Stephen Doyle

List of Publications by Year
in descending order

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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	Phenotypic and genotypic analysis of benzimidazole resistance in reciprocal genetic crosses of Haemonchus contortus. International Journal for Parasitology: Drugs and Drug Resistance, 2022, 18, 1-11.	1.4	3
2	Genome-wide analysis of the response to ivermectin treatment by a Swedish field population of Haemonchus contortus. International Journal for Parasitology: Drugs and Drug Resistance, 2022, 18, 12-19.	1.4	4
3	A genetic TRP down the channel to praziquantel resistance. Trends in Parasitology, 2022, 38, 351-352.	1.5	5
4	Worms and bugs of the gut: the search for diagnostic signatures using barcoding, and metagenomicsâ€“metabolomics. Parasites and Vectors, 2022, 15, 118.	1.0	7
5	Transcriptomic analyses implicate neuronal plasticity and chloride homeostasis in ivermectin resistance and response to treatment in a parasitic nematode. PLoS Pathogens, 2022, 18, e1010545.	2.1	19
6	Ivermectin and albendazole coadministration: opportunities for strongyloidiasis control. Lancet Infectious Diseases, The, 2022, 22, e341-e347.	4.6	9
7	Improving helminth genome resources in the post-genomic era. Trends in Parasitology, 2022, 38, 831-840.	1.5	18
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19	Genome-wide Approaches to Investigate Anthelmintic Resistance. Trends in Parasitology, 2019, 35, 289-301.	1.5	61
20	Refugia and anthelmintic resistance: Concepts and challenges. International Journal for Parasitology: Drugs and Drug Resistance, 2019, 10, 51-57.	1.4	65
21	Population genomic and evolutionary modelling analyses reveal a single major QTL for ivermectin drug resistance in the pathogenic nematode, Haemonchus contortus. BMC Genomics, 2019, 20, 218.	1.2	68
22	Comparative genomics of the major parasitic worms. Nature Genetics, 2019, 51, 163-174.	9.4	377
23	A Genome Resequencing-Based Genetic Map Reveals the Recombination Landscape of an Outbred Parasitic Nematode in the Presence of Polyploidy and Polyandry. Genome Biology and Evolution, 2018, 10, 396-409.	1.1	58
24	Outlier SNPs detect weak regional structure against a background of genetic homogeneity in the Eastern Rock Lobster, Sagmariasus verreauxi. Marine Biology, 2018, 165, 1.	0.7	20
25	Biology and genome of a newly discovered sibling species of Caenorhabditis elegans. Nature Communications, 2018, 9, 3216.	5.8	102
26	Significant heterogeneity in Wolbachia copy number within and between populations of Onchocerca volvulus. Parasites and Vectors, 2017, 10, 188.	1.0	15
27	PLAG1 deficiency impairs spermatogenesis and sperm motility in mice. Scientific Reports, 2017, 7, 5317.	1.6	24
28	The genome of Onchocerca volvulus, agent of river blindness. Nature Microbiology, 2017, 2, 16216.	5.9	107
29	You Are What You Eat: A Genomic Analysis of the Gut Microbiome of Captive and Wild Octopus vulgaris Paralarvae and Their Zooplankton Prey. Frontiers in Physiology, 2017, 8, 362.	1.3	27
30	Genomic introgression mapping of field-derived multiple-anthelmintic resistance in Teladorsagia circumcincta. PLoS Genetics, 2017, 13, e1006857.	1.5	67
31	Genome-wide analysis of ivermectin response by Onchocerca volvulus reveals that genetic drift and soft selective sweeps contribute to loss of drug sensitivity. PLoS Neglected Tropical Diseases, 2017, 11, e0005816.	1.3	87
32	Discrimination between Onchocerca volvulus and O. ochengi filarial larvae in Simulium damnosum (s.l.) and their distribution throughout central Ghana using a versatile high-resolution speciation assay. Parasites and Vectors, 2016, 9, 536.	1.0	11
33	Locating and Activating Molecular â€˜Time Bombsâ€™: Induction of Mycolata Prophages. PLoS ONE, 2016, 11, e0159957.	1.1	4
34	Massively parallel sequencing of customised forensically informative SNP panels on the MiSeq. Electrophoresis, 2016, 37, 2832-2840.	1.3	15
35	Outlier SNPs enable food traceability of the southern rock lobster, Jasus edwardsii. Marine Biology, 2016, 163, 1.	0.7	22
36	MethPat: a tool for the analysis and visualisation of complex methylation patterns obtained by massively parallel sequencing. BMC Bioinformatics, 2016, 17, 98.	1.2	22

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37	Exemplary multiplex bisulfite amplicon data used to demonstrate the utility of Methpat. GigaScience, 2015, 4, 55.	3.3	3
38	Low-coverage MiSeq next generation sequencing reveals the mitochondrial genome of the Eastern Rock Lobster,Sagmariasus verreauxi. Mitochondrial DNA, 2015, 26, 844-845.	0.6	6
39	Evidence of Evolutionary Constraints That Influences the Sequence Composition and Diversity of Mitochondrial Matrix Targeting Signals. PLoS ONE, 2013, 8, e67938.	1.1	11
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	Mitochondrial Gene Therapy: An Evaluation of Strategies for the Treatment of Mitochondrial DNA Disorders. Human Gene Therapy, 2008, 19, 1335-1348.	1.4	12
42	Mitochondrial gene therapy Â– an evaluation of strategies for the treatment of mitochondrial DNA disorders. Human Gene Therapy, 2008, .	1.4	0
43	Differential intracellular distribution of DNA complexed with polyethylenimine (PEI) and PEI-polyarginine PTD influences exogenous gene expression within live COS-7 cells. Genetic Vaccines and Therapy, 2007, 5, 11.	1.5	26
44	The genome sequence of the Australian filarial nematode, Cercopithifilaria johnstoni. Wellcome Open Research, 0, 6, 259.	0.9	2
45	An adaptive phase II/III safety and efficacy randomized controlled trial of single day or three-day fixed-dose albendazole-ivermectin co-formulation versus albendazole for the treatment of Trichuris trichiura and other STH infections. ALIVE trial protocol. Gates Open Research, 0, 6, 62.	2.0	5