flow in the global pest, <i>Helicoverpa armigera</i> . <i>Molecular Ecology</i> , 2016, 25, 5296-5311.	3.9	71
17	Nematode ligand-gated chloride channels: an appraisal of their involvement in macrocyclic lactone resistance and prospects for developing molecular markers. <i>Parasitology</i> , 2007, 134, 1111-1121.	1.5	68
18	Bt resistance in Australian insect pest species. <i>Current Opinion in Insect Science</i> , 2016, 15, 78-83.	4.4	67

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19	Juvenile hormone titre and related gene expression during the change of reproductive modes in the pea aphid. <i>Insect Molecular Biology</i> , 2012, 21, 49-60.	2.0	66
20	ABC transporter mis-splicing associated with resistance to Bt toxin Cry2Ab in laboratory- and field-selected pink bollworm. <i>Scientific Reports</i> , 2018, 8, 13531.	3.3	66
21	The cys-loop ligand-gated ion channel gene family of <i>Brugia malayi</i> and <i>Trichinella spiralis</i> : a comparison with <i>Caenorhabditis elegans</i> . <i>Invertebrate Neuroscience</i> , 2007, 7, 219-226.	1.8	64
22	Adaptive Introgression across Semipermeable Species Boundaries between Local <i>Helicoverpa zea</i> and Invasive <i>Helicoverpa armigera</i> Moths. <i>Molecular Biology and Evolution</i> , 2020, 37, 2568-2583.	8.9	64
23	Mitochondrial DNA and trade data support multiple origins of <i>Helicoverpa armigera</i> (Lepidoptera, Tj ETQq1 1 0.784314 rgBT /Overlo	3.3	61
24	Whole-genome sequencing to detect mutations associated with resistance to insecticides and Bt proteins in <i>Spodoptera frugiperda</i> . <i>Insect Science</i> , 2021, 28, 627-638.	3.0	61
25	Expansion of the miRNA Pathway in the Hemipteran Insect <i>Acyrtosiphon pisum</i> . <i>Molecular Biology and Evolution</i> , 2010, 27, 979-987.	8.9	56
26	Characterization of the resistance to Vip3Aa in <i>Helicoverpa armigera</i> from Australia and the role of midgut processing and receptor binding. <i>Scientific Reports</i> , 2016, 6, 24311.	3.3	52
27	Multiple recombination events between two cytochrome P450 loci contribute to global pyrethroid resistance in <i>Helicoverpa armigera</i> . <i>PLoS ONE</i> , 2018, 13, e0197760.	2.5	50
28	Transgenic cowpeas ( <i>Vigna unguiculata</i> L. Walp) expressing <i>Bacillus thuringiensis</i> Vip3Ba protein are protected against the Maruca pod borer ( <i>Maruca vitrata</i> ). <i>Plant Cell, Tissue and Organ Culture</i> , 2017, 131, 335-345.	2.3	48
29	Identification of ion channel genes in the <i>Acyrtosiphon pisum</i> genome. <i>Insect Molecular Biology</i> , 2010, 19, 141-153.	2.0	46
30	Expansion of Genes Encoding piRNA-Associated Argonaute Proteins in the Pea Aphid: Diversification of Expression Profiles in Different Plastic Morphs. <i>PLoS ONE</i> , 2011, 6, e28051.	2.5	38
31	Altered <i>avr-14B</i> gene transcription patterns in ivermectin-resistant isolates of the cattle parasites, <i>Cooperia oncophora</i> and <i>Ostertagia ostertagi</i> . <i>International Journal for Parasitology</i> , 2011, 41, 951-957.	3.1	37
32	Characterization of a Drinking Water Distribution Pipeline Terminally Colonized by <i>Naegleria fowleri</i> . <i>Environmental Science &amp; Technology</i> , 2016, 50, 2890-2898.	10.0	36
33	Mitochondrial DNA COI characterization of <i>Helicoverpa armigera</i> (Lepidoptera: Noctuidae) from Paraguay and Uruguay. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.2	34
34	Global population genomic signature of <i>Spodoptera frugiperda</i> (fall armyworm) supports complex introduction events across the Old World. <i>Communications Biology</i> , 2022, 5, 297.	4.4	34
35	Detection and measurement of benzimidazole resistance alleles in <i>Haemonchus contortus</i> using real-time PCR with locked nucleic acid Taqman probes. <i>Veterinary Parasitology</i> , 2007, 144, 304-312.	1.8	32
36	Geographic Monitoring of Insecticide Resistance Mutations in Native and Invasive Populations of the Fall Armyworm. <i>Insects</i> , 2021, 12, 468.	2.2	32

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37	A genomic approach to identify and monitor a novel pyrethroid resistance mutation in the redlegged earth mite, <i>Halotydeus destructor</i> . <i>Pesticide Biochemistry and Physiology</i> , 2018, 144, 83-90.	3.6	31
38	Determinants of Insecticide Resistance Evolution: Comparative Analysis Among Heliiothines. <i>Annual Review of Entomology</i> , 2022, 67, 387-406.	11.8	30
39	Variation in P450-mediated fenvalerate resistance levels is not correlated with CYP337B3 genotype in Chinese populations of <i>Helicoverpa armigera</i> . <i>Pesticide Biochemistry and Physiology</i> , 2015, 121, 129-135.	3.6	28
40	Dual Cry2Ab and Vip3A Resistant Strains of <i>Helicoverpa armigera</i> and <i>Helicoverpa punctigera</i> ; (Lepidoptera: Noctuidae); Testing Linkage Between Loci and Monitoring of Allele Frequencies. <i>Journal of Economic Entomology</i> , 2014, 107, 1610-1617.	1.8	22
41	Multiple incursion pathways for <i>Helicoverpa armigera</i> in Brazil show its genetic diversity spreading in a connected world. <i>Scientific Reports</i> , 2019, 9, 19380.	3.3	20
42	Cryptosporidiosis Modulates the Gut Microbiome and Metabolism in a Murine Infection Model. <i>Metabolites</i> , 2021, 11, 380.	2.9	20
43	Analysis of cross-resistance to Vip3 proteins in eight insect colonies, from four insect species, selected for resistance to <i>Bacillus thuringiensis</i> insecticidal proteins. <i>Journal of Invertebrate Pathology</i> , 2018, 155, 64-70.	3.2	19
44	Investigation into the microbial communities and associated crude oil-contamination along a Gulf War impacted groundwater system in Kuwait. <i>Water Research</i> , 2020, 170, 115314.	11.3	19
45	Bioaccumulation and impact of maternal PFAS offloading on egg biochemistry from wild-caught freshwater turtles ( <i>Emydura macquarii macquarii</i> ). <i>Science of the Total Environment</i> , 2022, 817, 153019.	8.0	19
46	Comparison of biofilm ecology supporting growth of individual <i>Naegleria</i> species in a drinking water distribution system. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	2.7	18
47	Genomics and transcriptomics yields a system-level view of the biology of the pathogen <i>Naegleria fowleri</i> . <i>BMC Biology</i> , 2021, 19, 142.	3.8	18
48	Insecticide resistance status of <i>Bemisia tabaci</i> MEAM1 (Hemiptera: Aleyrodidae) in Australian cotton production valleys. <i>Austral Entomology</i> , 2020, 59, 202-214.	1.4	16
49	Soybean Stem Fly, <i>Melanagromyza sojae</i> (Diptera: Agromyzidae), in the New World: detection of high genetic diversity from soybean fields in Brazil. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.2	15
50	Mitochondrial DNA genomes of five major <i>Helicoverpa</i> pest species from the Old and New Worlds (Lepidoptera: Noctuidae). <i>Ecology and Evolution</i> , 2019, 9, 2933-2944.	1.9	15
51	Complete Mitochondrial Genome of <i>Helicoverpa zea</i> (Lepidoptera: Noctuidae) and Expression Profiles of Mitochondrial-Encoded Genes in Early and Late Embryos. <i>Journal of Insect Science</i> , 2016, 16, 40.	1.5	14
52	Isolating, characterising and identifying a Cry1Ac resistance mutation in field populations of <i>Helicoverpa punctigera</i> . <i>Scientific Reports</i> , 2018, 8, 2626.	3.3	13
53	Efficacy and Resistance Management Potential of a Modified Vip3C Protein for Control of <i>Spodoptera frugiperda</i> in Maize. <i>Scientific Reports</i> , 2018, 8, 16204.	3.3	12
54	<i>Naegleria fowleri</i> in drinking water distribution systems. <i>Current Opinion in Environmental Science and Health</i> , 2020, 16, 22-27.	4.1	12

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55	Identification of cDNAs induced by the organophosphate trichlorphon in the parasitic copepod <i>Lepeophtheirus salmonis</i> (Copepoda; Caligidae). <i>Pesticide Biochemistry and Physiology</i> , 2007, 88, 26-30.	3.6	11
56	ACR-26: A novel nicotinic receptor subunit of parasitic nematodes. <i>Molecular and Biochemical Parasitology</i> , 2012, 183, 151-157.	1.1	10
57	Complete mitochondrial genome of the soybean stem fly <i>Melanagromyza sojae</i> (Diptera: Tj ETQq1 1 0.784314 rgBT /Overlock 0.7 10	0.7	10
58	Characterization of the complete mitochondrial genome of the Australian Heliothine moth, <i>Australothis rubrescens</i> (Lepidoptera: Noctuidae). <i>Mitochondrial DNA</i> , 2016, 27, 167-168.	0.6	10
59	The complete mitochondrial DNA genome of a Chloridea ( <i>Heliothis</i> ) <i>subflexa</i> (Lepidoptera: Noctuidae) morpho-species. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4532-4533.	0.7	10
60	Preferential feeding in <i>Naegleria fowleri</i> ; intracellular bacteria isolated from amoebae in operational drinking water distribution systems. <i>Water Research</i> , 2018, 141, 126-134.	11.3	10
61	Moving to Keep Fit: Feeding Behavior and Movement of <i>Helicoverpa armigera</i> (Lepidoptera: Noctuidae) on Artificial Diet With Different Protein: Carbohydrate Ratios. <i>Journal of Insect Science</i> , 2019, 19, .	1.5	10
62	Protein-carbohydrate regulation in <i>Helicoverpa armigera</i> and <i>H. punctigera</i> and how diet protein-carbohydrate content affects insect susceptibility to Bt toxins. <i>Journal of Insect Physiology</i> , 2018, 106, 88-95.	2.0	9
63	Biodegradability of legacy crude oil contamination in Gulf War damaged groundwater wells in Northern Kuwait. <i>Biodegradation</i> , 2019, 30, 71-85.	3.0	9
64	Oxidative stress delays development and alters gene expression in the agricultural pest moth, <i>Helicoverpa armigera</i> . <i>Ecology and Evolution</i> , 2020, 10, 5680-5693.	1.9	9
65	On species delimitation, hybridization and population structure of cassava whitefly in Africa. <i>Scientific Reports</i> , 2021, 11, 7923.	3.3	9
66	Omics-based ecosurveillance for the assessment of ecosystem function, health, and resilience. <i>Emerging Topics in Life Sciences</i> , 2022, 6, 185-199.	2.6	9
67	Unravelling Microbial Communities Associated with Different Light Non-Aqueous Phase Liquid Types Undergoing Natural Source Zone Depletion Processes at a Legacy Petroleum Site. <i>Water (Switzerland)</i> , 2021, 13, 898.	2.7	8
68	Omics-based ecosurveillance uncovers the influence of estuarine macrophytes on sediment microbial function and metabolic redundancy in a tropical ecosystem. <i>Science of the Total Environment</i> , 2022, 809, 151175.	8.0	8
69	The role of predicted chemotactic and hydrocarbon degrading taxa in natural source zone depletion at a legacy petroleum hydrocarbon site. <i>Journal of Hazardous Materials</i> , 2022, 430, 128482.	12.4	8
70	Linkage mapping an indoxacarb resistance locus in <i>Helicoverpa armigera</i> (Lepidoptera: Noctuidae) by genotype-by-sequence. <i>Pest Management Science</i> , 2020, 76, 617-627.	3.4	6
71	Screening for insecticide resistance in Australian field populations of <i>Bemisia tabaci</i> (Hemiptera: Aleyrodidae) using bioassays and DNA sequencing. <i>Pest Management Science</i> , 2022, 78, 3248-3259.	3.4	3
72	Genomic insights into a population of introduced European rabbits <i>Oryctolagus cuniculus</i> in Australia and the development of genetic resistance to rabbit hemorrhagic disease virus. <i>Transboundary and Emerging Diseases</i> , 2021, , .	3.0	2

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73	HearNPV susceptibility in <i>Helicoverpa armigera</i> and <i>Helicoverpa punctigera</i> strains resistant to Bt toxins Cry1Ac, Cry2Ab, and Vip3Aa. <i>Journal of Invertebrate Pathology</i> , 2021, 183, 107598.	3.2	2
74	Improving Risk Assessment of Noctuid Pests at North American Ports and Farms by Differentiating Egg Morphology. <i>Annals of the Entomological Society of America</i> , 2019, 112, 443-450.	2.5	1