

Robin B Gasser

List of Publications by Year in descending order

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637
papers

25,903
citations

9234

74
h-index

18075

120
g-index

645
all docs

645
docs citations

645
times ranked

18722
citing authors

#	ARTICLE	IF	CITATIONS
1	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	13.7	1,942
2	Clonorchiasis: a key foodborne zoonosis in China. <i>Lancet Infectious Diseases</i> , The, 2005, 5, 31-41.	4.6	513
3	Rapid sequencing of rDNA from single worms and eggs of parasitic helminths. <i>Nucleic Acids Research</i> , 1993, 21, 2525-2526.	6.5	394
4	Whole-genome sequence of <i>Schistosoma haematobium</i> . <i>Nature Genetics</i> , 2012, 44, 221-225.	9.4	383
5	SARS-CoV-2 seroprevalence worldwide: a systematic review and meta-analysis. <i>Clinical Microbiology and Infection</i> , 2021, 27, 331-340.	2.8	296
6	Human toxocariasis. <i>Lancet Infectious Diseases</i> , The, 2018, 18, e14-e24.	4.6	278
7	Differences in a ribosomal DNA sequence of morphologically indistinguishable species within the <i>Hypodontus macropi</i> complex (Nematoda: Strongyloidea). <i>International Journal for Parasitology</i> , 1995, 25, 647-651.	1.3	274
8	<i>Ascaris suum</i> draft genome. <i>Nature</i> , 2011, 479, 529-533.	13.7	246
9	Characterisation of anisakid nematodes with zoonotic potential by nuclear ribosomal dna sequences Note: Nucleotide sequence data reported in this paper are available in the embl, GenBank™ and DDJB databases under the accession numbers AJ225062-“AJ225070.. <i>International Journal for Parasitology</i> , 1998, 28, 1911-1921.	1.3	241
10	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.	1.0	238
11	A hitchhiker's guide to expressed sequence tag (EST) analysis. <i>Briefings in Bioinformatics</i> , 2006, 8, 6-21.	3.2	235
12	Single-strand conformation polymorphism (SSCP) for the analysis of genetic variation. <i>Nature Protocols</i> , 2006, 1, 3121-3128.	5.5	233
13	Molecular tools' advances, opportunities and prospects. <i>Veterinary Parasitology</i> , 2006, 136, 69-89.	0.7	198
14	The genome and developmental transcriptome of the strongylid nematode <i>Haemonchus contortus</i> . <i>Genome Biology</i> , 2013, 14, R89.	13.9	192
15	Ascaroside Signaling Is Widely Conserved among Nematodes. <i>Current Biology</i> , 2012, 22, 772-780.	1.8	177
16	Molecular and phylogenetic characterisation of <i>Cryptosporidium</i> from birds. <i>International Journal for Parasitology</i> , 2001, 31, 289-296.	1.3	174
17	Differentiation of <i>Haemonchus placei</i> from <i>H. contortus</i> (Nematoda: Trichostrongylidae) by the ribosomal DNA second internal transcribed spacer. <i>International Journal for Parasitology</i> , 1995, 25, 483-488.	1.3	168
18	Genome of the human hookworm <i>Necator americanus</i> . <i>Nature Genetics</i> , 2014, 46, 261-269.	9.4	166

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19	Differences in the second internal transcribed spacer (Ribosomal DNA) between five species of <i>Trichostrongylus</i> (Nematoda: Trichostrongylidae). <i>International Journal for Parasitology</i> , 1995, 25, 75-80.	1.3	156
20	The prevalence and epidemiology of gastrointestinal parasites of horses in Victoria, Australia. <i>International Journal for Parasitology</i> , 1995, 25, 711-724.	1.3	156
21	Structure and organization of the mitochondrial genome of the canine heartworm, <i>Dirofilaria immitis</i> . <i>Parasitology</i> , 2003, 127, 37-51.	0.7	156
22	Gene content evolution in the arthropods. <i>Genome Biology</i> , 2020, 21, 15.	3.8	150
23	PCR-based methods for identification of potentially zoonotic ascaridoid parasites of the dog, fox and cat. <i>Acta Tropica</i> , 1997, 68, 191-200.	0.9	149
24	The <i>Opisthorchis viverrini</i> genome provides insights into life in the bile duct. <i>Nature Communications</i> , 2014, 5, 4378.	5.8	144
25	Mitochondrial genomes of parasitic nematodes – progress and perspectives. <i>Trends in Parasitology</i> , 2006, 22, 78-84.	1.5	143
26	Unlocking the Transcriptomes of Two Carcinogenic Parasites, <i>Clonorchis sinensis</i> and <i>Opisthorchis viverrini</i> . <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e719.	1.3	141
27	Bovine ticks harbour a diverse array of microorganisms in Pakistan. <i>Parasites and Vectors</i> , 2020, 13, 1.	1.0	141
28	Assessing sequence variation in the internal transcribed spacers of ribosomal DNA within and among members of the <i>Contraecaecum osculatum</i> complex (Nematoda: Ascaridoidea: Anisakidae). <i>Parasitology Research</i> , 2000, 86, 677-683.	0.6	139
29	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.	6.0	139
30	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.	1.3	135
31	Toward practical, DNA-based diagnostic methods for parasitic nematodes of livestock – Bionomic and biotechnological implications. <i>Biotechnology Advances</i> , 2008, 26, 325-334.	6.0	134
32	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™ and DDBJ databases under the accession numbers AJ000894, AJ000896, AJ001506, AJ001507 and Y09491.. <i>International Journal for Parasitology</i> , 1999, 29, 469-478.	1.3	130
33	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.	1.3	130
34	An integrated pipeline for next-generation sequencing and annotation of mitochondrial genomes. <i>Nucleic Acids Research</i> , 2010, 38, 522-533.	6.5	129
35	Differences in a ribosomal DNA sequence of <i>Strongylus</i> species allows identification of single eggs. <i>International Journal for Parasitology</i> , 1995, 25, 359-365.	1.3	128
36	Elucidating the transcriptome of <i>Fasciola hepatica</i> – A key to fundamental and biotechnological discoveries for a neglected parasite. <i>Biotechnology Advances</i> , 2010, 28, 222-231.	6.0	119

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37	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.	1.3	118
38	Tick-borne diseases of bovines in Pakistan: major scope for future research and improved control. <i>Parasites and Vectors</i> , 2015, 8, 283.	1.0	117
39	Genomic and genetic research on bursate nematodes: significance, implications and prospects. <i>International Journal for Parasitology</i> , 2000, 30, 509-534.	1.3	116
40	<i>Cryptosporidium</i> " Biotechnological advances in the detection, diagnosis and analysis of genetic variation. <i>Biotechnology Advances</i> , 2008, 26, 304-317.	6.0	109
41	Phylogenomic and biogeographic reconstruction of the <i>Trichinella</i> complex. <i>Nature Communications</i> , 2016, 7, 10513.	5.8	107
42	Seroprevalence estimates for toxocariasis in people worldwide: A systematic review and meta-analysis. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007809.	1.3	107
43	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.	1.3	106
44	Low cost whole-organism screening of compounds for anthelmintic activity. <i>International Journal for Parasitology</i> , 2015, 45, 333-343.	1.3	106
45	Characterisation of taeniid cestode species by PCR-RFLP of ITS2 ribosomal DNA. <i>Acta Tropica</i> , 1995, 59, 31-40.	0.9	104
46	Genetic blueprint of the zoonotic pathogen <i>Toxocara canis</i> . <i>Nature Communications</i> , 2015, 6, 6145.	5.8	103
47	Exploration of extracellular vesicles from <i>Ascaris suum</i> provides evidence of parasite-host cross talk. <i>Journal of Extracellular Vesicles</i> , 2019, 8, 1578116.	5.5	103
48	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> , 2010, 156, 1100-1107.	1.0	50
49	The evolutionary origins of nematodes within the order Strongylida are related to predilection sites within hosts. <i>Molecular Phylogenetics and Evolution</i> , 2006, 40, 118-128.	1.2	99
50	Exploring the <i>Fasciola hepatica</i> tegument proteome. <i>International Journal for Parasitology</i> , 2011, 41, 1347-1359.	1.3	99
51	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.	1.3	98
52	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.	0.9	97
53	Long PCR amplification of the entire mitochondrial genome from individual helminths for direct sequencing. <i>Nature Protocols</i> , 2007, 2, 2339-2344.	5.5	97
54	Human Thelaziosis " A Neglected Parasitic Disease of the Eye. <i>Journal of Parasitology</i> , 2006, 92, 872-876.	0.3	95

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55	The ITS-2 rDNA of <i>Teladorsagia circumcincta</i> , <i>T. trifurcata</i> and <i>T. davtiani</i> (Nematoda): Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 747 1996, 26, 1123-1126.	1.3	94
56	Drug resistance in <i>Giardia duodenalis</i> . <i>Biotechnology Advances</i> , 2015, 33, 888-901.	6.0	94
57	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.	1.4	93
58	A combined microscopic-molecular method for the diagnosis of strongylid infections in sheep. <i>International Journal for Parasitology</i> , 2009, 39, 1277-1287.	1.3	93
59	Genome and transcriptome of the porcine whipworm <i>Trichuris suis</i> . <i>Nature Genetics</i> , 2014, 46, 701-706.	9.4	93
60	Toxocara eggs in public places worldwide - A systematic review and meta-analysis. <i>Environmental Pollution</i> , 2018, 242, 1467-1475.	3.7	93
61	PCR-based technology in veterinary parasitology. <i>Veterinary Parasitology</i> , 1999, 84, 229-258.	0.7	92
62	Relationships among some ascaridoid nematodes based on ribosomal DNA sequence data. <i>Parasitology Research</i> , 2000, 86, 738-744.	0.6	92
63	Biotechnological advances in the diagnosis of avian coccidiosis and the analysis of genetic variation in <i>Eimeria</i> . <i>Biotechnology Advances</i> , 2006, 24, 590-603.	6.0	91
64	Gene discovery for the carcinogenic human liver fluke, <i>Opisthorchis viverrini</i> . <i>BMC Genomics</i> , 2007, 8, 189.	1.2	90
65	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.	1.0	89
66	Foodborne anisakiasis and allergy. <i>Molecular and Cellular Probes</i> , 2014, 28, 167-174.	0.9	89
67	Using 454 technology for long-PCR based sequencing of the complete mitochondrial genome from single <i>Haemonchus contortus</i> (Nematoda). <i>BMC Genomics</i> , 2008, 9, 11.	1.2	88
68	Mutation scanning methods for the analysis of parasite genes. <i>International Journal for Parasitology</i> , 1997, 27, 1449-1463.	1.3	87
69	Phylogenetic relationships of Australian strongyloid nematodes inferred from ribosomal DNA sequence data. <i>International Journal for Parasitology</i> , 1997, 27, 1481-1494.	1.3	85
70	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.	1.3	84
71	Complete mitochondrial genomes of the â€”intermediate formâ€”™ 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.	1.0	80
72	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.	1.3	79

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73	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. <i>Biotechnology Advances</i> , 2010, 28, 17-26.	6.0	79
74	Genetic evidence for the existence of sibling species within <i>Contraecaecum rudolphii</i> (Hartwich, 1964) and the validity of <i>Contraecaecum septentrionale</i> (Kreis, 1955) (Nematoda: Anisakidae). <i>Parasitology Research</i> , 2005, 96, 361-366.	0.6	77
75	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.	1.3	77
76	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.	1.3	77
77	Drug target prediction and prioritization: using orthology to predict essentiality in parasite genomes. <i>BMC Genomics</i> , 2010, 11, 222.	1.2	76
78	Human toxocariasis – A look at a neglected disease through an epidemiological prism™. <i>Infection, Genetics and Evolution</i> , 2019, 74, 104002.	1.0	76
79	Acute <i>Toxoplasma</i> infection in pregnant women worldwide: A systematic review and meta-analysis. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007807.	1.3	76
80	Single-strand conformation polymorphism (SSCP)-based mutation scanning approaches to fingerprint sequence variation in ribosomal DNA of ascaridoid nematodes. <i>Electrophoresis</i> , 1998, 19, 1366-1373.	1.3	75
81	<i>Giardia/giardiasis</i> – A perspective on diagnostic and analytical tools. <i>Biotechnology Advances</i> , 2014, 32, 280-289.	6.0	73
82	Transcriptional Changes in the Hookworm, <i>Ancylostoma caninum</i> , during the Transition from a Free-Living to a Parasitic Larva. <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e130.	1.3	72
83	Prospects for exploring molecular developmental processes in <i>Haemonchus contortus</i> . <i>International Journal for Parasitology</i> , 2006, 36, 859-868.	1.3	71
84	Genetic markers in ribosomal DNA for hookworm identification. <i>Acta Tropica</i> , 1996, 62, 15-21.	0.9	70
85	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.	1.3	69
86	Oriental theileriosis in dairy cows causes a significant milk production loss. <i>Parasites and Vectors</i> , 2014, 7, 73.	1.0	68
87	<i>Lucilia cuprina</i> genome unlocks parasitic fly biology to underpin future interventions. <i>Nature Communications</i> , 2015, 6, 7344.	5.8	67
88	Massively Parallel Sequencing and Analysis of the <i>Necator americanus</i> Transcriptome. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e684.	1.3	66
89	A mutation scanning approach for the identification of hookworm species and analysis of population variation. <i>Molecular and Biochemical Parasitology</i> , 1998, 92, 303-312.	0.5	65
90	Redescription and genetic characterization of selected <i>Contraecaecum</i> spp. (Nematoda: Anisakidae) from various hosts in Australia. <i>Parasitology Research</i> , 2009, 104, 1507-1525.	0.6	65

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91	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.	5.3	65
92	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.	1.3	64
93	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.	1.2	63
94	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.	1.3	63
95	Omega-1 knockdown in <i>Schistosoma mansoni</i> eggs by lentivirus transduction reduces granuloma size in vivo. <i>Nature Communications</i> , 2014, 5, 5375.	5.8	63
96	Classification of <i>Cryptosporidium</i> Species from Patients with Sporadic Cryptosporidiosis by Use of Sequence-Based Multilocus Analysis following Mutation Scanning. <i>Journal of Clinical Microbiology</i> , 2008, 46, 2252-2262.	1.8	62
97	A practical, bioinformatic workflow system for large data sets generated by next-generation sequencing. <i>Nucleic Acids Research</i> , 2010, 38, e171-e171.	6.5	62
98	Global prevalence of <i>Toxocara</i> infection in dogs. <i>Advances in Parasitology</i> , 2020, 109, 561-583.	1.4	62
99	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.	1.4	61
100	Species identification of trichostrongyle nematodes by pcr-linked rflp. <i>International Journal for Parasitology</i> , 1994, 24, 291-293.	1.3	60
101	ESTExplorer: an expressed sequence tag (EST) assembly and annotation platform. <i>Nucleic Acids Research</i> , 2007, 35, W143-W147.	6.5	60
102	High resolution melting-curve (HRM) analysis for the diagnosis of cryptosporidiosis in humans. <i>Molecular and Cellular Probes</i> , 2009, 23, 10-15.	0.9	60
103	Infection with the carcinogenic human liver fluke, <i>Opisthorchis viverrini</i> . <i>Molecular BioSystems</i> , 2011, 7, 1367.	2.9	60
104	Genetic and morphological evidences for the existence of sibling species within <i>Contraecaecum rudolphii</i> (Hartwich, 1964) (Nematoda: Anisakidae) in Australia. <i>Parasitology Research</i> , 2009, 105, 529-538.	0.6	59
105	Molecular evidence for cryptic species within <i>Cylicostephanus minutus</i> (Nematoda: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 192 GenBank™ 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.	1.3	58
106	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.	1.3	58
107	The occurrence of <i>Toxocara malaysiensis</i> in cats in China, confirmed by sequence-based analyses of ribosomal DNA. <i>Parasitology Research</i> , 2006, 99, 554-557.	0.6	57
108	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.	6.0	57

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109	Sequence differences in the internal transcribed spacer ribosomal DNA among four species of hookworm (Ancylostomatoidea: Ancylostoma)1Note: Nucleotide sequence data reported in this paper are available in the EMBL, GenBank, and DDJB databases under the GenBank accession numbers A1001593-A1001594, A1001679 and Y19181-Y19183.1. International Journal for Parasitology, 1999, 29, 1971-1977.	1.3	56
110	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.	1.3	55
111	Identification of parasitic nematodes by PCR-SSCP of ITS-2 rDNA. Molecular and Cellular Probes, 1997, 11, 201-209.	0.9	55
112	First transcriptomic analysis of the economically important parasitic nematode, Trichostrongylus colubriformis, using a next-generation sequencing approach. Infection, Genetics and Evolution, 2010, 10, 1199-1207.	1.0	55
113	Human cyclosporiasis. Lancet Infectious Diseases, The, 2019, 19, e226-e236.	4.6	55
114	Distinguishing Echinococcus granulosus sensu stricto genotypes G1 and G3 with confidence: A practical guide. Infection, Genetics and Evolution, 2018, 64, 178-184.	1.0	54
115	Fingerprinting sequence variation in ribosomal DNA of parasites by DGGE. Molecular and Cellular Probes, 1996, 10, 99-105.	0.9	53
116	Comparison of bronchoalveolar lavage fluid examination and other diagnostic techniques with the Baermann technique for detection of naturally occurring Aelurostrongylus abstrusus infection in cats. Journal of the American Veterinary Medical Association, 2009, 235, 43-49.	0.2	53
117	Toward next-generation sequencing of mitochondrial genomes – Focus on parasitic worms of animals and biotechnological implications. Biotechnology Advances, 2010, 28, 151-159.	6.0	53
118	Transcriptional analysis identifies key genes involved in metabolism, fibrosis/tissue repair and the immune response against Fasciola hepatica in sheep liver. Parasites and Vectors, 2015, 8, 124.	1.0	53
119	Evolutionary Relationships of Trichostrongyloid Nematodes (Strongylida) Inferred from Ribosomal DNA Sequence Data. Molecular Phylogenetics and Evolution, 2001, 19, 367-386.	1.2	52
120	Soil-Transmitted Helminths of Humans in Southeast Asia – Towards Integrated Control. Advances in Parasitology, 2011, 74, 231-265.	1.4	52
121	Bovine theileriosis – An emerging problem in south-eastern Australia?. Infection, Genetics and Evolution, 2011, 11, 2095-2097.	1.0	52
122	Description and genetic characterisation of Hysterothylacium (Nematoda: Raphidascarididae) larvae parasitic in Australian marine fishes. Parasitology International, 2013, 62, 320-328.	0.6	52
123	The benefits of analysing complete mitochondrial genomes: Deep insights into the phylogeny and population structure of Echinococcus granulosus sensu lato genotypes G6 and G7. Infection, Genetics and Evolution, 2018, 64, 85-94.	1.0	52
124	An appraisal of natural products active against parasitic nematodes of animals. Parasites and Vectors, 2019, 12, 306.	1.0	52
125	Comparative analysis of mitochondrial genome data for Necator americanus from two endemic regions reveals substantial genetic variation. International Journal for Parasitology, 2003, 33, 955-963.	1.3	51
126	Epidemiological survey following oriental theileriosis outbreaks in Victoria, Australia, on selected cattle farms. Veterinary Parasitology, 2013, 197, 509-521.	0.7	51

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127	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.	1.0	51
128	Analysis of sequence homogenisation in rDNA arrays of <i>Haemonchus contortus</i> by denaturing gradient gel electrophoresis. <i>Electrophoresis</i> , 1998, 19, 2391-2395.	1.3	50
129	Insights into the epidemiology and genetic make-up of <i>Oesophagostomum bifurcum</i> from human and non-human primates using molecular tools. <i>Parasitology</i> , 2006, 132, 453-460.	0.7	50
130	Advances in the identification of <i>Malassezia</i> . <i>Molecular and Cellular Probes</i> , 2011, 25, 1-7.	0.9	50
131	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.	1.3	49
132	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.	1.3	49
133	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.	1.0	49
134	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.	0.9	49
135	Whole-genome sequence of the bovine blood fluke <i>Schistosoma bovis</i> supports interspecific hybridization with <i>S. haematobium</i> . <i>PLoS Pathogens</i> , 2019, 15, e1007513.	2.1	49
136	Update on SARS-CoV-2 seroprevalence: regional and worldwide. <i>Clinical Microbiology and Infection</i> , 2021, 27, 1762-1771.	2.8	49
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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636	Quantitative lipidomic analysis of <i>Ascaris suum</i> . , 2020, 14, e0008848.		0
637	Quantitative lipidomic analysis of <i>Ascaris suum</i> . , 2020, 14, e0008848.		0