

Stephen Doyle

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

1,714
citations

394286

19
h-index

360920

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. | 9.4 | 377 |
| 2 | The genome of <i>Onchocerca volvulus</i> , agent of river blindness. <i>Nature Microbiology</i> , 2017, 2, 16216. | 5.9 | 107 |
| 3 | Biology and genome of a newly discovered sibling species of <i>Caenorhabditis elegans</i> . <i>Nature Communications</i> , 2018, 9, 3216. | 5.8 | 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. | 2.0 | 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. | 1.3 | 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. | 1.2 | 68 |
| 7 | Genomic introgression mapping of field-derived multiple-anthelmintic resistance in <i>Teladorsagia circumcincta</i> . <i>PLoS Genetics</i> , 2017, 13, e1006857. | 1.5 | 67 |
| 8 | Refugia and anthelmintic resistance: Concepts and challenges. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2019, 10, 51-57. | 1.4 | 65 |
| 9 | The global diversity of <i>Haemonchus contortus</i> is shaped by human intervention and climate. <i>Nature Communications</i> , 2019, 10, 4811. | 5.8 | 63 |
| 10 | Genome-wide Approaches to Investigate Anthelmintic Resistance. <i>Trends in Parasitology</i> , 2019, 35, 289-301. | 1.5 | 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. | 1.1 | 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. | 5.8 | 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. | 1.4 | 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. | 1.1 | 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. | 1.3 | 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. | 1.6 | 24 |
| 18 | Outlier SNPs enable food traceability of the southern rock lobster, <i>Jasus edwardsii</i> . <i>Marine Biology</i> , 2016, 163, 1. | 0.7 | 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. | 1.2 | 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. | 0.7 | 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. | 1.7 | 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. | 2.1 | 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. | 1.3 | 18 |
| 24 | Improving helminth genome resources in the post-genomic era. <i>Trends in Parasitology</i> , 2022, 38, 831-840. | 1.5 | 18 |
| 25 | Massively parallel sequencing of customised forensically informative SNP panels on the MiSeq. <i>Electrophoresis</i> , 2016, 37, 2832-2840. | 1.3 | 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. | 1.0 | 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. | 1.4 | 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. | 1.1 | 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. | 1.0 | 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. | 1.3 | 10 |
| 31 | Ivermectin and albendazole coadministration: opportunities for strongyloidiasis control. <i>Lancet Infectious Diseases</i> , The, 2022, 22, e341-e347. | 4.6 | 9 |
| 32 | | | |

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|----|--|-----|-----------|
| 37 | Locating and Activating Molecular "Time Bombs": Induction of Mycolata Prophages. PLoS ONE, 2016, 11, e0159957. | 1.1 | 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, . | 1.4 | 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. | 1.4 | 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. | 1.7 | 3 |
| 41 | Exemplary multiplex bisulfite amplicon data used to demonstrate the utility of Methpat. GigaScience, 2015, 4, 55. | 3.3 | 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. | 1.4 | 3 |
| 43 | The genome sequence of the Australian filarial nematode, <i>Cercopithifilaria johnstoni</i> . Wellcome Open Research, 2021, 6, 259. | 0.9 | 2 |
| 44 | The genome sequence of the Australian filarial nematode, <i>Cercopithifilaria johnstoni</i> . Wellcome Open Research, 0, 6, 259. | 0.9 | 2 |
| 45 | Mitochondrial gene therapy – an evaluation of strategies for the treatment of mitochondrial DNA disorders. Human Gene Therapy, 2008, . | 1.4 | 0 |