

Karl H J Gordon

List of Publications by Year in descending order

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77
papers

9,123
citations

81743

39
h-index

69108

77
g-index

80
all docs

80
docs citations

80
times ranked

9173
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	2.0	34
2	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.	1.5	61
3	Geographic Monitoring of Insecticide Resistance Mutations in Native and Invasive Populations of the Fall Armyworm. <i>Insects</i> , 2021, 12, 468.	1.0	32
4	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.	1.7	6
5	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.	3.5	64
6	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.	0.8	15
7	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.	1.6	20
8	Going global – genomic insights into insect invasions. <i>Current Opinion in Insect Science</i> , 2019, 31, 123-130.	2.2	55
9	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.	3.3	113
10	Standardized molecular diagnostic tool for the identification of cryptic species within the <i>Bemisia tabaci</i> complex. <i>Pest Management Science</i> , 2018, 74, 170-173.	1.7	32
11	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.	1.6	66
12	Genome-wide analyses of the <i>Bemisia tabaci</i> species complex reveal contrasting patterns of admixture and complex demographic histories. <i>PLoS ONE</i> , 2018, 13, e0190555.	1.1	46
13	Mitochondrial DNA and trade data support multiple origins of <i>Helicoverpa armigera</i> (Lepidoptera, Tj ETQq1 1 0.784314 rgBT /Overlock 1.6 61	1.6	61
14	The Trouble with MEAM2: Implications of Pseudogenes on Species Delimitation in the Globally Invasive <i>Bemisia tabaci</i> (Hemiptera: Aleyrodidae) Cryptic Species Complex. <i>Genome Biology and Evolution</i> , 2017, 9, 2732-2738.	1.1	32
15	Two genomes of highly polyphagous lepidopteran pests (<i>Spodoptera frugiperda</i> , Noctuidae) with different host-plant ranges. <i>Scientific Reports</i> , 2017, 7, 11816.	1.6	242
16	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, .	0.3	15
17	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
18	Population structure and gene flow in the global pest, <i>Helicoverpa armigera</i> . <i>Molecular Ecology</i> , 2016, 25, 5296-5311.	2.0	71

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19	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.	1.2	154
20	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.	2.2	80
21	Complete mitochondrial DNA genome of <i>Bemisia tabaci</i> cryptic pest species complex Asia I (Hemiptera: Aleyrodidae). <i>Mitochondrial DNA</i> , 2016, 27, 972-973.	0.6	27
22	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.	1.5	155
23	<i>C. elegans</i> RNA-dependent RNA polymerases rrf-1 and ego-1 silence <i>Drosophila</i> transgenes by differing mechanisms. <i>Cellular and Molecular Life Sciences</i> , 2013, 70, 1469-1481.	2.4	9
24	Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. <i>Nature</i> , 2012, 487, 94-98.	13.7	1,086
25	RNA interference in Lepidoptera: An overview of successful and unsuccessful studies and implications for experimental design. <i>Journal of Insect Physiology</i> , 2011, 57, 231-245.	0.9	729
26	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.	1.1	38
27	Expression of <i>Caenorhabditis elegans</i> RNA-directed RNA polymerase in transgenic <i>Drosophila melanogaster</i> does not affect morphological development. <i>Transgenic Research</i> , 2010, 19, 1121-1128.	1.3	6
28	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.	1.2	95
29	<i>Euprosterna elaeasa</i> virus genome sequence and evolution of the Tetraviridae family: Emergence of bipartite genomes and conservation of the VPg signal with the dsRNA Birnaviridae family. <i>Virology</i> , 2010, 397, 145-154.	1.1	30
30	Comparative analysis of detoxification enzymes in <i>Acyrtosiphon pisum</i> and <i>Myzus persicae</i> . <i>Insect Molecular Biology</i> , 2010, 19, 155-164.	1.0	203
31	A functional DNA methylation system in the pea aphid, <i>Acyrtosiphon pisum</i> . <i>Insect Molecular Biology</i> , 2010, 19, 215-228.	1.0	123
32	Expansion of the miRNA Pathway in the Hemipteran Insect <i>Acyrtosiphon pisum</i> . <i>Molecular Biology and Evolution</i> , 2010, 27, 979-987.	3.5	56
33	Downregulation of a Chitin Deacetylase-Like Protein in Response to Baculovirus Infection and Its Application for Improving Baculovirus Infectivity. <i>Journal of Virology</i> , 2010, 84, 2547-2555.	1.5	47
34	Extensive synteny conservation of holocentric chromosomes in Lepidoptera despite high rates of local genome rearrangements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7680-7685.	3.3	147
35	Genome Sequence of the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>PLoS Biology</i> , 2010, 8, e1000313.	2.6	913
36	Gene identification and proteomic analysis of the esterases of the cotton bollworm, <i>Helicoverpa armigera</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2010, 40, 1-16.	1.2	71

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37	A peptidomics study reveals the impressive antimicrobial peptide arsenal of the wax moth <i>Galleria mellonella</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2009, 39, 792-800.	1.2	115
38	The evolution of RNAi as a defence against viruses and transposable elements. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2009, 364, 99-115.	1.8	423
39	The discovery and analysis of a diverged family of novel antifungal moricin-like peptides in the wax moth <i>Galleria mellonella</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 201-212.	1.2	68
40	Diversity of aminopeptidases, derived from four lepidopteran gene duplications, and polycalins expressed in the midgut of <i>Helicoverpa armigera</i> : Identification of proteins binding the I ¹ -endotoxin, Cry1Ac of <i>Bacillus thuringiensis</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 685-696.	1.2	71
41	Proteomic analysis of the peritrophic matrix from the gut of the caterpillar, <i>Helicoverpa armigera</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 950-958.	1.2	95
42	Induction of apoptosis in <i>Saccharomyces cerevisiae</i> results in the spontaneous maturation of tetravirus procapsids in vivo. <i>Journal of General Virology</i> , 2007, 88, 1576-1582.	1.3	21
43	RNAi for insect-proof plants. <i>Nature Biotechnology</i> , 2007, 25, 1231-1232.	9.4	305
44	Insights into social insects from the genome of the honeybee <i>Apis mellifera</i> . <i>Nature</i> , 2006, 443, 931-949.	13.7	1,648
45	Canonical TTAGG-repeat telomeres and telomerase in the honey bee, <i>Apis mellifera</i> . <i>Genome Research</i> , 2006, 16, 1345-1351.	2.4	47
46	Small RNA Viruses of Insects: Expression in Plants and RNA Silencing. <i>Advances in Virus Research</i> , 2006, 68, 459-502.	0.9	28
47	Kelp Fly Virus: a Novel Group of Insect Picorna-Like Viruses as Defined by Genome Sequence Analysis and a Distinctive Virion Structure. <i>Journal of Virology</i> , 2005, 79, 13385-13398.	1.5	21
48	Infection of its lepidopteran host by the <i>Helicoverpa armigera</i> stunt virus (Tetraviridae). <i>Journal of Invertebrate Pathology</i> , 2002, 80, 97-111.	1.5	20
49	The Palm Subdomain-based Active Site is Internally Permuted in Viral RNA-dependent RNA Polymerases of an Ancient Lineage. <i>Journal of Molecular Biology</i> , 2002, 324, 47-62.	2.0	202
50	Pathology and Properties of the Tetravirus <i>Helicoverpa armigera</i> Stunt Virus. <i>Biological Control</i> , 2001, 20, 65-75.	1.4	12
51	Replication-Independent Assembly of an Insect Virus (Tetraviridae) in Plant Cells. <i>Virology</i> , 2001, 288, 36-50.	1.1	14
52	Reverse Transcription of a Naturally Occurring Nonretroviral RNA Produces a Precise Deletion in the Majority of Its cDNA Products. <i>IUBMB Life</i> , 2000, 49, 223-227.	1.5	1
53	Sequence of the Genomic RNA of <i>Nudaurelia</i> I ² Virus (Tetraviridae) Defines a Novel Virus Genome Organization. <i>Virology</i> , 1999, 258, 42-53.	1.1	29
54	The Specificity of <i>Helicoverpa armigera</i> Stunt Virus Infectivity. <i>Journal of Invertebrate Pathology</i> , 1999, 74, 156-163.	1.5	14

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55	The Tetraviridae. <i>Advances in Virus Research</i> , 1997, , 101-168.	0.9	42
56	Were RNA replication and translation directly coupled in the RNA (+protein?) world?. <i>Journal of Theoretical Biology</i> , 1995, 173, 179-193.	0.8	32
57	The Larger Genomic RNA of <i>Helicoverpa armigera</i> Stunt Tetravirus Encodes the Viral RNA Polymerase and Has a Novel 3' Terminal tRNA-like Structure. <i>Virology</i> , 1995, 208, 84-98.	1.1	36
58	Sequence of RNA2 of the <i>Helicoverpa armigera</i> stunt virus (Tetraviridae) and bacterial expression of its genes. <i>Journal of General Virology</i> , 1995, 76, 799-811.	1.3	35
59	A novel small RNA virus isolated from the cotton bollworm, <i>Helicoverpa armigera</i> . <i>Journal of General Virology</i> , 1993, 74, 1805-1810.	1.3	29
60	Efficient initiation of translation at non-AUG triplets in plant cells. <i>Plant Journal</i> , 1992, 2, 809-813.	2.8	28
61	Differential inhibition of downstream gene expression by the cauliflower mosaic virus 35S RNA leader. <i>Virus Genes</i> , 1989, 3, 45-55.	0.7	64
62	The instability of a recombinant plasmid, caused by a prokaryotic-like promoter within the eukaryotic insert, can be alleviated by expression of antisense RNA. <i>Gene</i> , 1988, 67, 141-145.	1.0	15
63	The leading sequence of caulimovirus large RNA can be folded into a large stem-loop structure. <i>Nucleic Acids Research</i> , 1988, 16, 8377-8390.	6.5	60
64	Subgenomic RNAs with nucleotide sequences derived from RNAs 1 and 2 of cucumber mosaic virus can act as messenger RNAs in Vitro. <i>Virology</i> , 1985, 142, 144-157.	1.1	3
65	Nucleotide sequence of cucumber-mosaic-virus RNA 2 reveals a translation product significantly homologous to corresponding proteins of other viruses. <i>FEBS Journal</i> , 1984, 143, 277-284.	0.2	103
66	Construction of the physical map of the chloroplast DNA of <i>Phaseolus vulgaris</i> and localization of ribosomal and transfer RNA genes. <i>Gene</i> , 1983, 21, 257-266.	1.0	47
67	Satellite RNA of cucumber mosaic virus forms a secondary structure with partial 3'-terminal homology to genomic RNAs. <i>Nucleic Acids Research</i> , 1983, 11, 947-960.	6.5	77
68	Highly purified cucumber mosaic virus-induced RNA-dependent RNA polymerase does not contain any of the full length translation products of the genomic RNAs. <i>Virology</i> , 1982, 123, 284-295.	1.1	25
69	Physical mapping of differences in chloroplast DNA of the five wild-type plastomes in <i>Oenothera</i> subsection <i>Euoenothera</i> . <i>Theoretical and Applied Genetics</i> , 1982, 61, 373-384.	1.8	110
70	Compositional Heterogeneity of the Chloroplast DNAs from <i>Euglena gracilis</i> and <i>Spinacia oleracea</i> . <i>FEBS Journal</i> , 1981, 117, 375-382.	0.2	16
71	Restriction endonuclease cleavage site map of chloroplast DNA from <i>Oenothera parviflora</i> (<i>Euoenothera</i> plastome IV). <i>Theoretical and Applied Genetics</i> , 1981, 59, 281-296.	1.8	35
72	Analysis of the plastid DNA in an <i>Oenothera</i> plastome mutant deficient in ribulose biphosphate carboxylase. <i>Theoretical and Applied Genetics</i> , 1980, 57, 203-207.	1.8	15

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73	Homologies among ribosomal RNA and messenger RNA genes in chloroplasts, mitochondria and E. coli. <i>Molecular Genetics and Genomics</i> , 1980, 179, 539-545.	2.4	30
74	Transfer RNA genes associated with the 16S and 23S rRNA genes of <i>Euglena</i> chloroplast DNA. <i>Biochemical and Biophysical Research Communications</i> , 1980, 95, 47-54.	1.0	37
75	Presence of a transfer RNA gene in the spacer sequence between the 16 S and 23 S rRNA genes of spinach chloroplast DNA. <i>FEBS Letters</i> , 1979, 103, 52-56.	1.3	49
76	Fractionation and identification of spinach chloroplast transfer RNAs and mapping of their genes on the restriction map of chloroplast DNA. <i>Gene</i> , 1979, 6, 285-306.	1.0	129
77	AGEING-LINKED CHANGES IN PHOTOSYNTHETIC CAPACITY AND IN FRACTION I PROTEIN CONTENT OF THE FIRST LEAF OF PEA <i>PISUM SATIVUM L.</i> <i>New Phytologist</i> , 1978, 81, 35-42.	3.5	16