

Robin B Gasser

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4513222/publications.pdf>

Version: 2024-02-01

637
papers

25,903
citations

9264

74
h-index

18130

120
g-index

645
all docs

645
docs citations

645
times ranked

18722
citing authors

#	ARTICLE	IF	CITATIONS
1	Harnessing model organism genomics to underpin the machine learning-based prediction of essential genes in eukaryotes – Biotechnological implications. <i>Biotechnology Advances</i> , 2022, 54, 107822.	11.7	9
2	An RNA Interference Tool to Silence Genes in <i>Sarcoptes scabiei</i> Eggs. <i>International Journal of Molecular Sciences</i> , 2022, 23, 873.	4.1	2
3	A High-Throughput Phenotypic Screen of the –Pandemic Response Box™ Identifies a Quinoline Derivative with Significant Anthelmintic Activity. <i>Pharmaceuticals</i> , 2022, 15, 257.	3.8	14
4	Nuclear genome of <i>Bulinus truncatus</i> , an intermediate host of the carcinogenic human blood fluke <i>Schistosoma haematobium</i> . <i>Nature Communications</i> , 2022, 13, 977.	12.8	14
5	Chromosome-level genome of <i>Schistosoma haematobium</i> underpins genome-wide explorations of molecular variation. <i>PLoS Pathogens</i> , 2022, 18, e1010288.	4.7	13
6	Assessing the Anthelmintic Candidates BLK127 and HBK4 for Their Efficacy on <i>Haemonchus contortus</i> Adults and Eggs, and Their Hepatotoxicity and Biotransformation. <i>Pharmaceutics</i> , 2022, 14, 754.	4.5	1
7	–Escalibur– A practical pipeline for the de novo analysis of nucleotide variation in nonmodel eukaryotes. <i>Molecular Ecology Resources</i> , 2022, , .	4.8	2
8	Chromosome-scale <i>Echinococcus granulosus</i> (genotype G1) genome reveals the Eg95 gene family and conservation of the EG95-vaccine molecule. <i>Communications Biology</i> , 2022, 5, 199.	4.4	7
9	Worms and bugs of the gut: the search for diagnostic signatures using barcoding, and metagenomics–metabolomics. <i>Parasites and Vectors</i> , 2022, 15, 118.	2.5	7
10	Whole-organism phenotypic screening methods used in early-phase anthelmintic drug discovery. <i>Biotechnology Advances</i> , 2022, 57, 107937.	11.7	17
11	A Perspective on the Molecular Identification, Classification, and Epidemiology of <i>Enterocytozoon bieneusi</i> of Animals. <i>Experientia Supplementum</i> (2012), 2022, 114, 389-415.	0.9	2
12	–FeatureOmega– an integrative platform for engineering, visualization and analysis of features from molecular sequences, structural and ligand data sets. <i>Nucleic Acids Research</i> , 2022, 50, W434-W447.	14.5	24
13	Novel High-Throughput Fluorescence-Based Assay for the Identification of Nematocidal Compounds That Target the Blood-Feeding Pathway. <i>Pharmaceuticals</i> , 2022, 15, 669.	3.8	1
14	Evolution of sexual systems, sex chromosomes and sex-linked gene transcription in flatworms and roundworms. <i>Nature Communications</i> , 2022, 13, .	12.8	6
15	Identification of Anthelmintic Bishomoscalarane Sesterterpenes from the Australian Marine Sponge –Phyllospongia bergquistae– and Structure Revision of Phyllolactones A–D. <i>Journal of Natural Products</i> , 2022, 85, 1723-1729.	3.0	3
16	Ubiquitination pathway model for the barber– pole worm – <i>Haemonchus contortus</i> . <i>International Journal for Parasitology</i> , 2022, 52, 581-590.	3.1	3
17	OGEE v3: Online GENE Essentiality database with increased coverage of organisms and human cell lines. <i>Nucleic Acids Research</i> , 2021, 49, D998-D1003.	14.5	42
18	1-Methyl-1H-pyrazole-5-carboxamide Derivatives Exhibit Unexpected Acute Mammalian Toxicity. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 840-844.	6.4	3

#	ARTICLE	IF	CITATIONS
19	SARS-CoV-2 seroprevalence worldwide: a systematic review and meta-analysis. <i>Clinical Microbiology and Infection</i> , 2021, 27, 331-340.	6.0	296
20	<i>Enterocytozoon bieneusi</i> of animalsâ€”With an â€”Australian twistâ€™. <i>Advances in Parasitology</i> , 2021, 111, 1-73.	3.2	26
21	<i>Bulinus truncatus</i> transcriptome â€” a resource to enable molecular studies of snail and schistosome biology. <i>Current Research in Parasitology and Vector-borne Diseases</i> , 2021, 1, 100015.	1.9	5
22	Nanopore Sequencing Resolves Elusive Long Tandem-Repeat Regions in Mitochondrial Genomes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1811.	4.1	18
23	Phytochemical Profiling and Biological Activity of the Australian Carnivorous Plant, <i>Drosera magna</i> . <i>Journal of Natural Products</i> , 2021, 84, 964-971.	3.0	8
24	Molecular diagnosis of scabies using a novel probe-based polymerase chain reaction assay targeting high-copy number repetitive sequences in the <i>Sarcoptes scabiei</i> genome. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009149.	3.0	7
25	High-quality reference genome for <i>Clonorchis sinensis</i> . <i>Genomics</i> , 2021, 113, 1605-1615.	2.9	19
26	<i>Dipylidium caninum</i> draft genome - a new resource for comparative genomic and genetic explorations of flatworms. <i>Genomics</i> , 2021, 113, 1272-1280.	2.9	8
27	Three Small Molecule Entities (MPK18, MPK334 and YAK308) with Activity against <i>Haemonchus contortus</i> In Vitro. <i>Molecules</i> , 2021, 26, 2819.	3.8	2
28	Prospects of Using High-Throughput Proteomics to Underpin the Discovery of Animal Hostâ€”Nematode Interactions. <i>Pathogens</i> , 2021, 10, 825.	2.8	6
29	High-Throughput Phenotypic Assay to Screen for Anthelmintic Activity on <i>Haemonchus contortus</i> . <i>Pharmaceuticals</i> , 2021, 14, 616.	3.8	22
30	First Evidence of Function for <i>Schistosoma japonicum</i> riok-1 and RIOK-1. <i>Pathogens</i> , 2021, 10, 862.	2.8	3
31	Practical High-Throughput Method to Screen Compounds for Anthelmintic Activity against <i>Caenorhabditis elegans</i> . <i>Molecules</i> , 2021, 26, 4156.	3.8	12
32	Detection of <i>Breinlia</i> sp. (Nematoda) in the Leadbeater's possum (<i>Gymnobelideus leadbeateri</i>). <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2021, 15, 249-254.	1.5	3
33	How qPCR complements the WHO roadmap (2021â€”2030) for soil-transmitted helminths. <i>Trends in Parasitology</i> , 2021, 37, 698-708.	3.3	12
34	The mitogenome of <i>Halotydeus destructor</i> (Tucker) and its relationships with other trombidiform mites as inferred from nucleotide sequences and gene arrangements. <i>Ecology and Evolution</i> , 2021, 11, 14162-14174.	1.9	5
35	Update on SARS-CoV-2 seroprevalence: regional and worldwide. <i>Clinical Microbiology and Infection</i> , 2021, 27, 1762-1771.	6.0	49
36	Seroprevalence Estimates of Latent and Acute <i>Toxoplasma</i> Infections in HIV+ Peopleâ€”Call for Action in Underprivileged Communities. <i>Microorganisms</i> , 2021, 9, 2034.	3.6	9

#	ARTICLE	IF	CITATIONS
37	High Throughput Screening of the NatureBank [®] Marine Collection [™] in a Haemonchus Bioassay Identifies Anthelmintic Activity in Extracts from a Range of Sponges from Australian Waters. <i>Molecules</i> , 2021, 26, 5846.	3.8	7
38	Design, synthesis and screening of a drug discovery library based on an Eremophila-derived serrulatane scaffold. <i>Phytochemistry</i> , 2021, 190, 112887.	2.9	4
39	Mitochondrial genome of <i>Bulinus truncatus</i> (Gastropoda: Lymnaeoidea): Implications for snail systematics and schistosome epidemiology. <i>Current Research in Parasitology and Vector-borne Diseases</i> , 2021, 1, 100017.	1.9	6
40	Helminth lipidomics: Technical aspects and future prospects. <i>Current Research in Parasitology and Vector-borne Diseases</i> , 2021, 1, 100018.	1.9	6
41	Cryptosporidium of birds in pet markets in Wuhan city, Hubei, China. <i>Current Research in Parasitology and Vector-borne Diseases</i> , 2021, 1, 100025.	1.9	3
42	Ocular Filariasis in Human Caused by <i>Brelinia</i> (<i>Johnstonema</i>) <i>annulipapillata</i> Nematode, Australia. <i>Emerging Infectious Diseases</i> , 2021, 27, 297-300.	4.3	4
43	Advances in the discovery and development of anthelmintics by harnessing natural product scaffolds. <i>Advances in Parasitology</i> , 2021, 111, 203-251.	3.2	14
44	Targeted Next-Generation Sequencing and Informatics as an Effective Tool to Establish the Composition of Bovine Piroplasm Populations in Endemic Regions. <i>Microorganisms</i> , 2021, 9, 21.	3.6	10
45	Phylogenetic relationships of the nematode subfamily Phascolostrongylinae from macropodid and vombatid marsupials inferred using mitochondrial protein sequence data. <i>Parasites and Vectors</i> , 2021, 14, 523.	2.5	2
46	Case-Control Study to Assess the Association between Epilepsy and Toxocara Infection/Exposure. <i>Microorganisms</i> , 2021, 9, 2091.	3.6	5
47	Advances in the treatment, diagnosis, control and scientific understanding of taeniid cestode parasite infections over the past 50 years. <i>International Journal for Parasitology</i> , 2021, 51, 1167-1192.	3.1	21
48	Translational Research of Zoonotic Parasites: Toward Improved Tools for Diagnosis, Treatment and Control. <i>Pathogens</i> , 2021, 10, 1416.	2.8	1
49	Phytochemical Profiling and Biological Testing of the Constituents of the Australian Plant <i>Haemodorum brevisepalum</i> . <i>Journal of Natural Products</i> , 2021, 84, 2832-2844.	3.0	1
50	Ticks and tick-borne diseases of bovines in a smallholder livestock context: The Pakistani example. <i>Advances in Parasitology</i> , 2021, 114, 167-244.	3.2	3
51	Dysidenin from the Marine Sponge <i>Citronia</i> sp. Affects the Motility and Morphology of <i>Haemonchus contortus</i> Larvae In Vitro. <i>Marine Drugs</i> , 2021, 19, 698.	4.6	4
52	A serine/threonine-specific protein kinase of <i>Haemonchus contortus</i> with a role in the development. <i>FASEB Journal</i> , 2020, 34, 2075-2086.	0.5	8
53	Bovine ticks harbour a diverse array of microorganisms in Pakistan. <i>Parasites and Vectors</i> , 2020, 13, 1.	2.5	141
54	The developmental phosphoproteome of <i>Haemonchus contortus</i> . <i>Journal of Proteomics</i> , 2020, 213, 103615.	2.4	21

#	ARTICLE	IF	CITATIONS
55	An appraisal of oriental theileriosis and the <i>Theileria orientalis</i> complex, with an emphasis on diagnosis and genetic characterisation. <i>Parasitology Research</i> , 2020, 119, 11-22.	1.6	33
56	Combined use of feature engineering and machine-learning to predict essential genes in <i>Drosophila melanogaster</i> . <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa051.	3.2	10
57	High-quality nuclear genome for <i>Sarcoptes scabiei</i> —A critical resource for a neglected parasite. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008720.	3.0	25
58	Disseminated protozoal infection in a wild feathertail glider (<i>Acrobates pygmaeus</i>) in Australia. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2020, 13, 46-50.	1.5	1
59	<i>Cryptosporidium</i> cf. <i>avium</i> in an inland-bearded dragon (<i>Pogona vitticeps</i>) — A case report and review of the literature. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2020, 13, 150-159.	1.5	2
60	Natural Compounds from the Marine Brown Alga <i>Caulocystis cephalornithos</i> with Potent In Vitro-Activity against the Parasitic Nematode <i>Haemonchus contortus</i> . <i>Pathogens</i> , 2020, 9, 550.	2.8	17
61	Major SCP/TAPS protein expansion in <i>Lucilia cuprina</i> is associated with novel tandem array organisation and domain architecture. <i>Parasites and Vectors</i> , 2020, 13, 598.	2.5	1
62	“Begging the Question”—Does <i>Toxocara</i> Infection/Exposure Associate with Multiple Sclerosis-Risk?. <i>Pathogens</i> , 2020, 9, 938.	2.8	9
63	Eukaryote-Conserved Methylarginine Is Absent in Diplomonads and Functionally Compensated in <i>Giardia</i> . <i>Molecular Biology and Evolution</i> , 2020, 37, 3525-3549.	8.9	9
64	Use of kinase inhibitors against schistosomes to improve and broaden praziquantel efficacy. <i>Parasitology</i> , 2020, 147, 1488-1498.	1.5	7
65	Toward integrative omics of the barber’s pole worm and related parasitic nematodes. <i>Infection, Genetics and Evolution</i> , 2020, 85, 104500.	2.3	11
66	Diversity in the intrinsic apoptosis pathway of nematodes. <i>Communications Biology</i> , 2020, 3, 478.	4.4	4
67	DNA Footprints: Using Parasites to Detect Elusive Animals, Proof of Principle in Hedgehogs. <i>Animals</i> , 2020, 10, 1420.	2.3	5
68	An Assessment of the Molecular Diversity of Ticks and Tick-Borne Microorganisms of Small Ruminants in Pakistan. <i>Microorganisms</i> , 2020, 8, 1428.	3.6	21
69	First record of a tandem-repeat region within the mitochondrial genome of <i>Clonorchis sinensis</i> using a long-read sequencing approach. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008552.	3.0	18
70	Marked mitochondrial genetic variation in individuals and populations of the carcinogenic liver fluke <i>Clonorchis sinensis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008480.	3.0	6
71	Phylogenetic Analysis of Mitogenomic Data Sets Resolves the Relationship of Seven <i>Macropostrongyloides</i> Species from Australian Macropodid and Vombatid Marsupials. <i>Pathogens</i> , 2020, 9, 1042.	2.8	5
72	Global and regional seroprevalence estimates for human toxocariasis: A call for action. <i>Advances in Parasitology</i> , 2020, 109, 275-290.	3.2	37

#	ARTICLE	IF	CITATIONS
73	Comatulins Aâ€“E, Taurine-Conjugated Anthraquinones from the Australian Crinoid <i>Comatula rotularia</i> . Journal of Natural Products, 2020, 83, 1971-1979.	3.0	5
74	Predicting gene essentiality in <i>Caenorhabditis elegans</i> by feature engineering and machine-learning. Computational and Structural Biotechnology Journal, 2020, 18, 1093-1102.	4.1	15
75	Exploring the prevalence and diversity of bovine ticks in five agro-ecological zones of Pakistan using phenetic and genetic tools. Ticks and Tick-borne Diseases, 2020, 11, 101472.	2.7	26
76	Age of first infection across a range of parasite taxa in a wild mammalian population. Biology Letters, 2020, 16, 20190811.	2.3	16
77	Multiplex PCRs for the specific identification of marsupial and deer species from faecal samples as a basis for non-invasive epidemiological studies of parasites. Parasites and Vectors, 2020, 13, 144.	2.5	3
78	Global Prevalence Estimates of <i>Toxascaris leonina</i> Infection in Dogs and Cats. Pathogens, 2020, 9, 503.	2.8	13
79	A Targeted “Next-Generation” Sequencing-Informatic Approach to Define Genetic Diversity in <i>Theileria orientalis</i> Populations within Individual Cattle: Proof-of-Principle. Pathogens, 2020, 9, 448.	2.8	6
80	Lipid composition and abundance in the reproductive and alimentary tracts of female <i>Haemonchus contortus</i> . Parasites and Vectors, 2020, 13, 338.	2.5	13
81	Global prevalence of <i>Toxocara</i> infection in dogs. Advances in Parasitology, 2020, 109, 561-583.	3.2	62
82	Elucidating cryptic dynamics of <i>Theileria</i> communities in African buffalo using a high-throughput sequencing informatics approach. Ecology and Evolution, 2020, 10, 70-80.	1.9	19
83	Elucidating the molecular and developmental biology of parasitic nematodes: Moving to a multiomics paradigm. Advances in Parasitology, 2020, 108, 175-229.	3.2	17
84	High anti- <i>Ascaris</i> seroprevalence in fattening pigs in Sichuan, China, calls for improved management strategies. Parasites and Vectors, 2020, 13, 60.	2.5	10
85	Gene content evolution in the arthropods. Genome Biology, 2020, 21, 15.	8.8	150
86	Synthesis and structure-activity relationship study of pyrrolidine-oxadiazoles as anthelmintics against <i>Haemonchus contortus</i> . European Journal of Medicinal Chemistry, 2020, 190, 112100.	5.5	15
87	Expanded complement of Niemann-Pick type C2-like protein genes in <i>Clonorchis sinensis</i> suggests functions beyond sterol binding and transport. Parasites and Vectors, 2020, 13, 38.	2.5	3
88	Synthetic Kavalactone Analogues with Increased Potency and Selective Anthelmintic Activity against Larvae of <i>Haemonchus contortus</i> In Vitro. Molecules, 2020, 25, 2004.	3.8	4
89	Identification and characterization of an R-Smad homologue (Hco-DAF-8) from <i>Haemonchus contortus</i> . Parasites and Vectors, 2020, 13, 164.	2.5	4
90	Global prevalence of <i>Toxocara</i> infection in cats. Advances in Parasitology, 2020, 109, 615-639.	3.2	48

#	ARTICLE	IF	CITATIONS
91	Synthesis, characterization and antiparasitic activity of organometallic derivatives of the anthelmintic drug albendazole. Dalton Transactions, 2020, 49, 6616-6626.	3.3	11
92	A perspective on the discovery of selected compounds with anthelmintic activity against the barber's pole worm "Where to from here?". Advances in Parasitology, 2020, 108, 1-45.	3.2	17
93	Quantitative lipidomic analysis of <i>Ascaris suum</i> . PLoS Neglected Tropical Diseases, 2020, 14, e0008848.	3.0	5
94	A Participatory Investigation of Bovine Health and Production Issues in Pakistan. Frontiers in Veterinary Science, 2020, 7, 248.	2.2	14
95	Quantitative lipidomic analysis of <i>Ascaris suum</i> . , 2020, 14, e0008848.		0
96	Quantitative lipidomic analysis of <i>Ascaris suum</i> . , 2020, 14, e0008848.		0
97	Quantitative lipidomic analysis of <i>Ascaris suum</i> . , 2020, 14, e0008848.		0
98	Quantitative lipidomic analysis of <i>Ascaris suum</i> . , 2020, 14, e0008848.		0
99	<i>Enterocytozoon bienersi</i> genotypes in cats and dogs in Victoria, Australia. BMC Microbiology, 2019, 19, 183.	3.3	22
100	Human toxocariasis "A look at a neglected disease through an epidemiological prism". Infection, Genetics and Evolution, 2019, 74, 104002.	2.3	76
101	An Evaluation of Machine Learning Approaches for the Prediction of Essential Genes in Eukaryotes Using Protein Sequence-Derived Features. Computational and Structural Biotechnology Journal, 2019, 17, 785-796.	4.1	31
102	Dafachronic acid promotes larval development in <i>Haemonchus contortus</i> by modulating dauer signalling and lipid metabolism. PLoS Pathogens, 2019, 15, e1007960.	4.7	31
103	Acute <i>Toxoplasma</i> infection in pregnant women worldwide: A systematic review and meta-analysis. PLoS Neglected Tropical Diseases, 2019, 13, e0007807.	3.0	76
104	A suicide inhibitor of nematode trehalose-6-phosphate phosphatases. Scientific Reports, 2019, 9, 16165.	3.3	4
105	Identification of Fromiamycalin and Halaminol A from Australian Marine Sponge Extracts with Anthelmintic Activity against <i>Haemonchus contortus</i> . Marine Drugs, 2019, 17, 598.	4.6	17
106	The Challenge of Developing a Single-Dose Treatment for Scabies. Trends in Parasitology, 2019, 35, 931-943.	3.3	29
107	High-quality <i>Schistosoma haematobium</i> genome achieved by single-molecule and long-range sequencing. GigaScience, 2019, 8, .	6.4	41
108	Whole-genome sequence of the bovine blood fluke <i>Schistosoma bovis</i> supports interspecific hybridization with <i>S. haematobium</i> . PLoS Pathogens, 2019, 15, e1007513.	4.7	49

#	ARTICLE	IF	CITATIONS
109	Haem Biology in Metazoan Parasites – The Bright Side of Haem™. Trends in Parasitology, 2019, 35, 213-225.	3.3	17
110	Albendazole resistance induced in <i>Ancylostoma ceylanicum</i> is not due to single-nucleotide polymorphisms (SNPs) at codons 167, 198, or 200 of the beta-tubulin gene, indicating another resistance mechanism. Parasitology Research, 2019, 118, 837-849.	1.6	17
111	Long-read sequencing reveals a 4.4kb tandem repeat region in the mitogenome of <i>Echinococcus granulosus</i> (sensu stricto) genotype G1. Parasites and Vectors, 2019, 12, 238.	2.5	31
112	An appraisal of natural products active against parasitic nematodes of animals. Parasites and Vectors, 2019, 12, 306.	2.5	52
113	Comparative genome analysis indicates high evolutionary potential of pathogenicity genes in <i>Colletotrichum tanacetii</i> . PLoS ONE, 2019, 14, e0212248.	2.5	19
114	High throughput LC-MS/MS-based proteomic analysis of excretory-secretory products from short-term in vitro culture of <i>Haemonchus contortus</i> . Journal of Proteomics, 2019, 204, 103375.	2.4	44
115	Quantitative PCR-Based Diagnosis of Soil-Transmitted Helminth Infections: Faecal or Fickle?. Trends in Parasitology, 2019, 35, 491-500.	3.3	46
116	DRfit: a Java tool for the analysis of discrete data from multi-well plate assays. BMC Bioinformatics, 2019, 20, 262.	2.6	3
117	Phenotypic screening of the Kurz-box™ of chemicals identifies two compounds (BLK127 and HBK4) with anthelmintic activity in vitro against parasitic larval stages of <i>Haemonchus contortus</i> . Parasites and Vectors, 2019, 12, 191.	2.5	10
118	Dauer signalling pathway model for <i>Haemonchus contortus</i> . Parasites and Vectors, 2019, 12, 187.	2.5	25
119	Transcriptional alterations in <i>Caenorhabditis elegans</i> following exposure to an anthelmintic fraction of the plant <i>Picris fel-terrae</i> Lour.. Parasites and Vectors, 2019, 12, 181.	2.5	2
120	Novel 1-Methyl-1 <i>H</i> -pyrazole-5-carboxamide Derivatives with Potent Anthelmintic Activity. Journal of Medicinal Chemistry, 2019, 62, 3367-3380.	6.4	15
121	Human cyclosporiasis. Lancet Infectious Diseases, The, 2019, 19, e226-e236.	9.1	55
122	Common workflow language (CWL)-based software pipeline for de novo genome assembly from long- and short-read data. GigaScience, 2019, 8, .	6.4	17
123	Exploration of extracellular vesicles from <i>Ascaris suum</i> provides evidence of parasite-host cross talk. Journal of Extracellular Vesicles, 2019, 8, 1578116.	12.2	103
124	Molecular evidence for distinct modes of nutrient acquisition between visceral and neurotropic schistosomes of birds. Scientific Reports, 2019, 9, 1347.	3.3	17
125	Selected δ -pyrones from the plants <i>Cryptocarya novoguineensis</i> (Lauraceae) and <i>Piper methysticum</i> (Piperaceae) with activity against <i>Haemonchus contortus</i> in vitro. International Journal for Parasitology: Drugs and Drug Resistance, 2019, 9, 72-79.	3.4	10
126	Somatic proteome of <i>Haemonchus contortus</i> . International Journal for Parasitology, 2019, 49, 311-320.	3.1	38

#	ARTICLE	IF	CITATIONS
127	Seroprevalence estimates for toxocariasis in people worldwide: A systematic review and meta-analysis. PLoS Neglected Tropical Diseases, 2019, 13, e0007809.	3.0	107
128	A TGF- β 2 type II receptor that associates with developmental transition in <i>Haemonchus contortus</i> in vitro. PLoS Neglected Tropical Diseases, 2019, 13, e0007913.	3.0	12
129	Structure-Activity Relationship Studies of Tolfenpyrad Reveal Subnanomolar Inhibitors of <i>Haemonchus contortus</i> Development. Journal of Medicinal Chemistry, 2019, 62, 1036-1053.	6.4	17
130	Comparative bioinformatic analysis suggests that specific dauer-like signalling pathway components regulate <i>Toxocara canis</i> development and migration in the mammalian host. Parasites and Vectors, 2019, 12, 32.	2.5	15
131	Tetrahydroquinoxalines induce a lethal evisceration phenotype in <i>Haemonchus contortus</i> in vitro. International Journal for Parasitology: Drugs and Drug Resistance, 2019, 9, 59-71.	3.4	15
132	Transcriptomic Resources for Parasitic Nematodes of Veterinary Importance. Trends in Parasitology, 2019, 35, 72-84.	3.3	20
133	<i>Enterocytozoon bienersi</i> Genotypes in Cattle on Farms Located within a Water Catchment Area. Journal of Eukaryotic Microbiology, 2019, 66, 553-559.	1.7	26
134	Helminth Microbiomes – A Hidden Treasure Trove?. Trends in Parasitology, 2019, 35, 13-22.	3.3	36
135	Phylogenetic relationships of three tribes of cloacine nematodes (Strongylida: Chabertiidae) from macropodid marsupials. Journal of Helminthology, 2019, 93, 486-493.	1.0	3
136	Improved genomic resources and new bioinformatic workflow for the carcinogenic parasite <i>Clonorchis sinensis</i> : Biotechnological implications. Biotechnology Advances, 2018, 36, 894-904.	11.7	20
137	First detection and genetic characterisation of <i>Enterocytozoon bienersi</i> in wild deer in Melbourne's water catchments in Australia. Parasites and Vectors, 2018, 11, 2.	2.5	41
138	Multiplexed Tandem PCR (MT-PCR) Assay Using the Major Piroplasm Surface Protein Gene for the Diagnosis of <i>Theileria orientalis</i> Infection in Cattle. Journal of Clinical Microbiology, 2018, 56, .	3.9	5
139	Special issue – Learning and teaching of veterinary parasitology. Veterinary Parasitology, 2018, 253, 120-121.	1.8	6
140	Parasites of the Giant Panda: A Risk Factor in the Conservation of a Species. Advances in Parasitology, 2018, 99, 1-33.	3.2	28
141	Advances in kinome research of parasitic worms - implications for fundamental research and applied biotechnological outcomes. Biotechnology Advances, 2018, 36, 915-934.	11.7	8
142	<i>Cryptosporidium viatorum</i> from the native Australian swamp rat <i>Rattus lutreolus</i> - An emerging zoonotic pathogen?. International Journal for Parasitology: Parasites and Wildlife, 2018, 7, 18-26.	1.5	33
143	Human toxocariasis. Lancet Infectious Diseases, The, 2018, 18, e14-e24.	9.1	278
144	Working towards New Drugs against Parasitic Worms in a Public-Development Partnership. Trends in Parasitology, 2018, 34, 4-6.	3.3	18

#	ARTICLE	IF	CITATIONS
145	Using PCR-Based Sequencing to Diagnose <i>Haycocknema perplexum</i> Infection in Human Myositis Case, Australia. <i>Emerging Infectious Diseases</i> , 2018, 24, 2368-2370.	4.3	5
146	Optimization of Novel 1-Methyl-1 <i>H</i> -Pyrazole-5-carboxamides Leads to High Potency Larval Development Inhibitors of the Barber's Pole Worm. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 10875-10894.	6.4	29
147	Interactive online application for the prediction, ranking and prioritisation of drug targets in <i>Schistosoma haematobium</i> . <i>Parasites and Vectors</i> , 2018, 11, 605.	2.5	0
148	A TGF- β type I receptor-like molecule with a key functional role in <i>Haemonchus contortus</i> development. <i>International Journal for Parasitology</i> , 2018, 48, 1023-1033.	3.1	16
149	PCR-coupled sequencing achieves specific diagnosis of onchocerciasis in a challenging clinical case, to underpin effective treatment and clinical management. <i>Infection, Genetics and Evolution</i> , 2018, 66, 192-194.	2.3	4
150	Molecular investigation of <i>Cryptosporidium</i> in farmed chickens in Hubei Province, China, identifies "zoonotic" subtypes of <i>C. meleagridis</i> . <i>Parasites and Vectors</i> , 2018, 11, 484.	2.5	31
151	Advancing the multi-disciplinarity of parasitology within the British Society for Parasitology: studies of host-parasite evolution in an ever-changing world. <i>Parasitology</i> , 2018, 145, 1641-1646.	1.5	4
152	First cross-sectional, molecular epidemiological survey of <i>Cryptosporidium</i> , <i>Giardia</i> and <i>Enterocytozoon</i> in alpaca (<i>Vicugna pacos</i>) in Australia. <i>Parasites and Vectors</i> , 2018, 11, 498.	2.5	25
153	The developmental lipidome of <i>Haemonchus contortus</i> . <i>International Journal for Parasitology</i> , 2018, 48, 887-895.	3.1	30
154	Molecular alterations during larval development of <i>Haemonchus contortus</i> in vitro are under tight post-transcriptional control. <i>International Journal for Parasitology</i> , 2018, 48, 763-772.	3.1	30
155	Global phylogeography and genetic diversity of the zoonotic tapeworm <i>Echinococcus granulosus sensu stricto</i> genotype G1. <i>International Journal for Parasitology</i> , 2018, 48, 729-742.	3.1	77
156	Arylpyrrole and fipronil analogues that inhibit the motility and/or development of <i>Haemonchus contortus</i> in vitro. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2018, 8, 379-385.	3.4	9
157	Distinguishing <i>Echinococcus granulosus sensu stricto</i> genotypes G1 and G3 with confidence: A practical guide. <i>Infection, Genetics and Evolution</i> , 2018, 64, 178-184.	2.3	54
158	Trehalose 6-phosphate phosphatases of <i>Pseudomonas aeruginosa</i> . <i>FASEB Journal</i> , 2018, 32, 5470-5482.	0.5	9
159	Serine/threonine protein phosphatase 1 (PP1) controls growth and reproduction in <i>Schistosoma japonicum</i> . <i>FASEB Journal</i> , 2018, 32, 6626-6642.	0.5	14
160	New operational taxonomic units of <i>Enterocytozoon</i> in three marsupial species. <i>Parasites and Vectors</i> , 2018, 11, 371.	2.5	20
161	<i>Toxocara</i> eggs in public places worldwide - A systematic review and meta-analysis. <i>Environmental Pollution</i> , 2018, 242, 1467-1475.	7.5	93
162	Improved strategy for the curation and classification of kinases, with broad applicability to other eukaryotic protein groups. <i>Scientific Reports</i> , 2018, 8, 6808.	3.3	10

#	ARTICLE	IF	CITATIONS
163	The small RNA complement of adult <i>Schistosoma haematobium</i> . <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006535.	3.0	17
164	<i>Enterocytozoon bieneusi</i> genotypes in people with gastrointestinal disorders in Queensland and Western Australia. <i>Infection, Genetics and Evolution</i> , 2018, 65, 293-299.	2.3	22
165	The benefits of analysing complete mitochondrial genomes: Deep insights into the phylogeny and population structure of <i>Echinococcus granulosus sensu lato</i> genotypes G6 and G7. <i>Infection, Genetics and Evolution</i> , 2018, 64, 85-94.	2.3	52
166	<i>Opisthorchis viverrini</i> Draft Genome – Biomedical Implications and Future Avenues. <i>Advances in Parasitology</i> , 2018, 101, 125-148.	3.2	7
167	<i>Clonorchis sinensis</i> and Clonorchiasis: The Relevance of Exploring Genetic Variation. <i>Advances in Parasitology</i> , 2018, 100, 155-208.	3.2	18
168	Proteomic identification of galectin-11 and 14 ligands from <i>Haemonchus contortus</i> . <i>PeerJ</i> , 2018, 6, e4510.	2.0	7
169	Genomics of worms, with an emphasis on <i>Opisthorchis viverrini</i> – opportunities for fundamental discovery and biomedical outcomes. <i>Parasitology International</i> , 2017, 66, 341-345.	1.3	7
170	An outbreak of oriental theileriosis in dairy cattle imported to Vietnam from Australia. <i>Parasitology</i> , 2017, 144, 738-746.	1.5	24
171	Mitochondrial genomic comparison of <i>Clonorchis sinensis</i> from South Korea with other isolates of this species. <i>Infection, Genetics and Evolution</i> , 2017, 51, 160-166.	2.3	13
172	Probing function and structure of trehalose-6-phosphate phosphatases from pathogenic organisms suggests distinct molecular groupings. <i>FASEB Journal</i> , 2017, 31, 920-926.	0.5	9
173	Mitochondrial genomes of two <i>Babesia</i> taxa from sheep in China as a foundation for population genetic and epidemiological investigations. <i>Infection, Genetics and Evolution</i> , 2017, 47, 51-55.	2.3	6
174	Screening of the “Open Scaffolds”™ collection from Compounds Australia identifies a new chemical entity with anthelmintic activities against different developmental stages of the barber’s pole worm and other parasitic nematodes. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2017, 7, 286-294.	3.4	33
175	Whipworm kinomes reflect a unique biology and adaptation to the host animal. <i>International Journal for Parasitology</i> , 2017, 47, 857-866.	3.1	10
176	First survey of <i>Cryptosporidium</i> , <i>Giardia</i> and <i>Enterocytozoon</i> in diarrhoeic children from Wuhan, China. <i>Infection, Genetics and Evolution</i> , 2017, 51, 127-131.	2.3	51
177	Inadequate Differentiation of <i>Theileria orientalis</i> Genotypes buffeli and ikeda in a Multiplexed Tandem PCR (MT-PCR) Assay Using the p23 Gene as a Marker. <i>Journal of Clinical Microbiology</i> , 2017, 55, 641-644.	3.9	3
178	The apicoplast genomes of two taxonomic units of <i>Babesia</i> from sheep. <i>Veterinary Parasitology</i> , 2017, 233, 123-128.	1.8	10
179	<i>Ascaris</i> phylogeny based on multiple whole mtDNA genomes. <i>Infection, Genetics and Evolution</i> , 2017, 48, 4-9.	2.3	19
180	A communal catalogue reveals Earth’s multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	27.8	1,942

#	ARTICLE	IF	CITATIONS
181	Molecular and immunological characterisation of tropomyosin from <i>Anisakis pegreffii</i> . <i>Parasitology Research</i> , 2017, 116, 3291-3301.	1.6	11
182	Structural and developmental expression of Ss-riok-2, an RIO protein kinase encoding gene of <i>Strongyloides stercoralis</i> . <i>Scientific Reports</i> , 2017, 7, 8693.	3.3	6
183	Speciation in the genus <i>Cloacina</i> (Nematoda: Strongylida): species flocks and intra-host speciation. <i>Parasitology</i> , 2017, 144, 1828-1840.	1.5	8
184	Enzyme characteristics of pathogen-specific trehalose-6-phosphate phosphatases. <i>Scientific Reports</i> , 2017, 7, 2015.	3.3	12
185	Functional genomic exploration reveals that Ss-RIOK-1 is essential for the development and survival of <i>Strongyloides stercoralis</i> larvae. <i>International Journal for Parasitology</i> , 2017, 47, 933-940.	3.1	7
186	Genetic diversity in the C-terminus of merozoite surface protein 1 among <i>Plasmodium knowlesi</i> isolates from Selangor and Sabah Borneo, Malaysia. <i>Infection, Genetics and Evolution</i> , 2017, 54, 39-46.	2.3	15
187	Deguelin exerts potent nematocidal activity via the mitochondrial respiratory chain. <i>FASEB Journal</i> , 2017, 31, 4515-4532.	0.5	25
188	Screening of a small, well-curated natural product-based library identifies two rotenoids with potent nematocidal activity against <i>Haemonchus contortus</i> . <i>Veterinary Parasitology</i> , 2017, 244, 172-175.	1.8	19
189	Phylogenetic analysis of the Australasian paralysis ticks and their relatives (Ixodidae: Ixodes:). <i>Tj ETQq1 1 0.784314</i> <i>rgBT /Overlock 10</i>	2.5	17
190	Assessing the anthelmintic activity of pyrazole-5-carboxamide derivatives against <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , 2017, 10, 272.	2.5	25
191	Comparative transcriptomic analyses of male and female adult <i>Toxocara canis</i> . <i>Gene</i> , 2017, 600, 85-89.	2.2	12
192	Assessing the performance of multiplexed tandem PCR for the diagnosis of pathogenic genotypes of <i>Theileria orientalis</i> using pooled blood samples from cattle. <i>Molecular and Cellular Probes</i> , 2017, 31, 70-75.	2.1	8
193	Predominance of <i>Streptococcus suis</i> ST1 and ST7 in human cases in China, and detection of a novel sequence type, ST658. <i>Virulence</i> , 2017, 8, 1031-1035.	4.4	14
194	Molecular characterisation of <i>Theileria orientalis</i> in imported and native bovines from Pakistan. <i>Infection, Genetics and Evolution</i> , 2017, 47, 19-25.	2.3	22
195	Application of PCR-Based Tools to Explore <i>Strongyloides</i> Infection in People in Parts of Northern Australia. <i>Tropical Medicine and Infectious Disease</i> , 2017, 2, 62.	2.3	15
196	Transcriptomics Indicates Active and Passive Metronidazole Resistance Mechanisms in Three Seminal <i>Giardia</i> Lines. <i>Frontiers in Microbiology</i> , 2017, 8, 398.	3.5	31
197	Screening of the <i>Stasis Box</i> ™ identifies two kinase inhibitors under pharmaceutical development with activity against <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , 2017, 10, 323.	2.5	22
198	Use of a bioinformatic-assisted primer design strategy to establish a new nested PCR-based method for <i>Cryptosporidium</i> . <i>Parasites and Vectors</i> , 2017, 10, 509.	2.5	18

#	ARTICLE	IF	CITATIONS
199	Molecular investigation of <i>Cryptosporidium</i> and <i>Giardia</i> in pre- and post-weaned calves in Hubei Province, China. <i>Parasites and Vectors</i> , 2017, 10, 519.	2.5	37
200	The RIO protein kinase-encoding gene <i>Sj-riok-2</i> is involved in key reproductive processes in <i>Schistosoma japonicum</i> . <i>Parasites and Vectors</i> , 2017, 10, 604.	2.5	9
201	The Battle Against Flystrike “ Past Research and New Prospects Through Genomics. <i>Advances in Parasitology</i> , 2017, 98, 227-281.	3.2	6
202	Trehalose-6-phosphate phosphatase as a broad-spectrum therapeutic target against eukaryotic and prokaryotic pathogens. <i>Emerging Topics in Life Sciences</i> , 2017, 1, 675-683.	2.6	4
203	Time-Course Study of the Transcriptome of Peripheral Blood Mononuclear Cells (PBMCs) from Sheep Infected with <i>Fasciola hepatica</i> . <i>PLoS ONE</i> , 2016, 11, e0159194.	2.5	29
204	Harnessing the <i>Toxocara</i> Genome to Underpin Toxocariasis Research and New Interventions. <i>Advances in Parasitology</i> , 2016, 91, 87-110.	3.2	23
205	Mitochondrial Phylogenomics yields Strongly Supported Hypotheses for Ascaridomorph Nematodes. <i>Scientific Reports</i> , 2016, 6, 39248.	3.3	26
206	<i>Dictyocaulus viviparus</i> genome, variome and transcriptome elucidate lungworm biology and support future intervention. <i>Scientific Reports</i> , 2016, 6, 20316.	3.3	23
207	Analyses of Compact <i>Trichinella</i> Kinomes Reveal a MOS-Like Protein Kinase with a Unique N-Terminal Domain. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2847-2856.	1.8	6
208	Population structure of <i>Haemonchus contortus</i> from seven geographical regions in China, determined on the basis of microsatellite markers. <i>Parasites and Vectors</i> , 2016, 9, 586.	2.5	14
209	CAP protein superfamily members in <i>Toxocara canis</i> . <i>Parasites and Vectors</i> , 2016, 9, 360.	2.5	6
210	Molecular characterization of <i>Theileria orientalis</i> from cattle in Ethiopia. <i>Ticks and Tick-borne Diseases</i> , 2016, 7, 742-747.	2.7	28
211	A blow to the fly “ <i>Lucilia cuprina</i> draft genome and transcriptome to support advances in biology and biotechnology. <i>Biotechnology Advances</i> , 2016, 34, 605-620.	11.7	23
212	Anthelmintic activity of selected ethno-medicinal plant extracts on parasitic stages of <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , 2016, 9, 187.	2.5	34
213	Can New Digital Technologies Support Parasitology Teaching and Learning?. <i>Trends in Parasitology</i> , 2016, 32, 522-530.	3.3	24
214	First survey of parasitic helminths of goats along the Han River in Hubei Province, China. <i>Acta Parasitologica</i> , 2016, 61, 602-6.	1.1	8
215	Two benzimidazole resistance-associated SNPs in the isotype-1 β -tubulin gene predominate in <i>Haemonchus contortus</i> populations from eight regions in China. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2016, 6, 199-206.	3.4	27
216	<i>Pharyngostromylus thylogale</i> n. sp. (Nematoda: Strongylida) from the stomachs of macropodid marsupials defined by morphological and molecular criteria. <i>Systematic Parasitology</i> , 2016, 93, 749-760.	1.1	4

#	ARTICLE	IF	CITATIONS
217	Synthesis, Characterization, and Biological Activity of Ferrocenyl Analogues of the Anthelmintic Drug Monepantel. <i>Organometallics</i> , 2016, 35, 3369-3377.	2.3	21
218	Screening of the "Pathogen Box"™ identifies an approved pesticide with major anthelmintic activity against the barber's pole worm. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2016, 6, 329-334.	3.4	61
219	Molecular characterization of species of <i>Cloacina</i> (Strongyloidea: Cloacininae) from the common wallaroo, <i>Macropus robustus</i> (Marsupialia: Macropodidae) in Australia. <i>Infection, Genetics and Evolution</i> , 2016, 44, 245-253.	2.3	3
220	Organometallic Derivatization of the Nematocidal Drug Monepantel Leads to Promising Antiparasitic Drug Candidates. <i>Chemistry - A European Journal</i> , 2016, 22, 16602-16612.	3.3	19
221	Selenophene and thiophene-core estrogen receptor ligands that inhibit motility and development of parasitic stages of <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , 2016, 9, 346.	2.5	8
222	Divergent Transcriptional Responses to Physiological and Xenobiotic Stress in <i>Giardia duodenalis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 6034-6045.	3.2	33
223	Is <i>Cryptosporidium</i> from the common wombat (<i>Vombatus ursinus</i>) a new species and distinct from <i>Cryptosporidium ubiquitum</i> ?. <i>Infection, Genetics and Evolution</i> , 2016, 44, 28-33.	2.3	6
224	Metabolic profiling and in vitro assessment of anthelmintic fractions of <i>Picria fel-terrae</i> Lour.. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2016, 6, 171-178.	3.4	16
225	Understanding <i>Haemonchus contortus</i> Better Through Genomics and Transcriptomics. <i>Advances in Parasitology</i> , 2016, 93, 519-567.	3.2	36
226	Genomic resources for a unique, low-virulence <i>Babesia</i> taxon from China. <i>Parasites and Vectors</i> , 2016, 9, 564.	2.5	17
227	Assessment of the nematocidal activity of metallocenyl analogues of monepantel. <i>Dalton Transactions</i> , 2016, 45, 17662-17671.	3.3	9
228	MicroRNAs of <i>Toxocara canis</i> and their predicted functional roles. <i>Parasites and Vectors</i> , 2016, 9, 229.	2.5	37
229	Recent Advances in Elucidating Nematode Moulting " Prospects of Using <i>Oesophagostomum dentatum</i> as a Model. <i>Advances in Parasitology</i> , 2016, 91, 233-264.	3.2	6
230	More parasitic myositis cases in humans in Australia, and the definition of genetic markers for the causative agents as a basis for molecular diagnosis. <i>Infection, Genetics and Evolution</i> , 2016, 44, 69-75.	2.3	4
231	<i>Cryptosporidium</i> and <i>Giardia</i> taxa in faecal samples from animals in catchments supplying the city of Melbourne with drinking water (2011 to 2015). <i>Parasites and Vectors</i> , 2016, 9, 315.	2.5	48
232	Phylogenetic relationships of species of the oesophageal parasitic nematode genera <i>Cyclostrongylus</i> and <i>Spirostrongylus</i> (Strongyloidea: Chabertiidae: Cloacininae) with their wallaby hosts (Marsupialia: Tj ETQq0 0 0zBT /Overclock 10 Tf		
233	Detection of cryptic species of <i>Rugopharynx</i> (Nematoda: Strongylida) from the stomachs of Australian macropodid marsupials. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2016, 5, 124-133.	1.5	12
234	Reconstruction of the insulin-like signalling pathway of <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , 2016, 9, 64.	2.5	12

#	ARTICLE	IF	CITATIONS
235	Molecular characterization of the <i>Haemonchus contortus</i> phosphoinositide-dependent protein kinase-1 gene (Hc-pdk-1). <i>Parasites and Vectors</i> , 2016, 9, 65.	2.5	13
236	Pipeline for the identification and classification of ion channels in parasitic flatworms. <i>Parasites and Vectors</i> , 2016, 9, 155.	2.5	4
237	Molecular analysis of <i>Cryptosporidium</i> from cattle from five states of Peninsular Malaysia. <i>Molecular and Cellular Probes</i> , 2016, 30, 39-43.	2.1	7
238	Practical and low cost whole-organism motility assay: A step-by-step protocol. <i>Molecular and Cellular Probes</i> , 2016, 30, 13-17.	2.1	30
239	Phylogenomic and biogeographic reconstruction of the <i>Trichinella</i> complex. <i>Nature Communications</i> , 2016, 7, 10513.	12.8	107
240	Making sense of genomes of parasitic worms: Tackling bioinformatic challenges. <i>Biotechnology Advances</i> , 2016, 34, 663-686.	11.7	30
241	<i>Toxocara malaysiensis</i> infection in domestic cats in Vietnam – An emerging zoonotic issue?. <i>Infection, Genetics and Evolution</i> , 2016, 37, 94-98.	2.3	17
242	The complement of family M1 aminopeptidases of <i>Haemonchus contortus</i> – Biotechnological implications. <i>Biotechnology Advances</i> , 2016, 34, 65-76.	11.7	8
243	A perspective on genomic-guided anthelmintic discovery and repurposing using <i>Haemonchus contortus</i> . <i>Infection, Genetics and Evolution</i> , 2016, 40, 368-373.	2.3	19
244	Comparative Transcriptomic Exploration Reveals Unique Molecular Adaptations of Neuropathogenic <i>Trichobilharzia</i> to Invade and Parasitize Its Avian Definitive Host. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004406.	3.0	25
245	Exploring molecular variation in <i>Schistosoma japonicum</i> in China. <i>Scientific Reports</i> , 2015, 5, 17345.	3.3	33
246	Defining the <i>Schistosoma haematobium</i> kinome enables the prediction of essential kinases as anti-schistosome drug targets. <i>Scientific Reports</i> , 2015, 5, 17759.	3.3	37
247	A practical Java tool for small-molecule compound appraisal. <i>Journal of Cheminformatics</i> , 2015, 7, 28.	6.1	11
248	Tick-borne diseases of bovines in Pakistan: major scope for future research and improved control. <i>Parasites and Vectors</i> , 2015, 8, 283.	2.5	117
249	The <i>Haemonchus contortus</i> kinome - a resource for fundamental molecular investigations and drug discovery. <i>Parasites and Vectors</i> , 2015, 8, 623.	2.5	14
250	Detection of <i>Cyclospora</i> in captive chimpanzees and macaques by a quantitative PCR-based mutation scanning approach. <i>Parasites and Vectors</i> , 2015, 8, 274.	2.5	22
251	Time-Dependent Transcriptional Changes in Axenic <i>Giardia duodenalis</i> Trophozoites. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0004261.	3.0	16
252	Investigating the first outbreak of oriental theileriosis in cattle in South Australia using multiplexed tandem PCR (MT-PCR). <i>Ticks and Tick-borne Diseases</i> , 2015, 6, 574-578.	2.7	16

#	ARTICLE	IF	CITATIONS
253	First Human Case of Fatal <i>Halicephalobus gingivalis</i> Meningoencephalitis in Australia. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1768-1774.	3.9	19
254	Assessment of sequence variability in a p23 gene region within and among three genotypes of the <i>Theileria orientalis</i> complex from south-eastern Australia. <i>Ticks and Tick-borne Diseases</i> , 2015, 6, 123-128.	2.7	9
255	New Research Tools for Urogenital Schistosomiasis. <i>Journal of Infectious Diseases</i> , 2015, 211, 861-869.	4.0	24
256	Multiplex PCR for the detection and quantification of zoonotic taxa of <i>Giardia</i> , <i>Cryptosporidium</i> and <i>Toxoplasma</i> in wastewater and mussels. <i>Molecular and Cellular Probes</i> , 2015, 29, 122-125.	2.1	44
257	Genetic blueprint of the zoonotic pathogen <i>Toxocara canis</i> . <i>Nature Communications</i> , 2015, 6, 6145.	12.8	103
258	The barber's pole worm CAP protein superfamily – A basis for fundamental discovery and biotechnology advances. <i>Biotechnology Advances</i> , 2015, 33, 1744-1754.	11.7	16
259	Cracking the nodule worm code advances knowledge of parasite biology and biotechnology to tackle major diseases of livestock. <i>Biotechnology Advances</i> , 2015, 33, 980-991.	11.7	21
260	Molecular detection of <i>Cyclospora</i> in water, soil, vegetables and humans in southern Italy signals a need for improved monitoring by health authorities. <i>International Journal of Food Microbiology</i> , 2015, 211, 95-100.	4.7	41
261	Drug resistance in <i>Giardia duodenalis</i> . <i>Biotechnology Advances</i> , 2015, 33, 888-901.	11.7	94
262	New Editor-in-Chief of the <i>International Journal for Parasitology</i> . <i>International Journal for Parasitology</i> , 2015, 45, 283.	3.1	0
263	Low cost whole-organism screening of compounds for anthelmintic activity. <i>International Journal for Parasitology</i> , 2015, 45, 333-343.	3.1	106
264	A Perspective on <i>Cryptosporidium</i> and <i>Giardia</i> , with an Emphasis on Bovines and Recent Epidemiological Findings. <i>Advances in Parasitology</i> , 2015, 88, 243-301.	3.2	48
265	Use of multiplexed tandem PCR to estimate the prevalence and intensity of <i>Theileria orientalis</i> infections in cattle. <i>Infection, Genetics and Evolution</i> , 2015, 32, 68-73.	2.3	9
266	Transcriptional analysis identifies key genes involved in metabolism, fibrosis/tissue repair and the immune response against <i>Fasciola hepatica</i> in sheep liver. <i>Parasites and Vectors</i> , 2015, 8, 124.	2.5	53
267	Mitochondrial genome of <i>Hypoderaeum conoideum</i> – comparison with selected trematodes. <i>Parasites and Vectors</i> , 2015, 8, 97.	2.5	30
268	Comparison of the performance of three PCR assays for the detection and differentiation of <i>Theileria orientalis</i> genotypes. <i>Parasites and Vectors</i> , 2015, 8, 192.	2.5	20
269	Prospects for Vector-Based Gene Silencing to Explore Immunobiological Features of <i>Schistosoma mansoni</i> . <i>Advances in Parasitology</i> , 2015, 88, 85-122.	3.2	8
270	Knocking down schistosomes – promise for lentiviral transduction in parasites. <i>Trends in Parasitology</i> , 2015, 31, 324-332.	3.3	19

271	Lucilia cuprina genome unlocks parasitic fly biology to underpin future interventions. Nature Communications, 2015, 6, 7344.	12.8	67
272	Genetic analysis of Giardia and Cryptosporidium from people in Northern Australia using PCR-based tools. Infection, Genetics and Evolution, 2015, 36, 389-395.	2.3	25
273	The phylogenetic relationships of endemic Australasian trichostrongylin families (Nematoda): Tj ETQq1 1 0.784314 _{rgBT} / Overlock 10 ₆	1.8	6
274	Probing of a Human Proteome Microarray With a Recombinant Pathogen Protein Reveals a Novel Mechanism by Which Hookworms Suppress B-Cell Receptor Signaling. Journal of Infectious Diseases, 2015, 211, 416-425.	4.0	47
275	Semiquantitative Multiplexed Tandem PCR for Detection and Differentiation of Four Theileria orientalis Genotypes in Cattle. Journal of Clinical Microbiology, 2015, 53, 79-87.	3.9	27
276	Sequencing and Annotation of Mitochondrial Genomes from Individual Parasitic Helminths. Methods in Molecular Biology, 2015, 1201, 51-63.	0.9	5
277	A Real-Time PCR Assay for the Diagnosis of Gastrointestinal Nematode Infections of Small Ruminants. Methods in Molecular Biology, 2015, 1247, 145-152.	0.9	7
278	Impact of Next-Generation Technologies on Exploring Socioeconomically Important Parasites and Developing New Interventions. Methods in Molecular Biology, 2015, 1247, 437-474.	0.9	9
279	Flatworms have lost the right open reading frame kinase 3 gene during evolution. Scientific Reports, 2015, 5, 9417.	3.3	7
280	Mitochondrial Genome Analyses Suggest Multiple Trichuris Species in Humans, Baboons, and Pigs from Different Geographical Regions. PLoS Neglected Tropical Diseases, 2015, 9, e0004059.	3.0	45
281	Investigating the Role of RIO Protein Kinases in Caenorhabditis elegans. PLoS ONE, 2015, 10, e0117444.	2.5	15
282	Cryptosporidium cuniculus - new records in human and kangaroo in Australia. Parasites and Vectors, 2014, 7, 492.	2.5	44
283	Exploring the role of two interacting phosphoinositide 3-kinases of Haemonchus contortus. Parasites and Vectors, 2014, 7, 498.	2.5	13
284	Exploring features and function of Ss-riok-3, an enigmatic kinase gene from Strongyloides stercoralis. Parasites and Vectors, 2014, 7, 561.	2.5	6
285	Toward Understanding the Functional Role of Ss-riok-1, a RIO Protein Kinase-Encoding Gene of Strongyloides stercoralis. PLoS Neglected Tropical Diseases, 2014, 8, e3062.	3.0	13
286	Characterization of the Ca ²⁺ -Gated and Voltage-Dependent K ⁺ -Channel Slo-1 of Nematodes and Its Interaction with Emodepside. PLoS Neglected Tropical Diseases, 2014, 8, e3401.	3.0	40
287	Bioinformatic exploration of RIO protein kinases of parasitic and free-living nematodes. International Journal for Parasitology, 2014, 44, 827-836.	3.1	13

#	ARTICLE	IF	CITATIONS
289	The Relevance of Structural Biology in Studying Molecules Involved in Parasite–Host Interactions: Potential for Designing New Interventions. <i>Australian Journal of Chemistry</i> , 2014, 67, 1732.	0.9	2
290	Omega-1 knockdown in <i>Schistosoma mansoni</i> eggs by lentivirus transduction reduces granuloma size in vivo. <i>Nature Communications</i> , 2014, 5, 5375.	12.8	63
291	First genetic analysis of <i>Cryptosporidium</i> from humans from Tasmania, and identification of a new genotype from a traveller to Bali. <i>Electrophoresis</i> , 2014, 35, 2600-2607.	2.4	26
292	Crystal structure and immunological properties of the first annexin from <i>Schistosoma mansoni</i> : insights into the structural integrity of the schistosomal tegument. <i>FEBS Journal</i> , 2014, 281, 1209-1225.	4.7	21
293	The mitochondrial genome of <i>Parascaris univalens</i> - implications for a ‘forgotten’ parasite. <i>Parasites and Vectors</i> , 2014, 7, 428.	2.5	30
294	Genome of the human hookworm <i>Necator americanus</i> . <i>Nature Genetics</i> , 2014, 46, 261-269.	21.4	166
295	Oriental theileriosis in dairy cows causes a significant milk production loss. <i>Parasites and Vectors</i> , 2014, 7, 73.	2.5	68
296	Analysis of the transcriptome of adult <i>Dictyocaulus filaria</i> and comparison with <i>Dictyocaulus viviparus</i> , with a focus on molecules involved in host–parasite interactions. <i>International Journal for Parasitology</i> , 2014, 44, 251-261.	3.1	6
297	<i>Giardia/giardiasis</i> – A perspective on diagnostic and analytical tools. <i>Biotechnology Advances</i> , 2014, 32, 280-289.	11.7	73
298	Probing the equatorial groove of the hookworm protein and vaccine candidate antigen, Na-ASP-2. <i>International Journal of Biochemistry and Cell Biology</i> , 2014, 50, 146-155.	2.8	18
299	<i>Cryptosporidium parvum</i> genotype IIa and <i>Giardia duodenalis</i> assemblage A in <i>Mytilus galloprovincialis</i> on sale at local food markets. <i>International Journal of Food Microbiology</i> , 2014, 171, 62-67.	4.7	33
300	Mitochondrial genomes of <i>Anisakis simplex</i> and <i>Contracaecum osculatum</i> (sensu stricto) – Comparisons with selected nematodes. <i>Infection, Genetics and Evolution</i> , 2014, 21, 452-462.	2.3	25
301	Apoptosis in schistosomes: toward novel targets for the treatment of schistosomiasis. <i>Trends in Parasitology</i> , 2014, 30, 75-84.	3.3	33
302	Genetic variation within and among species of <i>Cloacina</i> (Strongyloidea: Cloacinine) from the swamp wallaby, <i>Wallabia bicolor</i> (Marsupialia: Macropodidae). <i>Infection, Genetics and Evolution</i> , 2014, 28, 261-269.	2.3	8
303	President’s message. <i>International Journal for Parasitology</i> , 2014, 44, 847.	3.1	0
304	Diversity in parasitic helminths of Australasian marsupials and monotremes: a molecular perspective. <i>International Journal for Parasitology</i> , 2014, 44, 859-864.	3.1	12
305	Discovery of acrylonitrile-based small molecules active against <i>Haemonchus contortus</i> . <i>MedChemComm</i> , 2014, 5, 159-164.	3.4	13
306	Genome and transcriptome of the porcine whipworm <i>Trichuris suis</i> . <i>Nature Genetics</i> , 2014, 46, 701-706.	21.4	93

#	ARTICLE	IF	CITATIONS
307	Proteomics elucidates key molecules involved in exsheathment in vitro in <i>Oesophagostomum dentatum</i> . <i>International Journal for Parasitology</i> , 2014, 44, 759-764.	3.1	3
308	Mitochondrial genomes of <i>Trichinella</i> species and genotypes as a basis for diagnosis, and systematic and epidemiological explorations. <i>International Journal for Parasitology</i> , 2014, 44, 1073-1080.	3.1	40
309	First insight into CD59-like molecules of adult <i>Fasciola hepatica</i> . <i>Experimental Parasitology</i> , 2014, 144, 57-64.	1.2	12
310	Genetic identification of an oxyurid from a captive, black-handed spider monkey—implications for treatment and control. <i>Parasitology Research</i> , 2014, 113, 3445-3448.	1.6	5
311	Identification of G protein-coupled receptors in <i>Schistosoma haematobium</i> and <i>S. mansoni</i> by comparative genomics. <i>Parasites and Vectors</i> , 2014, 7, 242.	2.5	37
312	Description of <i>Cloacina atthis</i> sp. nov. from the stomach of the euro (<i>Macropus robustus</i>) (Marsupialia: Macropodidae) from Western Australia based on morphological and molecular criteria. <i>Parasitology Research</i> , 2014, 113, 3485-3493.	1.6	11
313	Characterisation of the mitochondrial genome of <i>Parafilaroides normani</i> (lungworm) of <i>Arctocephalus pusillus doriferus</i> (Australian fur seal). <i>Parasitology Research</i> , 2014, 113, 3049-3055.	1.6	9
314	Complete mitochondrial genomes of the intermediate form of <i>Fasciola</i> and <i>Fasciola gigantica</i> , and their comparison with <i>F. hepatica</i> . <i>Parasites and Vectors</i> , 2014, 7, 150.	2.5	80
315	First molecular characterization of <i>Cryptosporidium</i> and <i>Giardia</i> from bovines (<i>Bos taurus</i> and) Tj ETQq1 1 0.784314 rgBT /Overlock 10. <i>Vectors</i> , 2014, 7, 75.	2.5	34
316	Foodborne anisakiasis and allergy. <i>Molecular and Cellular Probes</i> , 2014, 28, 167-174.	2.1	89
317	Hc-daf-2 encodes an insulin-like receptor kinase in the barber's pole worm, <i>Haemonchus contortus</i> , and restores partial dauer regulation. <i>International Journal for Parasitology</i> , 2014, 44, 485-496.	3.1	25
318	Unexpected occurrence of <i>Haemonchus placei</i> in cattle in southern Western Australia. <i>Infection, Genetics and Evolution</i> , 2014, 21, 252-258.	2.3	11
319	Techniques for the Diagnosis of <i>Fasciola</i> Infections in Animals. <i>Advances in Parasitology</i> , 2014, 85, 65-107.	3.2	40
320	<i>Cryptosporidium</i> : Current State of Genomics and Systems Biological Research. , 2014, , 327-344.		1
321	Impact of gastrointestinal parasitic nematodes of sheep, and the role of advanced molecular tools for exploring epidemiology and drug resistance - an Australian perspective. <i>Parasites and Vectors</i> , 2013, 6, 153.	2.5	238
322	Decoding the <i>Ascaris suum</i> Genome using Massively Parallel Sequencing and Advanced Bioinformatic Methods—Unprecedented Prospects for Fundamental and Applied Research. , 2013, , 287-314.		1
323	Description and genetic characterisation of <i>Hysterothylacium</i> (Nematoda: Raphidascarididae) larvae parasitic in Australian marine fishes. <i>Parasitology International</i> , 2013, 62, 320-328.	1.3	52
324	Molecular-based investigation of <i>Cryptosporidium</i> and <i>Giardia</i> from animals in water catchments in southeastern Australia. <i>Water Research</i> , 2013, 47, 1726-1740.	11.3	65

#	ARTICLE	IF	CITATIONS
325	Transcriptome analyses reveal protein and domain families that delineate stage-related development in the economically important parasitic nematodes, <i>Ostertagia ostertagi</i> and <i>Cooperia oncophora</i> . <i>BMC Genomics</i> , 2013, 14, 118.	2.8	31
326	Comparative evaluation of two DNA isolation techniques for PCR-based diagnosis of gastrointestinal nematode infections in sheep. <i>Molecular and Cellular Probes</i> , 2013, 27, 153-157.	2.1	18
327	Mutation scanning analysis of genetic variation within and among <i>Echinococcus</i> species: Implications and future prospects. <i>Electrophoresis</i> , 2013, 34, 1852-1862.	2.4	2
328	Getting the most out of parasitic helminth transcriptomes using HelmDB: Implications for biology and biotechnology. <i>Biotechnology Advances</i> , 2013, 31, 1109-1119.	11.7	23
329	Insights into the immuno-molecular biology of <i>Angiostrongylus vasorum</i> through transcriptomics—Prospects for new interventions. <i>Biotechnology Advances</i> , 2013, 31, 1486-1500.	11.7	18
330	Getting to the guts of the matter: The status and potential of “omics” research of parasitic protists of the human gastrointestinal system. <i>International Journal for Parasitology</i> , 2013, 43, 971-982.	3.1	11
331	The mitochondrial genome of <i>Aelurostrongylus abstrusus</i> —diagnostic, epidemiological and systematic implications. <i>Gene</i> , 2013, 516, 294-300.	2.2	17
332	The mitochondrial genome of <i>Protostrongylus rufescens</i> —implications for population and systematic studies. <i>Parasites and Vectors</i> , 2013, 6, 263.	2.5	18
333	Genetic variability within and among <i>Haemonchus contortus</i> isolates from goats and sheep in China. <i>Parasites and Vectors</i> , 2013, 6, 279.	2.5	41
334	First report of anthelmintic resistance in <i>Haemonchus contortus</i> in alpacas in Australia. <i>Parasites and Vectors</i> , 2013, 6, 243.	2.5	32
335	Molecular characterization of anisakid nematode larvae from 13 species of fish from Western Australia. <i>International Journal of Food Microbiology</i> , 2013, 161, 247-253.	4.7	32
336	First molecular characterisation of <i>Cryptosporidium</i> and <i>Giardia</i> from <i>Bubalus bubalis</i> (water) Tj ETQqO 0 0 rgBT /Overlock 10 Tf 50 302	2.3	28
337	Epidemiological survey following oriental theileriosis outbreaks in Victoria, Australia, on selected cattle farms. <i>Veterinary Parasitology</i> , 2013, 197, 509-521.	1.8	51
338	Rapid, multiplex-tandem PCR assay for automated detection and differentiation of toxigenic cyanobacterial blooms. <i>Molecular and Cellular Probes</i> , 2013, 27, 208-214.	2.1	25
339	A perfect time to harness advanced molecular technologies to explore the fundamental biology of <i>Toxocara</i> species. <i>Veterinary Parasitology</i> , 2013, 193, 353-364.	1.8	41
340	An improved molecular diagnostic assay for canine and feline dermatophytosis. <i>Medical Mycology</i> , 2013, 51, 136-143.	0.7	39
341	Genetic characterization of selected parasites from people with histories of gastrointestinal disorders using a mutation scanning—coupled approach. <i>Electrophoresis</i> , 2013, 34, 1720-1728.	2.4	47
342	Advances in the diagnosis of key gastrointestinal nematode infections of livestock, with an emphasis on small ruminants. <i>Biotechnology Advances</i> , 2013, 31, 1135-1152.	11.7	57

#	ARTICLE	IF	CITATIONS
343	[(I^{6} -Praziquantel) $\text{Cr}(\text{CO})_3$] Derivatives with Remarkable In Vitro Anti- <i>Schistosomal</i> Activity. <i>Chemistry - A European Journal</i> , 2013, 19, 2232-2235.	3.3	33
344	First molecular characterization of <i>Giardia duodenalis</i> from goats in Malaysia. <i>Molecular and Cellular Probes</i> , 2013, 27, 28-31.	2.1	25
345	Analyses of mitochondrial amino acid sequence datasets support the proposal that specimens of <i>Hypodontus macropi</i> from three species of macropodid hosts represent distinct species. <i>BMC Evolutionary Biology</i> , 2013, 13, 259.	3.2	17
346	Mitochondrial Genome of the Eyeworm, <i>Thelazia callipaeda</i> (Nematoda: Spirurida), as the First Representative from the Family Thelaziidae. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2029.	3.0	36
347	Proteomic Analysis of the Excretory-Secretory Products from Larval Stages of <i>Ascaris suum</i> Reveals High Abundance of Glycosyl Hydrolases. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2467.	3.0	63
348	The genome and developmental transcriptome of the strongylid nematode <i>Haemonchus contortus</i> . <i>Genome Biology</i> , 2013, 14, R89.	9.6	192
349	A genome-wide analysis of annexins from parasitic organisms and their vectors. <i>Scientific Reports</i> , 2013, 3, 2893.	3.3	31
350	Next-Generation Molecular-Diagnostic Tools for Gastrointestinal Nematodes of Livestock, with an Emphasis on Small Ruminants. <i>Advances in Parasitology</i> , 2013, 83, 267-333.	3.2	39
351	Assessing calves as carriers of <i>Cryptosporidium</i> and <i>Giardia</i> with zoonotic potential on dairy and beef farms within a water catchment area by mutation scanning. <i>Electrophoresis</i> , 2013, 34, 2259-2267.	2.4	21
352	Identification and genetic characterization of <i>Anisakis</i> larvae from marine fishes in the South China Sea using an electrophoretic-guided approach. <i>Electrophoresis</i> , 2013, 34, 888-894.	2.4	16
353	SOX9 Duplication Linked to Intersex in Deer. <i>PLoS ONE</i> , 2013, 8, e73734.	2.5	18
354	Proteomic Analysis of <i>Oesophagostomum dentatum</i> (Nematoda) during Larval Transition, and the Effects of Hydrolase Inhibitors on Development. <i>PLoS ONE</i> , 2013, 8, e63955.	2.5	16
355	Mitochondrial and Nuclear Ribosomal DNA Evidence Supports the Existence of a New <i>Trichuris</i> Species in the Endangered <i>Presbytis</i> Leaf-Monkey. <i>PLoS ONE</i> , 2013, 8, e66249.	2.5	40
356	Clear Genetic Distinctiveness between Human- and Pig-Derived <i>Trichuris</i> Based on Analyses of Mitochondrial Datasets. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1539.	3.0	98
357	Molecular Changes in <i>Opisthorchis viverrini</i> (Southeast Asian Liver Fluke) during the Transition from the Juvenile to the Adult Stage. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1916.	3.0	19
358	SBAL: a practical tool to generate and edit structure-based amino acid sequence alignments. <i>Bioinformatics</i> , 2012, 28, 1026-1027.	4.1	21
359	Larval anisakid nematodes in teleost fishes from Lizard Island, northern Great Barrier Reef, Australia. <i>Marine and Freshwater Research</i> , 2012, 63, 1283.	1.3	29
360	Genetic characterisation and taxonomy of species of <i>Anisakis</i> (Nematoda: Anisakidae) parasitic in Australian marine mammals. <i>Invertebrate Systematics</i> , 2012, 26, 204.	1.3	34

#	ARTICLE	IF	CITATIONS
361	A Deep Exploration of the Transcriptome and “Excretory/Secretory” Proteome of Adult <i>Fascioloides magna</i> . <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1340-1353.	3.8	35
362	Genetic variation within the <i>Hypodontus macropi</i> (Nematoda: Strongyloidea) complex from macropodid marsupial hosts in Australia. <i>Electrophoresis</i> , 2012, 33, 3544-3554.	2.4	20
363	Establishment of a robotic, high-throughput platform for the specific diagnosis of gastrointestinal nematode infections in sheep. <i>International Journal for Parasitology</i> , 2012, 42, 1151-1158.	3.1	37
364	Molecular diagnosis of sparganosis associated with pneumothorax in a dog. <i>Molecular and Cellular Probes</i> , 2012, 26, 60-62.	2.1	7
365	SCP/TAPS proteins in helminths “Where to from now?”. <i>Molecular and Cellular Probes</i> , 2012, 26, 54-59.	2.1	44
366	Detection of diarrhoeal pathogens in human faeces using an automated, robotic platform. <i>Molecular and Cellular Probes</i> , 2012, 26, 11-15.	2.1	27
367	An assessment of genetic variability in the mitochondrial cytochrome c oxidase subunit 1 gene of <i>Cercopithifilaria</i> sp. (Spirurida, Onchocercidae) from dog and <i>Rhipicephalus sanguineus</i> populations. <i>Molecular and Cellular Probes</i> , 2012, 26, 81-89.	2.1	14
368	Molecular evidence for a cryptic species within the parasitic nematode <i>Macroponema comani</i> (Strongyloidea: Cloacininae). <i>Molecular and Cellular Probes</i> , 2012, 26, 170-174.	2.1	18
369	Assessment of the genetic relationship between <i>Dictyocaulus</i> species from <i>Bos taurus</i> and <i>Cervus elaphus</i> using complete mitochondrial genomic datasets. <i>Parasites and Vectors</i> , 2012, 5, 241.	2.5	36
370	Mitochondrial genome of <i>Angiostrongylus vasorum</i> : Comparison with congeners and implications for studying the population genetics and epidemiology of this parasite. <i>Infection, Genetics and Evolution</i> , 2012, 12, 1884-1891.	2.3	34
371	Genetic characterisation of <i>Cryptosporidium</i> and <i>Giardia</i> from dairy calves: Discovery of species/genotypes consistent with those found in humans. <i>Infection, Genetics and Evolution</i> , 2012, 12, 1984-1993.	2.3	47
372	Whole-genome sequence of <i>Schistosoma haematobium</i> . <i>Nature Genetics</i> , 2012, 44, 221-225.	21.4	383
373	SchistoDB: an updated genome resource for the three key schistosomes of humans. <i>Nucleic Acids Research</i> , 2012, 41, D728-D731.	14.5	45
374	TranSeqAnnotator: large-scale analysis of transcriptomic data. <i>BMC Bioinformatics</i> , 2012, 13, S24.	2.6	6
375	An analysis of the transcriptome of <i>Teladorsagia circumcincta</i> : its biological and biotechnological implications. <i>BMC Genomics</i> , 2012, 13, S10.	2.8	18
376	Ascaroside Signaling Is Widely Conserved among Nematodes. <i>Current Biology</i> , 2012, 22, 772-780.	3.9	177
377	Mutation scanning-based analysis of <i>scp</i> <i>T</i> populations in cattle following an outbreak. <i>Electrophoresis</i> , 2012, 33, 2036-2040.	2.4	38
378	Key strongylid nematodes of animals “Impact of next-generation transcriptomics on systems biology and biotechnology. <i>Biotechnology Advances</i> , 2012, 30, 469-488.	11.7	37

#	ARTICLE	IF	CITATIONS
379	Hookworm SCP/TAPS protein structureâ€”A key to understanding hostâ€”parasite interactions and developing new interventions. <i>Biotechnology Advances</i> , 2012, 30, 652-657.	11.7	31
380	Transcription profiles for two key gender-specific gene families in <i>Oesophagostomum dentatum</i> during development in vivo and in vitro. <i>Infection, Genetics and Evolution</i> , 2012, 12, 137-141.	2.3	4
381	Use of a molecular approach for the definitive diagnosis of proliferative larval mesocestoidiasis in a cat. <i>Infection, Genetics and Evolution</i> , 2012, 12, 1377-1380.	2.3	19
382	Monoaminergic signaling as a target for anthelmintic drug discovery: Receptor conservation among the free-living and parasitic nematodes. <i>Molecular and Biochemical Parasitology</i> , 2012, 183, 1-7.	1.1	16
383	Bioinformatics meets parasitology. <i>Parasite Immunology</i> , 2012, 34, 265-275.	1.5	23
384	Mutation scanningâ€”based analysis of anisakid larvae from <i>Sillago flindersi</i> from Bass Strait, Australia. <i>Electrophoresis</i> , 2012, 33, 499-505.	2.4	16
385	Insights into SCP/TAPS Proteins of Liver Flukes Based on Large-Scale Bioinformatic Analyses of Sequence Datasets. <i>PLoS ONE</i> , 2012, 7, e31164.	2.5	24
386	A Molecular Diagnostic Tool to Replace Larval Culture in Conventional Faecal Egg Count Reduction Testing in Sheep. <i>PLoS ONE</i> , 2012, 7, e37327.	2.5	47
387	Infection with the carcinogenic human liver fluke, <i>Opisthorchis viverrini</i> . <i>Molecular BioSystems</i> , 2011, 7, 1367.	2.9	60
388	Soil-Transmitted Helminths of Humans in Southeast Asiaâ€”Towards Integrated Control. <i>Advances in Parasitology</i> , 2011, 74, 231-265.	3.2	52
389	Heartworm Genomics: Unprecedented Opportunities for Fundamental Molecular Insights and New Intervention Strategies. <i>Topics in Companion Animal Medicine</i> , 2011, 26, 193-199.	0.9	5
390	A Portrait of the Transcriptome of the Neglected Trematode, <i>Fasciola gigantica</i> â€”Biological and Biotechnological Implications. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1004.	3.0	84
391	RNA interference targeting cathepsin B of the carcinogenic liver fluke, <i>Opisthorchis viverrini</i> . <i>Parasitology International</i> , 2011, 60, 283-288.	1.3	32
392	Phylogenetic relationships of species within the tribe Labiostrongylinea (Nematoda: Cloacinidae) from Australian marsupials based on ribosomal DNA spacer sequence data. <i>Parasitology International</i> , 2011, 60, 381-387.	1.3	14
393	Mutation scanning-coupled sequencing of nuclear ribosomal DNA spacers as a tool for the specific identification of different <i>Contracaecum</i> (Nematoda: Anisakidae) larval types. <i>Molecular and Cellular Probes</i> , 2011, 25, 13-18.	2.1	47
394	A first insight into the genotypes of <i>Echinococcus granulosus</i> from humans in Mongolia. <i>Molecular and Cellular Probes</i> , 2011, 25, 49-54.	2.1	47
395	Advances in the identification of <i>Malassezia</i> . <i>Molecular and Cellular Probes</i> , 2011, 25, 1-7.	2.1	50
396	The Transcriptome of <i>Trichuris suis</i> â€” First Molecular Insights into a Parasite with Curative Properties for Key Immune Diseases of Humans. <i>PLoS ONE</i> , 2011, 6, e23590.	2.5	43

#	ARTICLE	IF	CITATIONS
397	Bovine theileriosis “An emerging problem in south-eastern Australia?. Infection, Genetics and Evolution, 2011, 11, 2095-2097.	2.3	52
398	Exploring the Fasciola hepatica tegument proteome. International Journal for Parasitology, 2011, 41, 1347-1359.	3.1	99
399	Serine/threonine phosphatases in socioeconomically important parasitic nematodes”Prospects as novel drug targets?. Biotechnology Advances, 2011, 29, 28-39.	11.7	35
400	Deep insights into Dictyocaulus viviparus transcriptomes provides unique prospects for new drug targets and disease intervention. Biotechnology Advances, 2011, 29, 261-271.	11.7	31
401	Atypical (RIO) protein kinases from Haemonchus contortus “ Promise as new targets for nematocidal drugs. Biotechnology Advances, 2011, 29, 338-350.	11.7	28
402	Ascaris suum draft genome. Nature, 2011, 479, 529-533.	27.8	246
403	Ancipirhynchus afossalis n. g., n. sp. (Trypanorhyncha: Otophriidae), from two species of sharks off Indonesian and Malaysian Borneo. Systematic Parasitology, 2011, 80, 1-15.	1.1	13
404	Occurrence and abundance of anisakid nematode larvae in five species of fish from southern Australian waters. Parasitology Research, 2011, 108, 927-934.	1.6	41
405	Another case of canine amoebic meningoencephalitis”the challenges of reaching a rapid diagnosis. Parasitology Research, 2011, 108, 1069-1073.	1.6	17
406	Major prospects for exploring canine vector borne diseases and novel intervention methods using 'omic technologies. Parasites and Vectors, 2011, 4, 53.	2.5	2
407	Barcoding of <i>Giardia duodenalis</i> isolates and derived lines from an established cryobank by a mutation scanning-based approach. Electrophoresis, 2011, 32, 2075-2090.	2.4	17
408	Norcantharidin analogues with nematocidal activity in Haemonchus contortus. Bioorganic and Medicinal Chemistry Letters, 2011, 21, 3277-3281.	2.2	36
409	Evaluation and application of a molecular method to assess the composition of strongylid nematode populations in sheep with naturally acquired infections. Infection, Genetics and Evolution, 2011, 11, 849-854.	2.3	47
410	First genetic classification of Cryptosporidium and Giardia from HIV/AIDS patients in Malaysia. Infection, Genetics and Evolution, 2011, 11, 968-974.	2.3	48
411	Cryptic Parasite Revealed. Advances in Parasitology, 2011, 77, 141-173.	3.2	21
412	Vaccinomics for the Major Blood Feeding Helminths of Humans. OMICS A Journal of Integrative Biology, 2011, 15, 567-577.	2.0	48
413	LIN-39 and the EGFR/RAS/MAPK pathway regulate <i>C. elegans</i> vulval morphogenesis via the VAB-23 zinc finger protein. Development (Cambridge), 2011, 138, 4649-4660.	2.5	22
414	Cryptosporidiosis. , 2011, , .		3

#	ARTICLE	IF	CITATIONS
415	Resurrection and redescription of <i>Globocephaloides wallabiae</i> Johnston et Mawson, 1939 (Nematoda,) Tj ETQq1 1 0.784314 rgBT /Over 2010, 55, .	1.1	5
416	Drug target prediction and prioritization: using orthology to predict essentiality in parasite genomes. BMC Genomics, 2010, 11, 222.	2.8	76
417	Differences in transcription between free-living and CO2-activated third-stage larvae of <i>Haemonchus contortus</i> . BMC Genomics, 2010, 11, 266.	2.8	47
418	Genetic richness and diversity in <i>Cryptosporidium hominis</i> and <i>C. parvum</i> reveals major knowledge gaps and a need for the application of “next generation” technologies “ Research review. Biotechnology Advances, 2010, 28, 17-26.	11.7	79
419	Elucidating ANTs in worms using genomic and bioinformatic tools “ Biotechnological prospects?. Biotechnology Advances, 2010, 28, 49-60.	11.7	13
420	Toward next-generation sequencing of mitochondrial genomes “ Focus on parasitic worms of animals and biotechnological implications. Biotechnology Advances, 2010, 28, 151-159.	11.7	53
421	Elucidating the transcriptome of <i>Fasciola hepatica</i> “ A key to fundamental and biotechnological discoveries for a neglected parasite. Biotechnology Advances, 2010, 28, 222-231.	11.7	119
422	Progress on the transcriptomics of carcinogenic liver flukes of humans“Unique biological and biotechnological prospects. Biotechnology Advances, 2010, 28, 859-870.	11.7	26
423	Structural and functional characterisation of the fork head transcription factor-encoding gene, <i>Hc-daf-16</i> , from the parasitic nematode <i>Haemonchus contortus</i> (Strongylida). International Journal for Parasitology, 2010, 40, 405-415.	3.1	48
424	Analysis of nucleotide variation within the triose-phosphate isomerase gene of <i>Giardia duodenalis</i> from sheep and its zoonotic implications. Electrophoresis, 2010, 31, 287-298.	2.4	37
425	Elucidating the identity of <i>Anisakis</i> larvae from a broad range of marine fishes from the Yellow Sea, China, using a combined electrophoretic-sequencing approach. Electrophoresis, 2010, 31, 654-658.	2.4	29
426	Highly sensitive non-isotopic restriction endonuclease fingerprinting of nucleotide variability in the <i>gp60</i> gene within <i>Cryptosporidium</i> species, genotypes and subgenotypes infective to humans, and its implications. Electrophoresis, 2010, 31, 1637-1647.	2.4	17
427	Molecular detection of <i>Cryptosporidium cuniculus</i> in rabbits in Australia. Infection, Genetics and Evolution, 2010, 10, 1179-1187.	2.3	41
428	First transcriptomic analysis of the economically important parasitic nematode, <i>Trichostrongylus colubriformis</i> , using a next-generation sequencing approach. Infection, Genetics and Evolution, 2010, 10, 1199-1207.	2.3	55
429	A practical, bioinformatic workflow system for large data sets generated by next-generation sequencing. Nucleic Acids Research, 2010, 38, e171-e171.	14.5	62
430	Massively Parallel Sequencing and Analysis of the <i>Necator americanus</i> Transcriptome. PLoS Neglected Tropical Diseases, 2010, 4, e684.	3.0	66
431	Unlocking the Transcriptomes of Two Carcinogenic Parasites, <i>Clonorchis sinensis</i> and <i>Opisthorchis viverrini</i> . PLoS Neglected Tropical Diseases, 2010, 4, e719.	3.0	141
432	The Rise and Fall of Human Oesophagostomiasis. Advances in Parasitology, 2010, 71, 93-155.	3.2	8

#	ARTICLE	IF	CITATIONS
433	Cryptosporidiosis in Southeast Asia. <i>Advances in Parasitology</i> , 2010, , 1-31.	3.2	14
434	Characterization of a <i>Caenorhabditis elegans</i> glc seven-like phosphatase (<i>gsp</i>) orthologue from <i>Haemonchus contortus</i> (Nematoda). <i>Molecular and Cellular Probes</i> , 2010, 24, 178-189.	2.1	12
435	A vacuolar-type proton (H ⁺) translocating ATPase $\hat{1}\pm$ subunit encoded by the Hc-vha-6 gene of <i>Haemonchus contortus</i> . <i>Molecular and Cellular Probes</i> , 2010, 24, 196-203.	2.1	3
436	A theoretical study to establish the relationship between the three-dimensional structure of triose-phosphate isomerase of <i>Giardia duodenalis</i> and point mutations in the respective gene. <i>Molecular and Cellular Probes</i> , 2010, 24, 281-285.	2.1	3
437	Genetic classification of <i>Echinococcus granulosus</i> cysts from humans, cattle and camels in Libya using mutation scanning-based analysis of mitochondrial loci. <i>Molecular and Cellular Probes</i> , 2010, 24, 346-351.	2.1	46
438	An integrated pipeline for next-generation sequencing and annotation of mitochondrial genomes. <i>Nucleic Acids Research</i> , 2010, 38, 522-533.	14.5	129
439	Improved molecular diagnostic tools for human hookworms. <i>Expert Review of Molecular Diagnostics</i> , 2009, 9, 17-21.	3.1	18
440	Diagnostic and analytical mutation scanning of <i>Cryptosporidium</i> : utility and advantages. <i>Expert Review of Molecular Diagnostics</i> , 2009, 9, 179-185.	3.1	10
441	A polymerase chain reaction-coupled high-resolution melting curve analytical approach for the monitoring of monospecificity of avian <i>Eimeria</i> species. <i>Avian Pathology</i> , 2009, 38, 13-19.	2.0	14
442	Systematic analysis of insertions and deletions specific to nematode proteins and their proposed functional and evolutionary relevance. <i>BMC Evolutionary Biology</i> , 2009, 9, 23.	3.2	24
443	The mitochondrial genomes of <i>Ancylostoma caninum</i> and <i>Bunostomum phlebotomum</i> “two hookworms of animal health and zoonotic importance. <i>BMC Genomics</i> , 2009, 10, 79.	2.8	63
444	Improved insights into the transcriptomes of the human hookworm <i>Necator americanus</i> “Fundamental and biotechnological implications. <i>Biotechnology Advances</i> , 2009, 27, 122-132.	11.7	17
445	A portrait of the “SCP/TAPS”-proteins of eukaryotes “Developing a framework for fundamental research and biotechnological outcomes. <i>Biotechnology Advances</i> , 2009, 27, 376-388.	11.7	139
446	Advanced in silico analysis of expressed sequence tag (EST) data for parasitic nematodes of major socio-economic importance “Fundamental insights toward biotechnological outcomes. <i>Biotechnology Advances</i> , 2009, 27, 439-448.	11.7	29
447	A combined microscopic-molecular method for the diagnosis of strongylid infections in sheep. <i>International Journal for Parasitology</i> , 2009, 39, 1277-1287.	3.1	93
448	Genetic characterization of <i>Cryptosporidium parvum</i> from calves by mutation scanning and targeted sequencing “zoonotic implications. <i>Electrophoresis</i> , 2009, 30, 2640-2647.	2.4	26
449	Genetic categorization of <i>Echinococcus granulosus</i> from humans and herbivorous hosts in Iran using an integrated mutation scanning phylogenetic approach. <i>Electrophoresis</i> , 2009, 30, 2648-2655.	2.4	77
450	Analysis of genetic variation in <i>Globocephaloides</i> populations from macropodid marsupials using a mutation scanning-based approach. <i>Electrophoresis</i> , 2009, 30, 2758-2764.	2.4	8

#	ARTICLE	IF	CITATIONS
451	Molecular characterization of selected dermatophytes and their identification by electrophoretic mutation scanning. <i>Electrophoresis</i> , 2009, 30, 3555-3564.	2.4	24
452	Genetic divergence between island and continental populations of the parasitic nematode <i>Labiosimplex australis</i> in Australia. <i>Parasitology Research</i> , 2009, 104, 229-236.	1.6	12
453	Redescription and genetic characterization of selected <i>Contracaecum</i> spp. (Nematoda: Anisakidae) from various hosts in Australia. <i>Parasitology Research</i> , 2009, 104, 1507-1525.	1.6	65
454	Genetic and morphological evidences for the existence of sibling species within <i>Contracaecum rudolphii</i> (Hartwich, 1964) (Nematoda: Anisakidae) in Australia. <i>Parasitology Research</i> , 2009, 105, 529-538.	1.6	59
455	Investigation of the regulation of transcriptional changes in <i>Ancylostoma caninum</i> larvae following serum activation, with a focus on the insulin-like signalling pathway. <i>Veterinary Parasitology</i> , 2009, 159, 139-148.	1.8	13
456	Mutation scanning-coupled tools for the analysis of genetic variation in <i>Taenia</i> and diagnosis “ Status and prospects. <i>Infection, Genetics and Evolution</i> , 2009, 9, 740-747.	2.3	7
457	Strongyloid nematodes in the caeca of donkeys in Henan Province, China. <i>Acta Parasitologica</i> , 2009, 54, .	1.1	6
458	The conserved zinc finger protein VAB-23 is an essential regulator of epidermal morphogenesis in <i>Caenorhabditis elegans</i> . <i>Developmental Biology</i> , 2009, 336, 84-93.	2.0	4
459	Exploring transcriptional conservation between <i>Ancylostoma caninum</i> and <i>Haemonchus contortus</i> by oligonucleotide microarray and bioinformatic analyses. <i>Molecular and Cellular Probes</i> , 2009, 23, 1-9.	2.1	11
460	High resolution melting-curve (HRM) analysis for the diagnosis of cryptosporidiosis in humans. <i>Molecular and Cellular Probes</i> , 2009, 23, 10-15.	2.1	60
461	Bioinformatic analysis of abundant, gender-enriched transcripts of adult <i>Ascaris suum</i> (Nematoda) using a semi-automated workflow platform. <i>Molecular and Cellular Probes</i> , 2009, 23, 205-217.	2.1	16
462	Male-enriched transcription of genes encoding ASPs and Kunitz-type protease inhibitors in <i>Ancylostoma</i> species. <i>Molecular and Cellular Probes</i> , 2009, 23, 298-303.	2.1	9
463	Comparison of bronchoalveolar lavage fluid examination and other diagnostic techniques with the Baermann technique for detection of naturally occurring <i>Aelurostrongylus abstrusus</i> infection in cats. <i>Journal of the American Veterinary Medical Association</i> , 2009, 235, 43-49.	0.5	53
464	Genetic variation within species of the nematode genus <i>Cloacina</i> (Strongyloidea: Cloacininae) parasitic in the stomachs of rock wallabies, <i>Petrogale</i> spp. (Marsupialia: Macropodidae) in Queensland. <i>Australian Journal of Zoology</i> , 2009, 57, 1.	1.0	27
465	<i>Contracaecum pyripapillatum</i> n. sp. (Nematoda: Anisakidae) and a description of <i>C. multipapillatum</i> (von Drasche, 1882) from the Australian pelican, <i>Pelecanus conspicillatus</i> . <i>Parasitology Research</i> , 2008, 103, 1031-1039.	1.6	46
466	Analysis of the genetic diversity within <i>Cryptosporidium hominis</i> and <i>Cryptosporidium parvum</i> from imported and autochthonous cases of human cryptosporidiosis by mutation scanning. <i>Electrophoresis</i> , 2008, 29, 4119-4129.	2.4	32
467	Genetic characterization of three unique operational taxonomic units of <i>Eimeria</i> from chickens in Australia based on nuclear spacer ribosomal DNA. <i>Veterinary Parasitology</i> , 2008, 152, 226-234.	1.8	47
468	Genetic variants of <i>Malassezia pachydermatis</i> from canine skin: body distribution and phospholipase activity. <i>FEMS Yeast Research</i> , 2008, 8, 451-459.	2.3	47

#	ARTICLE	IF	CITATIONS
469	In silico analysis of expressed sequence tags from <i>Trichostrongylus vitrinus</i> (Nematoda): comparison of the automated ESTExplorer workflow platform with conventional database searches. BMC Bioinformatics, 2008, 9, S10.	2.6	17
470	Using 454 technology for long-PCR based sequencing of the complete mitochondrial genome from single <i>Haemonchus contortus</i> (Nematoda). BMC Genomics, 2008, 9, 11.	2.8	88
471	DNA technological progress toward advanced diagnostic tools to support human hookworm control. Biotechnology Advances, 2008, 26, 35-45.	11.7	30
472	<i>Cryptosporidium</i> " Biotechnological advances in the detection, diagnosis and analysis of genetic variation. Biotechnology Advances, 2008, 26, 304-317.	11.7	109
473	Toward practical, DNA-based diagnostic methods for parasitic nematodes of livestock " Bionomic and biotechnological implications. Biotechnology Advances, 2008, 26, 325-334.	11.7	134
474	Gender-enriched transcripts in <i>Haemonchus contortus</i> " predicted functions and genetic interactions based on comparative analyses with <i>Caenorhabditis elegans</i> . International Journal for Parasitology, 2008, 38, 65-83.	3.1	40
475	Genomics of reproduction in nematodes: prospects for parasite intervention?. Trends in Parasitology, 2008, 24, 89-95.	3.3	15
476	Parasite transmission by insects: a female affair?. Trends in Parasitology, 2008, 24, 116-120.	3.3	10
477	Tv-RIO1 " an atypical protein kinase from the parasitic nematode <i>Trichostrongylus vitrinus</i> . Parasites and Vectors, 2008, 1, 34.	2.5	9
478	Extensive and complex sequence diversity in mitochondrial cytochrome c oxidase subunit 1 within <i>Necator americanus</i> from Colombia revealed by SSCP-coupled sequencing. Molecular and Cellular Probes, 2008, 22, 234-237.	2.1	8
479	Assessing the relationship between <i>Malassezia</i> and leishmaniasis in dogs with or without skin lesions. Acta Tropica, 2008, 107, 25-29.	2.0	13
480	Molecular and phylogenetic characterization of cytochromes c from <i>Haemonchus contortus</i> and <i>Trichostrongylus vitrinus</i> (Nematoda: Trichostrongylida). Gene, 2008, 424, 121-129.	2.2	10
481	Classification of <i>Cryptosporidium</i> Species from Patients with Sporadic Cryptosporidiosis by Use of Sequence-Based Multilocus Analysis following Mutation Scanning. Journal of Clinical Microbiology, 2008, 46, 2252-2262.	3.9	62
482	Transcriptional Changes in the Hookworm, <i>Ancylostoma caninum</i> , during the Transition from a Free-Living to a Parasitic Larva. PLoS Neglected Tropical Diseases, 2008, 2, e130.	3.0	72
483	Genomic-Bioinformatic Analysis of Transcripts Enriched in the Third-Stage Larva of the Parasitic Nematode <i>Ascaris suum</i> . PLoS Neglected Tropical Diseases, 2008, 2, e246.	3.0	27
484	The Mitochondrial Genome of <i>Toxocara canis</i> . PLoS Neglected Tropical Diseases, 2008, 2, e273.	3.0	40
485	Needles in the EST Haystack: Large-Scale Identification and Analysis of Excretory-Secretory (ES) Proteins in Parasitic Nematodes Using Expressed Sequence Tags (ESTs). PLoS Neglected Tropical Diseases, 2008, 2, e301.	3.0	44
486	ESTExplorer: an expressed sequence tag (EST) assembly and annotation platform. Nucleic Acids Research, 2007, 35, W143-W147.	14.5	60

#	ARTICLE	IF	CITATIONS
487	Classification of <i>Mycoplasma synoviae</i> strains using single-strand conformation polymorphism and high-resolution melting-curve analysis of the <i>vlhA</i> gene single-copy region. <i>Microbiology (United Kingdom)</i> , 2007, 157, 1074-1084. ETQq1 1 0.784314 rgBT /Overlock 1	1.4	1
488	Genomic characterization of <i>Tv-ant-1</i> , a <i>Caenorhabditis elegans</i> tag-61 homologue from the parasitic nematode <i>Trichostrongylus vitrinus</i> . <i>Gene</i> , 2007, 397, 12-25.	2.2	8
489	PCR approach for the detection of <i>Trypanosoma brucei</i> and <i>T. equiperdum</i> and their differentiation from <i>T. evansi</i> based on maxicircle kinetoplast DNA. <i>Molecular and Cellular Probes</i> , 2007, 21, 1-7.	2.1	17
490	Nucleotide alterations in the D3 domain of the large subunit of ribosomal DNA among 21 species of equine strongyle. <i>Molecular and Cellular Probes</i> , 2007, 21, 111-115.	2.1	9
491	Molecular characterization of <i>Malassezia</i> isolates from dogs using three distinct genetic markers in nuclear DNA. <i>Molecular and Cellular Probes</i> , 2007, 21, 229-238.	2.1	33
492	The specific identification of anisakid larvae from fishes from the Yellow Sea, China, using mutation scanning-coupled sequence analysis of nuclear ribosomal DNA. <i>Molecular and Cellular Probes</i> , 2007, 21, 386-390.	2.1	49
493	The application of a polymerase chain reaction (PCR)-based capillary electrophoretic technique provides detailed insights into <i>Eimeria</i> populations in intensive poultry establishments. <i>Molecular and Cellular Probes</i> , 2007, 21, 288-294.	2.1	32
494	Multilocus mutation scanning for the analysis of genetic variation within <i>Malassezia</i> (Basidiomycota). <i>Trends in Microbiology</i> , 2007, 15, 254-264. ETQq0 0 0 rgBT /Overlock 10 Tf	2.4	18
495	Specific and genotypic identification of <i>Cryptosporidium</i> from a broad range of host species by nonisotopic SSCP analysis of nuclear ribosomal DNA. <i>Electrophoresis</i> , 2007, 28, 2818-2825.	2.4	29
496	A practical and cost-effective mutation scanning-based approach for investigating genetic variation in <i>Cryptosporidium</i> . <i>Electrophoresis</i> , 2007, 28, 3875-3883.	2.4	44
497	Long PCR amplification of the entire mitochondrial genome from individual helminths for direct sequencing. <i>Nature Protocols</i> , 2007, 2, 2339-2344.	12.0	97
498	Gene discovery for the carcinogenic human liver fluke, <i>Opisthorchis viverrini</i> . <i>BMC Genomics</i> , 2007, 8, 189.	2.8	90
499	A transcriptomic analysis of the adult stage of the bovine lungworm, <i>Dictyocaulus viviparus</i> . <i>BMC Genomics</i> , 2007, 8, 311.	2.8	17
500	<i>Oesophagostomum dentatum</i> – Potential as a model for genomic studies of strongylid nematodes, with biotechnological prospects. <i>Biotechnology Advances</i> , 2007, 25, 281-293.	11.7	19
501	<i>Trichostrongylus vitrinus</i> (Nematoda: Strongylida): Molecular characterization and transcriptional analysis of <i>Tv-stp-1</i> , a serine/threonine phosphatase gene. <i>Experimental Parasitology</i> , 2007, 117, 22-34.	1.2	27
502	Multifocal <i>Balamuthia mandrillaris</i> infection in a dog in Australia. <i>Parasitology Research</i> , 2007, 100, 423-426.	1.6	34
503	Initial support for the hypothesis that PAR2 is involved in the immune response to <i>Nippostrongylus brasiliensis</i> in mice. <i>Parasitology Research</i> , 2007, 101, 105-109.	1.6	14
504	Investigating a persistent coccidiosis problem on a commercial broiler breeder farm utilising PCR-coupled capillary electrophoresis. <i>Parasitology Research</i> , 2007, 101, 583-589.	1.6	48

#	ARTICLE	IF	CITATIONS
505	A hitchhiker's guide to expressed sequence tag (EST) analysis. Briefings in Bioinformatics, 2006, 8, 6-21.	6.5	235
506	Human Thelaziosisâ€”A Neglected Parasitic Disease of the Eye. Journal of Parasitology, 2006, 92, 872-876.	0.7	95
507	Characterisation of a DM domain-containing transcription factor from <i>Trichostrongylus vitrinus</i> (Nematoda: Strongylida). Parasitology International, 2006, 55, 155-157.	1.3	7
508	AFLP fingerprinting for the analysis of genetic diversity within <i>Necator americanus</i> . Molecular and Cellular Probes, 2006, 20, 317-321.	2.1	16
509	Insights into the epidemiology and genetic make-up of <i>Oesophagostomum bifurcum</i> from human and non-human primates using molecular tools. Parasitology, 2006, 132, 453-460.	1.5	50
510	Single-strand conformation polymorphism (SSCP) for the analysis of genetic variation. Nature Protocols, 2006, 1, 3121-3128.	12.0	233
511	Molecular toolsâ€”advances, opportunities and prospects. Veterinary Parasitology, 2006, 136, 69-89.	1.8	198
512	The evolutionary origins of nematodes within the order Strongylida are related to predilection sites within hosts. Molecular Phylogenetics and Evolution, 2006, 40, 118-128.	2.7	99
513	Reproductive characteristics of a precocious vaccine line (Rt3+15) of <i>Eimeria tenella</i> in embryonating chicken eggs. Acta Parasitologica, 2006, 51, .	1.1	0
514	Ubiquitin-conjugating enzyme genes in <i>Oesophagostomum dentatum</i> . Parasitology Research, 2006, 99, 119-125.	1.6	11
515	Isolation and characterization of class II myosin genes from <i>Haemonchus contortus</i> . Parasitology Research, 2006, 99, 200-203.	1.6	4
516	The occurrence of <i>Toxocara malaysiensis</i> in cats in China, confirmed by sequence-based analyses of ribosomal DNA. Parasitology Research, 2006, 99, 554-557.	1.6	57
517	<i>Haemonchus contortus</i> : Prokaryotic expression and enzyme activity of recombinant HcSTK, a serine/threonine protein kinase. Experimental Parasitology, 2006, 113, 207-214.	1.2	4
518	Prospects for exploring molecular developmental processes in <i>Haemonchus contortus</i> . International Journal for Parasitology, 2006, 36, 859-868.	3.1	71
519	Class II myosins in nematodes â€” genetic relationships, fundamental and applied implications. Biotechnology Advances, 2006, 24, 338-350.	11.7	7
520	Biotechnological advances in the diagnosis of avian coccidiosis and the analysis of genetic variation in <i>Eimeria</i> . Biotechnology Advances, 2006, 24, 590-603.	11.7	91
521	Mitochondrial genomes of parasitic nematodes â€” progress and perspectives. Trends in Parasitology, 2006, 22, 78-84.	3.3	143
522	Differentiation of <i>Entamoeba histolytica</i> from <i>Entamoeba dispar</i> by PCR-coupled nonisotopic SSCP analysis. Electrophoresis, 2006, 27, 4419-4422.	2.4	1

#	ARTICLE	IF	CITATIONS
523	Genetic analysis of <i>Trichinella</i> populations by "cold"™ single-strand conformation polymorphism analysis. <i>Veterinary Parasitology</i> , 2005, 132, 23-26.	1.8	12
524	Polymerase chain reaction-based differential diagnosis of <i>Ancylostoma duodenale</i> and <i>Necator americanus</i> infections in humans in northern Ghana. <i>Tropical Medicine and International Health</i> , 2005, 10, 574-580.	2.3	49
525	<i>Oesophagostomum bifurcum</i> in non-human primates is not a potential reservoir for human infection in Ghana. <i>Tropical Medicine and International Health</i> , 2005, 10, 1315-1320.	2.3	21
526	Direct comparison of selected methods for genetic categorisation of <i>Cryptosporidium parvum</i> and <i>Cryptosporidium hominis</i> species. <i>International Journal for Parasitology</i> , 2005, 35, 397-410.	3.1	130
527	High-throughput capillary electrophoresis for the identification and differentiation of seven species of <i>Eimeria</i> from chickens. <i>Electrophoresis</i> , 2005, 26, 3479-3485.	2.4	23
528	Mutation scanning-coupled analysis of haplotypic variability in mitochondrial DNA regions reveals low gene flow between human and porcine <i>Ascaris</i> in endemic regions of China. <i>Electrophoresis</i> , 2005, 26, 4317-4326.	2.4	69
529	PCR-based identification and delineation of members within the <i>Pseudorhabdosynochus lantauensis</i> complex (Monogenea: Diplectanidae). <i>Parasitology Research</i> , 2005, 98, 34-37.	1.6	3
530	Genetic evidence for the existence of sibling species within <i>Contracaecum rudolphii</i> (Hartwich, 1964) and the validity of <i>Contracaecum septentrionale</i> (Kreis, 1955) (Nematoda: Anisakidae). <i>Parasitology Research</i> , 2005, 96, 361-366.	1.6	77
531	Clonorchiasis: a key foodborne zoonosis in China. <i>Lancet Infectious Diseases</i> , The, 2005, 5, 31-41.	9.1	513
532	Analysis of genetic variability within <i>Thelazia callipaeda</i> (Nematoda: Thelazioidea) from Europe and Asia by sequencing and mutation scanning of the mitochondrial cytochrome c oxidase subunit 1 gene. <i>Molecular and Cellular Probes</i> , 2005, 19, 306-313.	2.1	97
533	Capillary electrophoretic analysis of fragment length polymorphism in ribosomal markers of <i>Cryptosporidium</i> from humans. <i>Molecular and Cellular Probes</i> , 2005, 19, 394-399.	2.1	23
534	Application of multiple DNA fingerprinting techniques to study the genetic relationships among three members of the subgenus <i>Trypanozoon</i> (Protozoa: Trypanosomatidae). <i>Molecular and Cellular Probes</i> , 2005, 19, 400-407.	2.1	18
535	Molecular biology of reproduction and development in parasitic nematodes: progress and opportunities. <i>International Journal for Parasitology</i> , 2004, 34, 125-138.	3.1	33
536	Profiling of gender-specific gene expression for <i>Trichostrongylus vitrinus</i> (Nematoda: Strongylida) by microarray analysis of expressed sequence tag libraries constructed by suppressive-subtractive hybridisation. <i>International Journal for Parasitology</i> , 2004, 34, 633-643.	3.1	64
537	Nonisotopic single-strand conformation polymorphism analysis of sequence variability in ribosomal DNA expansion segments within the genus <i>Trichinella</i> (Nematoda: Adenophorea). <i>Electrophoresis</i> , 2004, 25, 3357-3364.	2.4	25
538	Genomic organization and expression analysis for <i>hcstk</i> , a serine/threonine protein kinase gene of <i>Haemonchus contortus</i> , and comparison with <i>Caenorhabditis elegans par-1</i> . <i>Gene</i> , 2004, 343, 313-322.	2.2	10
539	Advances in developing molecular-diagnostic tools for strongyloid nematodes of equids: fundamental and applied implications. <i>Molecular and Cellular Probes</i> , 2004, 18, 3-16.	2.1	30
540	Mutation scanning analysis of <i>Marteilia sydneyi</i> populations from different geographical locations in eastern Australia. <i>Molecular and Cellular Probes</i> , 2004, 18, 133-138.	2.1	10

#	ARTICLE	IF	CITATIONS
541	Elucidating the ecology of bucephalid parasites using a mutation scanning approach. <i>Molecular and Cellular Probes</i> , 2004, 18, 139-146.	2.1	7
542	An electrophoretic tool for the genetic characterisation and delineation of lungworms. <i>Molecular and Cellular Probes</i> , 2004, 18, 197-203.	2.1	4
543	Specific identification of <i>Habronema microstoma</i> and <i>Habronema muscae</i> (Spirurida, Habronematidae) by PCR using markers in ribosomal DNA. <i>Molecular and Cellular Probes</i> , 2004, 18, 215-221.	2.1	33
544	An improved "cold SSCP"™ method for the genotypic and subgenotypic characterization of <i>Cryptosporidium</i> . <i>Molecular and Cellular Probes</i> , 2004, 18, 329-332.	2.1	23
545	GENETIC SUBSTRUCTURING WITHIN <i>OESOPHAGOSTOMUM BIFURCUM</i> (NEMATODA) FROM HUMAN AND NON-HUMAN PRIMATES FROM GHANA BASED ON RANDOM AMPLIFIED POLYMORPHIC DNA ANALYSIS. <i>American Journal of Tropical Medicine and Hygiene</i> , 2004, 71, 227-233.	1.4	34
546	Genomics of reproduction in parasitic nematodes—fundamental and biotechnological implications. <i>Biotechnology Advances</i> , 2003, 21, 103-108.	11.7	6
547	Molecular characterisation of a male-specific serine/threonine phosphatase from <i>Oesophagostomum dentatum</i> (Nematoda: Strongylida), and functional analysis of homologues in <i>Caenorhabditis elegans</i> . <i>International Journal for Parasitology</i> , 2003, 33, 313-325.	3.1	47
548	Comparative analysis of mitochondrial genome data for <i>Necator americanus</i> from two endemic regions reveals substantial genetic variation. <i>International Journal for Parasitology</i> , 2003, 33, 955-963.	3.1	51
549	The mitochondrial genome of <i>Strongyloides stercoralis</i> (Nematoda) — idiosyncratic gene order and evolutionary implications. <i>International Journal for Parasitology</i> , 2003, 33, 1393-1408.	3.1	106
550	Molecular epidemiological investigation of <i>Ascaris</i> genotypes in China based on single-strand conformation polymorphism analysis of ribosomal DNA. <i>Electrophoresis</i> , 2003, 24, 2308-2315.	2.4	49
551	The Mitochondrial Genomics of Parasitic Nematodes of Socio-Economic Importance: Recent Progress, and Implications for Population Genetics and Systematics. <i>Advances in Parasitology</i> , 2003, 56, 133-212.	3.2	93
552	First complete large subunit ribosomal RNA sequence and secondary structure for a parasitic nematode: phylogenetic and diagnostic implications. <i>Molecular and Cellular Probes</i> , 2003, 17, 33-39.	2.1	47
553	Survey of <i>Cryptosporidium parvum</i> genotypes in humans from the UK by mutation scanning analysis of a heat shock protein gene region. <i>Molecular and Cellular Probes</i> , 2003, 17, 127-134.	2.1	15
554	Electrophoretic Analysis of Genetic Variability within <i>Cryptosporidium parvum</i> from Imported and Autochthonous Cases of Human Cryptosporidiosis in the United Kingdom. <i>Applied and Environmental Microbiology</i> , 2003, 69, 2719-2730.	3.1	43
555	Structure and organization of the mitochondrial genome of the canine heartworm, <i>Dirofilaria immitis</i> . <i>Parasitology</i> , 2003, 127, 37-51.	1.5	156
556	The Value of Mutation Scanning Approaches for Detecting Genetic Variation — Implications for Studying Intestinal Nematodes of Humans. , 2002, , 219-233.		10
557	Opportunities and Prospects for Investigating Developmentally Regulated and Sex-Specific Genes and Their Expression in Intestinal Nematodes of Humans. , 2002, , 235-268.		8
558	The mitochondrial genomes of the human hookworms, <i>Ancylostoma duodenale</i> and <i>Necator americanus</i> (Nematoda: Secernentea). <i>International Journal for Parasitology</i> , 2002, 32, 145-158.	3.1	135

#	ARTICLE	IF	CITATIONS
559	HcSTK, a <i>Caenorhabditis elegans</i> PAR-1 homologue from the parasitic nematode, <i>Haemonchus contortus</i> . <i>International Journal for Parasitology</i> , 2002, 32, 749-758.	3.1	36
560	Single-strand conformation polymorphism-based analysis of mitochondrial cytochrome c oxidase subunit 1 reveals significant substructuring in hookworm populations. <i>Electrophoresis</i> , 2002, 23, 27.	2.4	79
561	Mutation scanning analysis of mitochondrial cytochrome c oxidase subunit 1 reveals limited gene flow among bovine lungworm subpopulations in Sweden. <i>Electrophoresis</i> , 2002, 23, 3357-3363.	2.4	33
562	Veterinary parasitology teaching in eastern Australia. <i>Veterinary Parasitology</i> , 2002, 108, 295-307.	1.8	3
563	Redescription of <i>Zoniolaimus mawsonae</i> Beveridge, 1983 (Nematoda: Strongyloidea) and the description of <i>Z. latebrosus</i> n. sp. from the red kangaroo <i>Macropus rufus</i> (Marsupialia: Macropodidae) based on morphological and molecular data. <i>Systematic Parasitology</i> , 2002, 51, 135-147.	1.1	20
564	Molecular aspects of sexual development and reproduction in nematodes and schistosomes. <i>Advances in Parasitology</i> , 2001, 50, 153-198.	3.2	38
565	Applications of single-strand conformation polymorphism (SSCP) to taxonomy, diagnosis, population genetics and molecular evolution of parasitic nematodes. <i>Veterinary Parasitology</i> , 2001, 101, 201-213.	1.8	38
566	Determining the prevalence of <i>Oesophagostomum bifurcum</i> and <i>Necator americanus</i> infections using specific PCR amplification of DNA from faecal samples. <i>Tropical Medicine and International Health</i> , 2001, 6, 726-731.	2.3	89
567	Evolutionary Relationships of Trichostrongyloid Nematodes (Strongylida) Inferred from Ribosomal DNA Sequence Data. <i>Molecular Phylogenetics and Evolution</i> , 2001, 19, 367-386.	2.7	52
568	Mutation scanning for sequence variation in three mitochondrial DNA regions for members of the <i>Contracaecum osculatum</i> (Nematoda: Ascaridoidea) complex. <i>Electrophoresis</i> , 2001, 22, 1069-1075.	2.4	30
569	Mutation scanning analysis of sequence heterogeneity in the second internal transcribed spacer (rDNA) within some members of the <i>Hypodontus macropi</i> (Nematoda: Strongyloidea) complex. <i>Electrophoresis</i> , 2001, 22, 1076-1085.	2.4	30
570	Genotyping <i>Cryptosporidium parvum</i> by single-strand conformation polymorphism analysis of ribosomal and heat shock gene regions. <i>Electrophoresis</i> , 2001, 22, 433-437.	2.4	40
571	Single-strand conformation polymorphism analysis of genetic variation in <i>Labiostongylus longispicularis</i> from kangaroos. <i>Electrophoresis</i> , 2001, 22, 1925-1929.	2.4	15
572	Electrophoretic detection of population variation within <i>Contracaecum ogmorhini</i> (Nematoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22	2.4	38
573	Automated, fluorescence-based approach for the specific diagnosis of chicken coccidiosis. <i>Electrophoresis</i> , 2001, 22, 3546-3550.	2.4	39
574	Molecular and phylogenetic characterisation of <i>Cryptosporidium</i> from birds. <i>International Journal for Parasitology</i> , 2001, 31, 289-296.	3.1	174
575	Molecular taxonomic, diagnostic and genetic studies of parasitic helminths. <i>International Journal for Parasitology</i> , 2001, 31, 860-864.	3.1	14
576	High-resolution electrophoretic procedures for the identification of five <i>Eimeria</i> species from chickens, and detection of population variation. <i>Electrophoresis</i> , 2000, 21, 3558-3563.	2.4	29

#	ARTICLE	IF	CITATIONS
577	Isolation and characterisation of sex-specific transcripts from <i>Oesophagostomum dentatum</i> by RNA arbitrarily-primed PCR. <i>Molecular and Biochemical Parasitology</i> , 2000, 108, 217-224.	1.1	33
578	ITS-1 ribosomal DNA sequence variants are maintained in different species and strains of <i>Echinococcus</i> . <i>International Journal for Parasitology</i> , 2000, 30, 157-169.	3.1	58
579	Genomic and genetic research on bursate nematodes: significance, implications and prospects. <i>International Journal for Parasitology</i> , 2000, 30, 509-534.	3.1	116
580	Mitochondrial DNA polymorphism within and among species of <i>Capillaria sensu lato</i> from Australian marsupials and rodents. <i>International Journal for Parasitology</i> , 2000, 30, 933-938.	3.1	36
581	A molecular systematic framework for equine strongyles based on ribosomal DNA sequence data Note: Nucleotide sequence data reported in this paper are available in GenBank [®] , [†] database under the accession numbers: AJ004835 [†] AJ004855; AJ228236 [†] AJ228247; AJ005831; AJ005832; X77807 [†] X77808 [†] ; X77863; X99345; Y08583 [†] Y08592.1. <i>International Journal for Parasitology</i> , 2000, 30, 95-103.	3.1	41
582	PCR assay for the specific amplification of <i>Oesophagostomum bifurcum</i> DNA from human faeces. <i>International Journal for Parasitology</i> , 2000, 30, 137-142.	3.1	49
583	Assessing sequence variation in the internal transcribed spacers of ribosomal DNA within and among members of the <i>Contraecum osculatum</i> complex (Nematoda: Ascaridoidea: Anisakidae). <i>Parasitology Research</i> , 2000, 86, 677-683.	1.6	139
584	Relationships among some ascaridoid nematodes based on ribosomal DNA sequence data. <i>Parasitology Research</i> , 2000, 86, 738-744.	1.6	92
585	Screening for different genotypes of <i>Echinococcus granulosus</i> within China and Argentina by single-strand conformation polymorphism (SSCP) analysis. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 1999, 93, 329-334.	1.8	33
586	PCR-based technology in veterinary parasitology. <i>Veterinary Parasitology</i> , 1999, 84, 229-258.	1.8	92
587	Sequence differences in the internal transcribed spacer ribosomal DNA among four species of hookworm (Ancylostomatoidea: Ancylostoma) Note: Nucleotide sequence data reported in this paper are available in the EMBL, GenBank [®] , [†] and DDJB databases under the GenBank accession numbers AI001593-AI001594, AI001679 and Y19181-Y19183.1. <i>International Journal for Parasitology</i> , 1999, 29, 1971-1977.	3.1	56
588	Intraspecific and interspecific variation in the second internal transcribed spacer sequence for <i>Metastrongylus</i> (Nematoda: Metastrongyloidea) detected by high resolution PCR-linked restriction fragment length polymorphism. <i>International Journal for Parasitology</i> , 1999, 29, 1935-1940.	3.1	29
589	NADH dehydrogenase subunit 1 and cytochrome c oxidase subunit I sequences compared for members of the genus <i>Taenia</i> (Cestoda). <i>International Journal for Parasitology</i> , 1999, 29, 1965-1970.	3.1	118
590	Screening for nucleotide variations in ribosomal DNA arrays of <i>Oesophagostomum bifurcum</i> by polymerase chain reaction-coupled single-strand conformation polymorphism. <i>Electrophoresis</i> , 1999, 20, 1486-1491.	2.4	26
591	Dideoxy fingerprinting of low-level nucleotide variation in mitochondrial DNA of the human blood fluke, <i>Schistosoma japonicum</i> . <i>Electrophoresis</i> , 1999, 20, 2830-2833.	2.4	13
592	Genotyping <i>Taenia</i> tapeworms by single-strand conformation polymorphism of mitochondrial DNA. <i>Electrophoresis</i> , 1999, 20, 2834-2837.	2.4	25
593	Molecular evidence for cryptic species within <i>Cylicostephanus minutus</i> (Nematoda: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 112 GenBank TM and DDBJ databases under the accession numbers AJ228241, AJ005831, AJ228239, AJ228240, aj 004843, AI005832, AI004841 and AI004842. <i>International Journal for Parasitology</i> , 1999, 29, 285-291.	3.1	58
594	Characterisation of <i>Ascaris</i> from human and pig hosts by nuclear ribosomal DNA sequences Note: Nucleotide sequence data reported in this paper are available in the embl, GenBank TM and DDJB databases under the accession numbers AJ000894 [†] AJ000896, AJ001506, AJ001507 and Y09491. <i>International Journal for Parasitology</i> , 1999, 29, 469-478.	3.1	130

#	ARTICLE	IF	CITATIONS
595	Identification of Nematodirus species (Nematoda: Molineidae) from wild ruminants in Italy using ribosomal DNA markers1Note: Nucleotide sequence data reported in this paper have been deposited in the GenBank, database under the accession numbers AJ239111â€AJ239114.1. International Journal for Parasitology, 1999, 29, 1809-1817.	3.1	22
596	Secondary structure model for the ITS-2 precursor rRNA of strongyloid nematodes of equids: implications for phylogenetic inference1Note: Nucleotide sequences used in this paper are in GenBank, under accession numbers AJ005832, AJ004835â€AJ004847, AJ228236, X77807, X77808, X77863, X99345, Y08585, Y08586, Y08587, Y08619, Y08584, Y08583 and Y08588â€Y08592.1. International Journal for Parasitology, 1999, 29, 1949-1964.	3.1	29
597	A mutation scanning approach for the identification of hookworm species and analysis of population variation. Molecular and Biochemical Parasitology, 1998, 92, 303-312.	1.1	65
598	Detection of sequence variation in parasite ribosomal DNA by electrophoresis in agarose gels supplemented with a DNA-intercalating agent. Electrophoresis, 1998, 19, 671-674.	2.4	6
599	Single-strand conformation polymorphism (SSCP)-based mutation scanning approaches to fingerprint sequence variation in ribosomal DNA of ascaridoid nematodes. Electrophoresis, 1998, 19, 1366-1373.	2.4	75
600	Analysis of sequence homogenisation in rDNA arrays of Haemonchus contortus by denaturing gradient gel electrophoresis. Electrophoresis, 1998, 19, 2391-2395.	2.4	50
601	Differences in the 5.8S rDNA sequences among ascarid nematodes. International Journal for Parasitology, 1998, 28, 617-622.	3.1	30
602	Whatâ€™s in that band?. International Journal for Parasitology, 1998, 28, 989-996.	3.1	20
603	Display of sequence variation in PCR-amplified mitochondrial DNA regions of Echinococcus by single-strand conformation polymorphism. Acta Tropica, 1998, 71, 107-115.	2.0	29
604	Dideoxy fingerprinting: application to the genotyping of Echinococcus. International Journal for Parasitology, 1998, 28, 1775-1779.	3.1	28
605	Common secondary structures for the second internal transcribed spacer pre-rRNA of two subfamilies of trichostrongylid nematodes1Note: Sequences reported in this paper are available in the embl, GenBankTM and DDJB databases (GenBank accession numbers Y14817, Y14818 and Y14819).. International Journal for Parasitology, 1998, 28, 1765-1773.	3.1	39
606	Distinguishing Oesophagostomum dentatum from Oesophagostomum quadrispinulatum developmental stages by a single-strand conformation polymorphism method. International Journal for Parasitology, 1998, 28, 1903-1909.	3.1	18
607	Systematic relationships of some members of the genera Oesophagostomum and Chabertia (Nematoda:) Tj ETQq1 T 0.784314 rgBT /Overlock 10 Tf 50 67 this paper are available in the embl, GenBankTM and DDJB databases under the accession numbers Y10790, Y11735, Y11736, Y11733, Y10789, AJ006149 and AJ006150.. International Journal for Parasitology, 1998, 28, 1763-1769.	3.1	36
608	Characterisation of anisakid nematodes with zoonotic potential by nuclear ribosomal dna sequences1Note: Nucleotide sequence data reported in this paper are available in the embl, GenBankTM and DDJB databases under the accession numbers AJ225062â€AJ225070.. International Journal for Parasitology, 1998, 28, 1911-1921.	3.1	241
609	Identification of parasitic nematodes by PCR-SSCP of ITS-2 rDNA. Molecular and Cellular Probes, 1997, 11, 201-209.	2.1	55
610	PCR-based methods for identification of potentially zoonotic ascaridoid parasites of the dog, fox and cat. Acta Tropica, 1997, 68, 191-200.	2.0	149
611	The 5.8S rDNA sequences of 18 species of bursate nematodes (order Strongylida): Comparison with rhabditid and tylenchid nematodes. International Journal for Parasitology, 1997, 27, 119-124.	3.1	29
612	Evidence for hybridisation between Paramacrostrongylus iugalis and P. typicus (Nematoda:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 67 eastern Australia. International Journal for Parasitology, 1997, 27, 475-482.	3.1	20

#	ARTICLE	IF	CITATIONS
613	Mutation scanning methods for the analysis of parasite genes. International Journal for Parasitology, 1997, 27, 1449-1463.	3.1	87
614	Phylogenetic relationships of Australian strongyloid nematodes inferred from ribosomal DNA sequence data. International Journal for Parasitology, 1997, 27, 1481-1494.	3.1	85
615	Echinococcus granulosus myophilin Relationship with protein homologues containing Calponin motifs. International Journal for Parasitology, 1997, 27, 1561-1567.	3.1	16
616	Polymerase chain reaction-linked single-strand conformation polymorphism of ribosomal DNA to fingerprint parasites. Electrophoresis, 1997, 18, 1564-1566.	2.4	17
617	Genetic markers in ribosomal DNA for hookworm identification. Acta Tropica, 1996, 62, 15-21.	2.0	70
618	Fingerprinting sequence variation in ribosomal DNA of parasites by DGGE. Molecular and Cellular Probes, 1996, 10, 99-105.	2.1	53
619	Use of RAPD for the detection of genetic variation in the human blood fluke, Schistosoma japonicum, from mainland China. Molecular and Cellular Probes, 1996, 10, 353-358.	2.1	25
620	Strongylus asini (Nematoda, Strongyloidea): Genetic relationships with other strongylus species determined by ribosomal DNA. International Journal for Parasitology, 1996, 26, 1407-1411.	3.1	42
621	The ITS-2 rDNA of Teladorsagia circumcincta, T. trifurcata and T. davtiani (Nematoda: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 487 1996, 26, 1123-1126.	3.1	94
622	The immunodiagnostic potential of Echinococcus granulosus adult-worm antigens in human cystic echinococcosis. Parasitology Research, 1996, 83, 90-92.	1.6	13
623	Identification and characterization of myophilin, a muscle-specific antigen of Echinococcus granulosus. Molecular and Biochemical Parasitology, 1995, 70, 139-148.	1.1	19
624	Characterisation of taeniid cestode species by PCR-RFLP of ITS2 ribosomal DNA. Acta Tropica, 1995, 59, 31-40.	2.0	104
625	Specific fingerprinting of nematodes by PCR with single primers to defined repetitive elements. Acta Tropica, 1995, 60, 127-131.	2.0	9
626	Differences in the second internal transcribed spacer (Ribosomal DNA) between five species of Trichostrongylus (Nematoda: Trichostrongylidae). International Journal for Parasitology, 1995, 25, 75-80.	3.1	156
627	Differences in a ribosomal DNA sequence of Strongylus species allows identification of single eggs. International Journal for Parasitology, 1995, 25, 359-365.	3.1	128
628	Differentiation of Haemonchus placei from H. contortus (Nematoda: Trichostrongylidae) by the ribosomal DNA second internal transcribed spacer. International Journal for Parasitology, 1995, 25, 483-488.	3.1	168
629	Differences in a ribosomal DNA sequence of morphologically indistinguishable species within the Hypodontus macropi complex (Nematoda: Strongyloidea). International Journal for Parasitology, 1995, 25, 647-651.	3.1	274
630	The prevalence and epidemiology of gastrointestinal parasites of horses in Victoria, Australia. International Journal for Parasitology, 1995, 25, 711-724.	3.1	156

#	ARTICLE	IF	CITATIONS
631	Species identification of trichostrongyle nematodes by pcr-linked rflp. International Journal for Parasitology, 1994, 24, 291-293.	3.1	60
632	Lack of intraspecific variation in the second Internal Transcribed Spacer (ITS-2) of Trichostrongylus colubriformis ribosomal DNA. International Journal for Parasitology, 1993, 23, 1069-1071.	3.1	55
633	Chromatographic and antigenic properties of Echinococcus granulosus hydatid cyst-derived glycolipids. Parasite Immunology, 1993, 15, 669-681.	1.5	23
634	Rapid sequencing of rDNA from single worms and eggs of parasitic helminths. Nucleic Acids Research, 1993, 21, 2525-2526.	14.5	394
635	Sexing single larval stages of Schistosoma mansoni by polymerase chain reaction. Molecular and Biochemical Parasitology, 1991, 47, 255-258.	1.1	44
636	Determination of the optimum cut-off value of a diagnostic test. Preventive Veterinary Medicine, 1990, 10, 137-143.	1.9	32
637	Identification of protein components of Echinococcus granulosus protoscolex antigens for specific serodiagnosis of E. granulosus infection in dogs. Parasite Immunology, 1989, 11, 279-291.	1.5	22