

Robin B Gasser

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

625
papers

20,337
citations

68
h-index

108
g-index

645
ext. papers

23,376
ext. citations

5.5
avg, IF

6.93
L-index

#	Paper	IF	Citations
625	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017 , 551, 457-463	50.4	1076
624	Clonorchiasis: a key foodborne zoonosis in China. <i>Lancet Infectious Diseases, The</i> , 2005 , 5, 31-41	25.5	437
623	Rapid sequencing of rDNA from single worms and eggs of parasitic helminths. <i>Nucleic Acids Research</i> , 1993 , 21, 2525-6	20.1	337
622	Whole-genome sequence of <i>Schistosoma haematobium</i> . <i>Nature Genetics</i> , 2012 , 44, 221-5	36.3	325
621	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, 647-51	4.3	264
620	<i>Ascaris suum</i> draft genome. <i>Nature</i> , 2011 , 479, 529-33	50.4	217
619	Single-strand conformation polymorphism (SSCP) for the analysis of genetic variation. <i>Nature Protocols</i> , 2006 , 1, 3121-8	18.8	210
618	Characterisation of anisakid nematodes with zoonotic potential by nuclear ribosomal DNA sequences. <i>International Journal for Parasitology</i> , 1998 , 28, 1911-21	4.3	202
617	A hitchhiker's guide to expressed sequence tag (EST) analysis. <i>Briefings in Bioinformatics</i> , 2007 , 8, 6-21	13.4	200
616	Human toxocariasis. <i>Lancet Infectious Diseases, The</i> , 2018 , 18, e14-e24	25.5	179
615	Molecular tools--advances, opportunities and prospects. <i>Veterinary Parasitology</i> , 2006 , 136, 69-89	2.8	177
614	The genome and developmental transcriptome of the strongylid nematode <i>Haemonchus contortus</i> . <i>Genome Biology</i> , 2013 , 14, R89	18.3	166
613	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	4	164
612	SARS-CoV-2 seroprevalence worldwide: a systematic review and meta-analysis. <i>Clinical Microbiology and Infection</i> , 2021 , 27, 331-340	9.5	162
611	Molecular and phylogenetic characterisation of <i>Cryptosporidium</i> from birds. <i>International Journal for Parasitology</i> , 2001 , 31, 289-96	4.3	161
610	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, 483-8	4.3	150
609	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	4.3	148

608	Structure and organization of the mitochondrial genome of the canine heartworm, <i>Dirofilaria immitis</i> . <i>Parasitology</i> , 2003 , 127, 37-51	2.7	143
607	Ascaroside signaling is widely conserved among nematodes. <i>Current Biology</i> , 2012 , 22, 772-80	6.3	141
606	Genome of the human hookworm <i>Necator americanus</i> . <i>Nature Genetics</i> , 2014 , 46, 261-269	36.3	139
605	PCR-based methods for identification of potentially zoonotic ascaridoid parasites of the dog, fox and cat. <i>Acta Tropica</i> , 1997 , 68, 191-200	3.2	131
604	Mitochondrial genomes of parasitic nematodes--progress and perspectives. <i>Trends in Parasitology</i> , 2006 , 22, 78-84	6.4	128
603	A portrait of the "SCP/TAPS" proteins of eukaryotes--developing a framework for fundamental research and biotechnological outcomes. <i>Biotechnology Advances</i> , 2009 , 27, 376-88	17.8	126
602	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	4.8	122
601	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, 145-58	4.3	122
600	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	4.3	120
599	Characterisation of <i>Ascaris</i> from human and pig hosts by nuclear ribosomal DNA sequences. <i>International Journal for Parasitology</i> , 1999 , 29, 469-78	4.3	119
598	Differences in a ribosomal DNA sequence of <i>Strongylus</i> species allows identification of single eggs. <i>International Journal for Parasitology</i> , 1995 , 25, 359-65	4.3	114
597	The <i>Opisthorchis viverrini</i> genome provides insights into life in the bile duct. <i>Nature Communications</i> , 2014 , 5, 4378	17.4	113
596	Toward practical, DNA-based diagnostic methods for parasitic nematodes of livestock--bionomic and biotechnological implications. <i>Biotechnology Advances</i> , 2008 , 26, 325-34	17.8	113
595	An integrated pipeline for next-generation sequencing and annotation of mitochondrial genomes. <i>Nucleic Acids Research</i> , 2010 , 38, 522-33	20.1	112
594	The prevalence and epidemiology of gastrointestinal parasites of horses in Victoria, Australia. <i>International Journal for Parasitology</i> , 1995 , 25, 711-24	4.3	111
593	Assessing sequence variation in the internal transcribed spacers of ribosomal DNA within and among members of the <i>Contracecum osculatum</i> complex (Nematoda: Ascaridoidea: Anisakidae). <i>Parasitology Research</i> , 2000 , 86, 677-83	2.4	110
592	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, 1965-70	4.3	105
591	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, 222-31	17.8	102

590	Genomic and genetic research on bursate nematodes: significance, implications and prospects. <i>International Journal for Parasitology</i> , 2000 , 30, 509-34	4.3	101
589	Characterisation of taeniid cestode species by PCR-RFLP of ITS2 ribosomal DNA. <i>Acta Tropica</i> , 1995 , 59, 31-40	3.2	97
588	The mitochondrial genome of <i>Strongyloides stercoralis</i> (Nematoda) - idiosyncratic gene order and evolutionary implications. <i>International Journal for Parasitology</i> , 2003 , 33, 1393-408	4.3	93
587	Cryptosporidium--biotechnological advances in the detection, diagnosis and analysis of genetic variation. <i>Biotechnology Advances</i> , 2008 , 26, 304-17	17.8	91
586	The ITS-2 rDNA of <i>Teladorsagia circumcincta</i> , <i>T. trifurcata</i> and <i>T. davtiani</i> (Nematoda: Trichostrongylidae) indicates that these taxa are one species. <i>International Journal for Parasitology</i> , 1996 , 26, 1123-1126	4.3	88
585	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	4.8	87
584	Mutation scanning methods for the analysis of parasite genes. <i>International Journal for Parasitology</i> , 1997 , 27, 1449-63	4.3	86
583	Long PCR amplification of the entire mitochondrial genome from individual helminths for direct sequencing. <i>Nature Protocols</i> , 2007 , 2, 2339-44	18.8	86
582	The evolutionary origins of nematodes within the order Strongylida are related to predilection sites within hosts. <i>Molecular Phylogenetics and Evolution</i> , 2006 , 40, 118-28	4.1	86
581	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, 726-31	2.3	86
580	Bovine ticks harbour a diverse array of microorganisms in Pakistan. <i>Parasites and Vectors</i> , 2020 , 13, 1	4	86
579	PCR-based technology in veterinary parasitology. <i>Veterinary Parasitology</i> , 1999 , 84, 229-58	2.8	85
578	The mitochondrial genomics of parasitic nematodes of socio-economic importance: recent progress, and implications for population genetics and systematics. <i>Advances in Parasitology</i> , 2004 , 56, 133-212	3.2	84
577	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 , 153, 2679-2688	2.9	83
576	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, 306-13	3.3	83
575	Human thelaziosis--a neglected parasitic disease of the eye. <i>Journal of Parasitology</i> , 2006 , 92, 872-5	0.9	83
574	Exploring the <i>Fasciola hepatica</i> tegument proteome. <i>International Journal for Parasitology</i> , 2011 , 41, 1347-59	4.3	82
573	A combined microscopic-molecular method for the diagnosis of strongylid infections in sheep. <i>International Journal for Parasitology</i> , 2009 , 39, 1277-87	4.3	82

572	Low cost whole-organism screening of compounds for anthelmintic activity. <i>International Journal for Parasitology</i> , 2015 , 45, 333-43	4.3	81
571	Phylogenomic and biogeographic reconstruction of the <i>Trichinella</i> complex. <i>Nature Communications</i> , 2016 , 7, 10513	17.4	81
570	Gene discovery for the carcinogenic human liver fluke, <i>Opisthorchis viverrini</i> . <i>BMC Genomics</i> , 2007 , 8, 189	4.5	81
569	Relationships among some ascaridoid nematodes based on ribosomal DNA sequence data. <i>Parasitology Research</i> , 2000 , 86, 738-44	2.4	79
568	Genetic blueprint of the zoonotic pathogen <i>Toxocara canis</i> . <i>Nature Communications</i> , 2015 , 6, 6145	17.4	77
567	Genome and transcriptome of the porcine whipworm <i>Trichuris suis</i> . <i>Nature Genetics</i> , 2014 , 46, 701-6	36.3	77
566	Phylogenetic relationships of Australian strongyloid nematodes inferred from ribosomal DNA sequence data. <i>International Journal for Parasitology</i> , 1997 , 27, 1481-94	4.3	77
565	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	4.5	74
564	Single-strand conformation polymorphism-based analysis of mitochondrial cytochrome c oxidase subunit 1 reveals significant substructuring in hookworm populations. <i>Electrophoresis</i> , 2002 , 23, 27-34	3.6	74
563	Drug resistance in <i>Giardia duodenalis</i> . <i>Biotechnology Advances</i> , 2015 , 33, 888-901	17.8	73
562	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	17.8	72
561	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	17.8	71
560	Tick-borne diseases of bovines in Pakistan: major scope for future research and improved control. <i>Parasites and Vectors</i> , 2015 , 8, 283	4	70
559	A portrait of the transcriptome of the neglected trematode, <i>Fasciola gigantica</i> --biological and biotechnological implications. <i>PLoS Neglected Tropical Diseases</i> , 2011 , 5, e1004	4.8	70
558	<i>Toxocara</i> eggs in public places worldwide - A systematic review and meta-analysis. <i>Environmental Pollution</i> , 2018 , 242, 1467-1475	9.3	68
557	Foodborne anisakiasis and allergy. <i>Molecular and Cellular Probes</i> , 2014 , 28, 167-74	3.3	67
556	Single-strand conformation polymorphism (SSCP)-based mutation scanning approaches to fingerprint sequence variation in ribosomal DNA of ascaridoid nematodes. <i>Electrophoresis</i> , 1998 , 19, 1366-73	3.6	67
555	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, 361-6	2.4	67

554	Massively parallel sequencing and analysis of the <i>Necator americanus</i> transcriptome. <i>PLoS Neglected Tropical Diseases</i> , 2010 , 4, e684	4.8	66
553	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	4.8	66
552	A mutation scanning approach for the identification of hookworm species and analysis of population variation. <i>Molecular and Biochemical Parasitology</i> , 1998 , 92, 303-12	1.9	65
551	Prospects for exploring molecular developmental processes in <i>Haemonchus contortus</i> . <i>International Journal for Parasitology</i> , 2006 , 36, 859-68	4.3	65
550	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	4	64
549	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, 633-43	4.3	64
548	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, 4317-26	3.6	64
547	Gene content evolution in the arthropods. <i>Genome Biology</i> , 2020 , 21, 15	18.3	63
546	<i>Giardia</i> /giardiasis - a perspective on diagnostic and analytical tools. <i>Biotechnology Advances</i> , 2014 , 32, 280-9	17.8	62
545	Drug target prediction and prioritization: using orthology to predict essentiality in parasite genomes. <i>BMC Genomics</i> , 2010 , 11, 222	4.5	62
544	A practical, bioinformatic workflow system for large data sets generated by next-generation sequencing. <i>Nucleic Acids Research</i> , 2010 , 38, e171	20.1	60
543	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, 2648-55	3.6	60
542	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, 2252-62	9.7	60
541	Genetic markers in ribosomal DNA for hookworm identification. <i>Acta Tropica</i> , 1996 , 62, 15-21	3.2	60
540	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, 1726-40	12.5	56
539	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	4.5	56
538	ESTExplorer: an expressed sequence tag (EST) assembly and annotation platform. <i>Nucleic Acids Research</i> , 2007 , 35, W143-7	20.1	56
537	High resolution melting-curve (HRM) analysis for the diagnosis of cryptosporidiosis in humans. <i>Molecular and Cellular Probes</i> , 2009 , 23, 10-5	3.3	55

536	Global phylogeography and genetic diversity of the zoonotic tapeworm <i>Echinococcus granulosus</i> sensu stricto genotype G1. <i>International Journal for Parasitology</i> , 2018 , 48, 729-742	4.3	54
535	Sequence differences in the internal transcribed spacers of DNA among four species of hookworm (Ancylostomatoidea: Ancylostoma). <i>International Journal for Parasitology</i> , 1999 , 29, 1971-7	4.3	53
534	Omega-1 knockdown in <i>Schistosoma mansoni</i> eggs by lentivirus transduction reduces granuloma size in vivo. <i>Nature Communications</i> , 2014 , 5, 5375	17.4	52
533	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, 529-38 ²⁻⁴	2.4	52
532	Identification of parasitic nematodes by PCR-SSCP of ITS-2 rDNA. <i>Molecular and Cellular Probes</i> , 1997 , 11, 201-9	3.3	52
531	Lack of intraspecific variation in the second internal transcribed spacer (ITS-2) of <i>Trichostrongylus colubriformis</i> ribosomal DNA. <i>International Journal for Parasitology</i> , 1993 , 23, 1069-71	4.3	52
530	<i>Lucilia cuprina</i> genome unlocks parasitic fly biology to underpin future interventions. <i>Nature Communications</i> , 2015 , 6, 7344	17.4	51
529	Species identification of trichostrongyle nematodes by PCR-linked RFLP. <i>International Journal for Parasitology</i> , 1994 , 24, 291-3	4.3	51
528	First transcriptomic analysis of the economically important parasitic nematode, <i>Trichostrongylus colubriformis</i> , using a next-generation sequencing approach. <i>Infection, Genetics and Evolution</i> , 2010 , 10, 1199-207	4.5	50
527	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, 157-69	4.3	50
526	Fingerprinting sequence variation in ribosomal DNA of parasites by DGGE. <i>Molecular and Cellular Probes</i> , 1996 , 10, 99-105	3.3	50
525	Oriental theileriosis in dairy cows causes a significant milk production loss. <i>Parasites and Vectors</i> , 2014 , 7, 73	4	49
524	Toward next-generation sequencing of mitochondrial genomes--focus on parasitic worms of animals and biotechnological implications. <i>Biotechnology Advances</i> , 2010 , 28, 151-9	17.8	49
523	Molecular evidence for cryptic species within <i>Cylicostephanus minutus</i> (Nematoda: Strongylidae). <i>International Journal for Parasitology</i> , 1999 , 29, 285-91	4.3	49
522	Seroprevalence estimates for toxocariasis in people worldwide: A systematic review and meta-analysis. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007809	4.8	49
521	Infection with the carcinogenic human liver fluke, <i>Opisthorchis viverrini</i> . <i>Molecular BioSystems</i> , 2011 , 7, 1367-75		48
520	Redescription and genetic characterization of selected <i>Contraecaecum</i> spp. (Nematoda: Anisakidae) from various hosts in Australia. <i>Parasitology Research</i> , 2009 , 104, 1507-25	2.4	48
519	Analysis of sequence homogenisation in rDNA arrays of <i>Haemonchus contortus</i> by denaturing gradient gel electrophoresis. <i>Electrophoresis</i> , 1998 , 19, 2391-5	3.6	48

518	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, 554-7	2.4	48
517	Screening of the Pathogen Box identifies an approved pesticide with major anthelmintic activity against the barber pole worm. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2016 , 6, 329-334	4	48
516	Acute <i>Toxoplasma</i> infection in pregnant women worldwide: A systematic review and meta-analysis. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007807	4.8	47
515	Description and genetic characterisation of <i>Hysterothylacium</i> (Nematoda: Raphidascarididae) larvae parasitic in Australian marine fishes. <i>Parasitology International</i> , 2013 , 62, 320-8	2.1	47
514	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, 386-90	3.3	47
513	Evolutionary relationships of trichostrongyloid nematodes (Strongylida) inferred from ribosomal DNA sequence data. <i>Molecular Phylogenetics and Evolution</i> , 2001 , 19, 367-86	4.1	47
512	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	4.8	46
511	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, 453-60	2.7	46
510	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, 955-63	4.3	46
509	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, 2308-15	3.6	46
508	Epidemiological survey following oriental theileriosis outbreaks in Victoria, Australia, on selected cattle farms. <i>Veterinary Parasitology</i> , 2013 , 197, 509-21	2.8	45
507	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). <i>International Journal for Parasitology</i> , 2010 , 40, 405-15	4.3	45
506	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, 33-9	3.3	45
505	PCR assay for the specific amplification of <i>Oesophagostomum bifurcum</i> DNA from human faeces. <i>International Journal for Parasitology</i> , 2000 , 30, 137-42	4.3	45
504	Human toxocariasis - A look at a neglected disease through an epidemiological prism. <i>Infection, Genetics and Evolution</i> , 2019 , 74, 104002	4.5	44
503	Advances in the diagnosis of key gastrointestinal nematode infections of livestock, with an emphasis on small ruminants. <i>Biotechnology Advances</i> , 2013 , 31, 1135-52	17.8	44
502	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	3.3	44
501	Bovine theileriosis—an emerging problem in south-eastern Australia?. <i>Infection, Genetics and Evolution</i> , 2011 , 11, 2095-7	4.5	44

500	Soil-transmitted helminths of humans in Southeast Asia--towards integrated control. <i>Advances in Parasitology</i> , 2011 , 74, 231-65	3.2	44
499	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, 43-9	1	44
498	Differences in transcription between free-living and CO ₂ -activated third-stage larvae of <i>Haemonchus contortus</i> . <i>BMC Genomics</i> , 2010 , 11, 266	4.5	44
497	A practical and cost-effective mutation scanning-based approach for investigating genetic variation in <i>Cryptosporidium</i> . <i>Electrophoresis</i> , 2007 , 28, 3875-83	3.6	44
496	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, 574-80	2.3	44
495	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, 1984-93	4.5	43
494	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, 313-25	4.3	43
493	Exploration of extracellular vesicles from provides evidence of parasite-host cross talk. <i>Journal of Extracellular Vesicles</i> , 2019 , 8, 1578116	16.4	42
492	SchistoDB: an updated genome resource for the three key schistosomes of humans. <i>Nucleic Acids Research</i> , 2013 , 41, D728-31	20.1	41
491	Genetic characterization of selected parasites from people with histories of gastrointestinal disorders using a mutation scanning-coupled approach. <i>Electrophoresis</i> , 2013 , 34, 1720-8	3.6	41
490	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, 346-51	3.3	41
489	Evaluation and application of a molecular method to assess the composition of strongylid nematode populations in sheep with naturally acquired infections. <i>Infection, Genetics and Evolution</i> , 2011 , 11, 849-54	4.5	41
488	First genetic classification of <i>Cryptosporidium</i> and <i>Giardia</i> from HIV/AIDS patients in Malaysia. <i>Infection, Genetics and Evolution</i> , 2011 , 11, 968-74	4.5	41
487	A molecular diagnostic tool to replace larval culture in conventional faecal egg count reduction testing in sheep. <i>PLoS ONE</i> , 2012 , 7, e37327	3.7	41
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485	<i>Cryptosporidium cuniculus</i> --new records in human and kangaroo in Australia. <i>Parasites and Vectors</i> , 2014 , 7, 492	4	40
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203	Identification of Fromiamycalin and Halaminol A from Australian Marine Sponge Extracts with Anthelmintic Activity against. <i>Marine Drugs</i> , 2019 , 17,	6	10
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