

Stephen Doyle

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

1,714
citations

394421

19
h-index

361022

35
g-index

64
all docs

64
docs citations

64
times ranked

2495
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative genomics of the major parasitic worms. <i>Nature Genetics</i> , 2019, 51, 163-174.	21.4	377
2	The genome of <i>Onchocerca volvulus</i> , agent of river blindness. <i>Nature Microbiology</i> , 2017, 2, 16216.	13.3	107
3	Biology and genome of a newly discovered sibling species of <i>Caenorhabditis elegans</i> . <i>Nature Communications</i> , 2018, 9, 3216.	12.8	102
4	Genomic and transcriptomic variation defines the chromosome-scale assembly of <i>Haemonchus contortus</i> , a model gastrointestinal worm. <i>Communications Biology</i> , 2020, 3, 656.	4.4	91
5	Genome-wide analysis of ivermectin response by <i>Onchocerca volvulus</i> reveals that genetic drift and soft selective sweeps contribute to loss of drug sensitivity. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005816.	3.0	87
6	Population genomic and evolutionary modelling analyses reveal a single major QTL for ivermectin drug resistance in the pathogenic nematode, <i>Haemonchus contortus</i> . <i>BMC Genomics</i> , 2019, 20, 218.	2.8	68
7	Genomic introgression mapping of field-derived multiple-anthelmintic resistance in <i>Teladorsagia circumcincta</i> . <i>PLoS Genetics</i> , 2017, 13, e1006857.	3.5	67
8	Refugia and anthelmintic resistance: Concepts and challenges. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2019, 10, 51-57.	3.4	65
9	The global diversity of <i>Haemonchus contortus</i> is shaped by human intervention and climate. <i>Nature Communications</i> , 2019, 10, 4811.	12.8	63
10	Genome-wide Approaches to Investigate Anthelmintic Resistance. <i>Trends in Parasitology</i> , 2019, 35, 289-301.	3.3	61
11	A Genome Resequencing-Based Genetic Map Reveals the Recombination Landscape of an Outbred Parasitic Nematode in the Presence of Polyploidy and Polyandry. <i>Genome Biology and Evolution</i> , 2018, 10, 396-409.	2.5	58
12	Single-cell atlas of the first intra-mammalian developmental stage of the human parasite <i>Schistosoma mansoni</i> . <i>Nature Communications</i> , 2020, 11, 6411.	12.8	51
13	Challenges and opportunities for the adoption of molecular diagnostics for anthelmintic resistance. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2020, 14, 264-273.	3.4	44
14	Evaluation of DNA Extraction Methods on Individual Helminth Egg and Larval Stages for Whole-Genome Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 826.	2.3	30
15	You Are What You Eat: A Genomic Analysis of the Gut Microbiome of Captive and Wild <i>Octopus vulgaris</i> Paralarvae and Their Zooplankton Prey. <i>Frontiers in Physiology</i> , 2017, 8, 362.	2.8	27
16	Differential intracellular distribution of DNA complexed with polyethylenimine (PEI) and PEI-polyarginine PTD influences exogenous gene expression within live COS-7 cells. <i>Genetic Vaccines and Therapy</i> , 2007, 5, 11.	1.5	26
17	PLAG1 deficiency impairs spermatogenesis and sperm motility in mice. <i>Scientific Reports</i> , 2017, 7, 5317.	3.3	24
18	Outlier SNPs enable food traceability of the southern rock lobster, <i>Jasus edwardsii</i> . <i>Marine Biology</i> , 2016, 163, 1.	1.5	22

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19	MethPat: a tool for the analysis and visualisation of complex methylation patterns obtained by massively parallel sequencing. <i>BMC Bioinformatics</i> , 2016, 17, 98.	2.6	22
20	Outlier SNPs detect weak regional structure against a background of genetic homogeneity in the Eastern Rock Lobster, <i>Sagmariasus verreauxi</i> . <i>Marine Biology</i> , 2018, 165, 1.	1.5	20
21	Complete representation of a tapeworm genome reveals chromosomes capped by centromeres, necessitating a dual role in segregation and protection. <i>BMC Biology</i> , 2020, 18, 165.	3.8	19
22	Transcriptomic analyses implicate neuronal plasticity and chloride homeostasis in ivermectin resistance and response to treatment in a parasitic nematode. <i>PLoS Pathogens</i> , 2022, 18, e1010545.	4.7	19
23	Population genomic evidence that human and animal infections in Africa come from the same populations of <i>Dracunculus medinensis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008623.	3.0	18
24	Improving helminth genome resources in the post-genomic era. <i>Trends in Parasitology</i> , 2022, 38, 831-840.	3.3	18
25	Massively parallel sequencing of customised forensically informative SNP panels on the MiSeq. <i>Electrophoresis</i> , 2016, 37, 2832-2840.	2.4	15
26	Significant heterogeneity in <i>Wolbachia</i> copy number within and between populations of <i>Onchocerca volvulus</i> . <i>Parasites and Vectors</i> , 2017, 10, 188.	2.5	15
27	Mitochondrial Gene Therapy: An Evaluation of Strategies for the Treatment of Mitochondrial DNA Disorders. <i>Human Gene Therapy</i> , 2008, 19, 1335-1348.	2.7	12
28	Evidence of Evolutionary Constraints That Influences the Sequence Composition and Diversity of Mitochondrial Matrix Targeting Signals. <i>PLoS ONE</i> , 2013, 8, e67938.	2.5	11
29	Discrimination between <i>Onchocerca volvulus</i> and <i>O. ochengi</i> filarial larvae in <i>Simulium damnosum</i> (s.l.) and their distribution throughout central Ghana using a versatile high-resolution speciation assay. <i>Parasites and Vectors</i> , 2016, 9, 536.	2.5	11
30	The confounding effects of high genetic diversity on the determination and interpretation of differential gene expression analysis in the parasitic nematode <i>Haemonchus contortus</i> . <i>International Journal for Parasitology</i> , 2019, 49, 847-858.	3.1	10
31	Ivermectin and albendazole coadministration: opportunities for strongyloidiasis control. <i>Lancet Infectious Diseases</i> , The, 2022, 22, e341-e347.	9.1	9
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37	Locating and Activating Molecular "Time Bombs": Induction of Mycolata Prophages. PLoS ONE, 2016, 11, e0159957.	2.5	4
38	Screening the <i>Saccharomyces cerevisiae</i> Nonessential Gene Deletion Library Reveals Diverse Mechanisms of Action for Antifungal Plant Defensins. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	4
39	Genome-wide analysis of the response to ivermectin treatment by a Swedish field population of <i>Haemonchus contortus</i> . International Journal for Parasitology: Drugs and Drug Resistance, 2022, 18, 12-19.	3.4	4
40	Enhanced annealing of mismatched oligonucleotides using a novel melting curve assay allows efficient in vitro discrimination and restriction of a single nucleotide polymorphism. BMC Biotechnology, 2011, 11, 83.	3.3	3
41	Exemplary multiplex bisulfite amplicon data used to demonstrate the utility of Methpat. GigaScience, 2015, 4, 55.	6.4	3
42	Phenotypic and genotypic analysis of benzimidazole resistance in reciprocal genetic crosses of <i>Haemonchus contortus</i> . International Journal for Parasitology: Drugs and Drug Resistance, 2022, 18, 1-11.	3.4	3
43	The genome sequence of the Australian filarial nematode, <i>Cercopithifilaria johnstoni</i> . Wellcome Open Research, 2021, 6, 259.	1.8	2
44	The genome sequence of the Australian filarial nematode, <i>Cercopithifilaria johnstoni</i> . Wellcome Open Research, 0, 6, 259.	1.8	2
45	Mitochondrial gene therapy – an evaluation of strategies for the treatment of mitochondrial DNA disorders. Human Gene Therapy, 2008, .	2.7	0