Aaron R Jex

List of Publications by Citations

156 papers	5,416 citations	41 h-index	66 g-index
165 ext. papers	6,191 ext. citations	7 avg, IF	5.48 L-index

#	Paper	IF	Citations
156	Whole-genome sequence of Schistosoma haematobium. *Nature Genetics*, **2012**, 44, 221-5	36.3	325
155	Ascaris suum draft genome. *Nature*, **2011**, 479, 529-33	50.4	217
154	Single-strand conformation polymorphism (SSCP) for the analysis of genetic variation. *Nature Protocols*, **2006**, 1, 3121-8	18.8	210
153	The genome and developmental transcriptome of the strongylid nematode Haemonchus contortus. *Genome Biology*, **2013**, 14, R89	18.3	166
152	Impact of gastrointestinal parasitic nematodes of sheep, and the role of advanced molecular tools for exploring epidemiology and drug resistance - an Australian perspective. *Parasites and Vectors*, **2013**, 6, 153	4	164
151	Recent advances in candidate-gene and whole-genome approaches to the discovery of anthelmintic resistance markers and the description of drug/receptor interactions. *International Journal for Parasitology: Drugs and Drug Resistance*, **2014**, 4, 164-84	4	125
150	Unlocking the transcriptomes of two carcinogenic parasites, Clonorchis sinensis and Opisthorchis viverrini. *PLoS Neglected Tropical Diseases*, **2010**, 4, e719	4.8	122
149	The Opisthorchis viverrini genome provides insights into life in the bile duct. *Nature Communications*, **2014**, 5, 4378	17.4	113
148	An integrated pipeline for next-generation sequencing and annotation of mitochondrial genomes. *Nucleic Acids Research*, **2010**, 38, 522-33	20.1	112
147	Elucidating the transcriptome of Fasciola hepatica - a key to fundamental and biotechnological discoveries for a neglected parasite. *Biotechnology Advances*, **2010**, 28, 222-31	17.8	102
146	Cryptosporidium--biotechnological advances in the detection, diagnosis and analysis of genetic variation. *Biotechnology Advances*, **2008**, 26, 304-17	17.8	91
145	Long PCR amplification of the entire mitochondrial genome from individual helminths for direct sequencing. *Nature Protocols*, **2007**, 2, 2339-44	18.8	86
144	Low cost whole-organism screening of compounds for anthelmintic activity. *International Journal for Parasitology*, **2015**, 45, 333-43	4.3	81
143	Phylogenomic and biogeographic reconstruction of the Trichinella complex. *Nature Communications*, **2016**, 7, 10513	17.4	81
142	Genetic blueprint of the zoonotic pathogen Toxocara canis. *Nature Communications*, **2015**, 6, 6145	17.4	77
141	Genome and transcriptome of the porcine whipworm Trichuris suis. *Nature Genetics*, **2014**, 46, 701-6	36.3	77
140	Using 454 technology for long-PCR based sequencing of the complete mitochondrial genome from single Haemonchus contortus (Nematoda). *BMC Genomics*, **2008**, 9, 11	4.5	74

139	Drug resistance in Giardia duodenalis. *Biotechnology Advances*, **2015**, 33, 888-901	17.8	73
138	Genetic richness and diversity in Cryptosporidium hominis and C. parvum reveals major knowledge gaps and a need for the application of "next generation" technologies--research review. *Biotechnology Advances*, **2010**, 28, 17-26	17.8	72
137	A portrait of the transcriptome of the neglected trematode, Fasciola gigantica--biological and biotechnological implications. *PLoS Neglected Tropical Diseases*, **2011**, 5, e1004	4.8	70
136	Massively parallel sequencing and analysis of the Necator americanus transcriptome. *PLoS Neglected Tropical Diseases*, **2010**, 4, e684	4.8	66
135	Giardia/giardiasis - a perspective on diagnostic and analytical tools. *Biotechnology Advances*, **2014**, 32, 280-9	17.8	62
134	A practical, bioinformatic workflow system for large data sets generated by next-generation sequencing. *Nucleic Acids Research*, **2010**, 38, e171	20.1	60
133	Genetic categorization of Echinococcus granulosus from humans and herbivorous hosts in Iran using an integrated mutation scanning-phylogenetic approach. *Electrophoresis*, **2009**, 30, 2648-55	3.6	60
132	Classification of Cryptosporidium species from patients with sporadic cryptosporidiosis by use of sequence-based multilocus analysis following mutation scanning. *Journal of Clinical Microbiology*, **2008**, 46, 2252-62	9.7	60
131	Comparative genomics of Cylindrospermopsis raciborskii strains with differential toxicities. *BMC Genomics*, **2014**, 15, 83	4.5	56
130	Molecular-based investigation of Cryptosporidium and Giardia from animals in water catchments in southeastern Australia. *Water Research*, **2013**, 47, 1726-40	12.5	56
129	The mitochondrial genomes of Ancylostoma caninum and Bunostomum phlebotomum--two hookworms of animal health and zoonotic importance. *BMC Genomics*, **2009**, 10, 79	4.5	56
128	High resolution melting-curve (HRM) analysis for the diagnosis of cryptosporidiosis in humans. *Molecular and Cellular Probes*, **2009**, 23, 10-5	3.3	55
127	Lucilia cuprina genome unlocks parasitic fly biology to underpin future interventions. *Nature Communications*, **2015**, 6, 7344	17.4	51
126	First transcriptomic analysis of the economically important parasitic nematode, Trichostrongylus colubriformis, using a next-generation sequencing approach. *Infection, Genetics and Evolution*, **2010**, 10, 1199-207	4.5	50
125	Toward next-generation sequencing of mitochondrial genomes--focus on parasitic worms of animals and biotechnological implications. *Biotechnology Advances*, **2010**, 28, 151-9	17.8	49
124	Proteogenomic analysis of the total and surface-exposed proteomes of Plasmodium vivax salivary gland sporozoites. *PLoS Neglected Tropical Diseases*, **2017**, 11, e0005791	4.8	48
123	Proteomic analysis of the excretory-secretory products from larval stages of Ascaris suum reveals high abundance of glycosyl hydrolases. *PLoS Neglected Tropical Diseases*, **2013**, 7, e2467	4.8	46
122	Advances in the diagnosis of key gastrointestinal nematode infections of livestock, with an emphasis on small ruminants. *Biotechnology Advances*, **2013**, 31, 1135-52	17.8	44

121	A first insight into the genotypes of Echinococcus granulosus from humans in Mongolia. *Molecular and Cellular Probes*, **2011**, 25, 49-54	3.3	44
120	Soil-transmitted helminths of humans in Southeast Asia--towards integrated control. *Advances in Parasitology*, **2011**, 74, 231-65	3.2	44
119	Differences in transcription between free-living and CO2-activated third-stage larvae of Haemonchus contortus. *BMC Genomics*, **2010**, 11, 266	4.5	44
118	A practical and cost-effective mutation scanning-based approach for investigating genetic variation in Cryptosporidium. *Electrophoresis*, **2007**, 28, 3875-83	3.6	44
117	Genetic characterisation of Cryptosporidium and Giardia from dairy calves: discovery of species/genotypes consistent with those found in humans. *Infection, Genetics and Evolution*, **2012**, 12, 1984-93	4.5	43
116	Exploration of extracellular vesicles from provides evidence of parasite-host cross talk. *Journal of Extracellular Vesicles*, **2019**, 8, 1578116	16.4	42
115	Genetic characterization of selected parasites from people with histories of gastrointestinal disorders using a mutation scanning-coupled approach. *Electrophoresis*, **2013**, 34, 1720-8	3.6	41
114	Genetic classification of Echinococcus granulosus cysts from humans, cattle and camels in Libya using mutation scanning-based analysis of mitochondrial loci. *Molecular and Cellular Probes*, **2010**, 24, 346-51	3.3	41
113	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, 849-54	4.5	41
112	First genetic classification of Cryptosporidium and Giardia from HIV/AIDS patients in Malaysia. *Infection, Genetics and Evolution*, **2011**, 11, 968-74	4.5	41
111	A molecular diagnostic tool to replace larval culture in conventional faecal egg count reduction testing in sheep. *PLoS ONE*, **2012**, 7, e37327	3.7	41
110	A perspective on Cryptosporidium and Giardia, with an emphasis on bovines and recent epidemiological findings. *Advances in Parasitology*, **2015**, 88, 243-301	3.2	40
109	The transcriptome of Trichuris suis--first molecular insights into a parasite with curative properties for key immune diseases of humans. *PLoS ONE*, **2011**, 6, e23590	3.7	40
108	Cryptosporidium and Giardia taxa in faecal samples from animals in catchments supplying the city of Melbourne with drinking water (2011 to 2015). *Parasites and Vectors*, **2016**, 9, 315	4	39
107	Molecular detection of Cryptosporidium cuniculus in rabbits in Australia. *Infection, Genetics and Evolution*, **2010**, 10, 1179-87	4.5	36
106	Analysis of nucleotide variation within the triose-phosphate isomerase gene of Giardia duodenalis from sheep and its zoonotic implications. *Electrophoresis*, **2010**, 31, 287-98	3.6	35
105	Mitochondrial genomes of Trichinella species and genotypes basis for diagnosis, and systematic and epidemiological explorations. *International Journal for Parasitology*, **2014**, 44, 1073-80	4.3	34
104	Establishment of a robotic, high-throughput platform for the specific diagnosis of gastrointestinal nematode infections in sheep. *International Journal for Parasitology*, **2012**, 42, 1151-8	4.3	34

103	The mitochondrial genome of Toxocara canis. *PLoS Neglected Tropical Diseases*, **2008**, 2, e273	4.8	34
102	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	4	32
101	Defining the Schistosoma haematobium kinome enables the prediction of essential kinases as anti-schistosome drug targets. *Scientific Reports*, **2015**, 5, 17759	4.9	32
100	Next-generation molecular-diagnostic tools for gastrointestinal nematodes of livestock, with an emphasis on small ruminants: a turning point?. *Advances in Parasitology*, **2013**, 83, 267-333	3.2	32
99	Characterization of the Ca2+-gated and voltage-dependent K+-channel Slo-1 of nematodes and its interaction with emodepside. *PLoS Neglected Tropical Diseases*, **2014**, 8, e3401	4.8	31
98	Mitochondrial genome of Angiostrongylus vasorum: comparison with congeners and implications for studying the population genetics and epidemiology of this parasite. *Infection, Genetics and Evolution*, **2012**, 12, 1884-91	4.5	31
97	Differential protein expression and post-translational modifications in metronidazole-resistant Giardia duodenalis. *GigaScience*, **2018**, 7,	7.6	29
96	First molecular characterization of Cryptosporidium and Giardia from bovines (Bos taurus and Bubalus bubalis) in Sri Lanka: unexpected absence of C. parvum from pre-weaned calves. *Parasites and Vectors*, **2014**, 7, 75	4	29
95	Assessment of the genetic relationship between Dictyocaulus species from Bos taurus and Cervus elaphus using complete mitochondrial genomic datasets. *Parasites and Vectors*, **2012**, 5, 241	4	29
94	Analysis of the genetic diversity within Cryptosporidium hominis and Cryptosporidium parvum from imported and autochtonous cases of human cryptosporidiosis by mutation scanning. *Electrophoresis*, **2008**, 29, 4119-29	3.6	29
93	Extracellular vesicles from early stage Plasmodium falciparum-infected red blood cells contain PfEMP1 and induce transcriptional changes in human monocytes. *Cellular Microbiology*, **2018**, 20, e12822	3.9	28
92	Specific and genotypic identification of Cryptosporidium from a broad range of host species by nonisotopic SSCP analysis of nuclear ribosomal DNA. *Electrophoresis*, **2007**, 28, 2818-25	3.6	28
91	Deep insights into Dictyocaulus viviparus transcriptomes provides unique prospects for new drug targets and disease intervention. *Biotechnology Advances*, **2011**, 29, 261-71	17.8	27
90	A self-sufficient pressure pump using latex balloons for microfluidic applications. *Lab on A Chip*, **2018**, 18, 2730-2740	7.2	26
89	Transcriptomics Indicates Active and Passive Metronidazole Resistance Mechanisms in Three Seminal Lines. *Frontiers in Microbiology*, **2017**, 8, 398	5.7	26
88	Techniques for the diagnosis of Fasciola infections in animals: room for improvement. *Advances in Parasitology*, **2014**, 85, 65-107	3.2	25
87	Detection of diarrhoeal pathogens in human faeces using an automated, robotic platform. *Molecular and Cellular Probes*, **2012**, 26, 11-5	3.3	25
86	Genome variation in nine co-occurring toxic Cylindrospermopsis raciborskii strains. *Harmful Algae*, **2018**, 73, 157-166	5.3	24

85	Responses of the Differentiated Intestinal Epithelial Cell Line Caco-2 to Infection With the GS Isolate. *Frontiers in Cellular and Infection Microbiology*, **2018**, 8, 244	5.9	24
84	First molecular characterization of Giardia duodenalis from goats in Malaysia. *Molecular and Cellular Probes*, **2013**, 27, 28-31	3.3	24
83	Time-Course Study of the Transcriptome of Peripheral Blood Mononuclear Cells (PBMCs) from Sheep Infected with Fasciola hepatica. *PLoS ONE*, **2016**, 11, e0159194	3.7	24
82	Transcriptome and histone epigenome of Plasmodium vivax salivary-gland sporozoites point to tight regulatory control and mechanisms for liver-stage differentiation in relapsing malaria. *International Journal for Parasitology*, **2019**, 49, 501-513	4.3	23
81	First molecular characterisation of Cryptosporidium and Giardia from Bubalus bubalis (water buffalo) in Victoria, Australia. *Infection, Genetics and Evolution*, **2013**, 20, 96-102	4.5	23
80	The mitochondrial genome of Parascaris univalens--implications for a "forgotten" parasite. *Parasites and Vectors*, **2014**, 7, 428	4	23
79	Genetic characterization of Cryptosporidium parvum from calves by mutation scanning and targeted sequencing--zoonotic implications. *Electrophoresis*, **2009**, 30, 2640-7	3.6	23
78	Genetic analysis of Giardia and Cryptosporidium from people in Northern Australia using PCR-based tools. *Infection, Genetics and Evolution*, **2015**, 36, 389-395	4.5	22
77	Self-sufficient, low-cost microfluidic pumps utilising reinforced balloons. *Lab on A Chip*, **2019**, 19, 2885-2896	7.2	22
76	Getting the most out of parasitic helminth transcriptomes using HelmDB: implications for biology and biotechnology. *Biotechnology Advances*, **2013**, 31, 1109-19	17.8	22
75	Progress on the transcriptomics of carcinogenic liver flukes of humans--unique biological and biotechnological prospects. *Biotechnology Advances*, **2010**, 28, 859-70	17.8	22
74	First genetic analysis of Cryptosporidium from humans from Tasmania, and identification of a new genotype from a traveller to Bali. *Electrophoresis*, **2014**, 35, 2600-7	3.6	21
73	The Thelastomatoidea (Nematoda: Oxyurida) of two sympatric Panesthiinae (Insecta: Blattodea) from southeastern Queensland, Australia: taxonomy, species richness and host specificity. *Nematology*, **2005**, 7, 543-575	0.9	21
72	Profiling circulating miRNAs in serum from pigs infected with the porcine whipworm, Trichuris suis. *Veterinary Parasitology*, **2016**, 223, 30-3	2.8	21
71	Mitochondrial genomes of Anisakis simplex and Contracaecum osculatum (sensu stricto)--comparisons with selected nematodes. *Infection, Genetics and Evolution*, **2014**, 21, 452-62	4.5	20
70	Rapid, multiplex-tandem PCR assay for automated detection and differentiation of toxigenic cyanobacterial blooms. *Molecular and Cellular Probes*, **2013**, 27, 208-14	3.3	20
69	Exploring molecular variation in Schistosoma japonicum in China. *Scientific Reports*, **2015**, 5, 17345	4.9	19
68	Assessing calves as carriers of Cryptosporidium and Giardia with zoonotic potential on dairy and beef farms within a water catchment area by mutation scanning. *Electrophoresis*, **2013**, 34, 2259-67	3.6	18

67	Cryptic parasite revealed improved prospects for treatment and control of human cryptosporidiosis through advanced technologies. *Advances in Parasitology*, **2011**, 77, 141-73	3.2	18
66	Molecular changes in Opisthorchis viverrini (Southeast Asian liver fluke) during the transition from the juvenile to the adult stage. *PLoS Neglected Tropical Diseases*, **2012**, 6, e1916	4.8	18
65	Genetic variation within the Hypodontus macropi (Nematoda: Strongyloidea) complex from macropodid marsupial hosts in Australia. *Electrophoresis*, **2012**, 33, 3544-54	3.6	17
64	Insights into the immuno-molecular biology of Angiostrongylus vasorum through transcriptomics--prospects for new interventions. *Biotechnology Advances*, **2013**, 31, 1486-500	17.8	16
63	Molecular evidence for a cryptic species within the parasitic nematode Macroponema comani (Strongyloidea: Cloacininae). *Molecular and Cellular Probes*, **2012**, 26, 170-4	3.3	16
62	Highly sensitive non-isotopic restriction endonuclease fingerprinting of nucleotide variability in the gp60 gene within Cryptosporidium species, genotypes and subgenotypes infective to humans, and its implications. *Electrophoresis*, **2010**, 31, 1637-47	3.6	16
61	Development and validation of a multiplexed-tandem qPCR tool for diagnostics of human soil-transmitted helminth infections. *PLoS Neglected Tropical Diseases*, **2019**, 13, e0007363	4.8	15
60	An improved method for PCR-based detection and routine monitoring of geosmin-producing cyanobacterial blooms. *Water Research*, **2018**, 136, 34-40	12.5	15
59	Mutation scanning-based analysis of anisakid larvae from Sillago flindersi from Bass Strait, Australia. *Electrophoresis*, **2012**, 33, 499-505	3.6	15
58	Analyses of mitochondrial amino acid sequence datasets support the proposal that specimens of Hypodontus macropi from three species of macropodid hosts represent distinct species. *BMC Evolutionary Biology*, **2013**, 13, 259	3	15
57	Transcriptomic Resources for Parasitic Nematodes of Veterinary Importance. *Trends in Parasitology*, **2019**, 35, 72-84	6.4	15
56	Barcoding of Giardia duodenalis isolates and derived lines from an established cryobank by a mutation scanning-based approach. *Electrophoresis*, **2011**, 32, 2075-90	3.6	14
55	Zoonotic Ancylostomiasis: An Update of a Continually Neglected Zoonosis. *American Journal of Tropical Medicine and Hygiene*, **2020**, 103, 64-68	3.2	14
54	Comparative evaluation of two DNA isolation techniques for PCR-based diagnosis of gastrointestinal nematode infections in sheep. *Molecular and Cellular Probes*, **2013**, 27, 153-7	3.3	13
53	The mitochondrial genome of Aelurostrongylus abstrusus-diagnostic, epidemiological and systematic implications. *Gene*, **2013**, 516, 294-300	3.8	13
52	The mitochondrial genome of Protostrongylus rufescens - implications for population and systematic studies. *Parasites and Vectors*, **2013**, 6, 263	4	13
51	Cryptosporidiosis in Southeast Asia. *Advances in Parasitology*, **2010**, 1-31	3.2	13
50	Divergent Transcriptional Responses to Physiological and Xenobiotic Stress in Giardia duodenalis. *Antimicrobial Agents and Chemotherapy*, **2016**, 60, 6034-45	5.9	13

49	Annotation of the Giardia proteome through structure-based homology and machine learning. *GigaScience*, **2019**, 8,	7.6	13
48	The barberR pole worm CAP protein superfamily--A basis for fundamental discovery and biotechnology advances. *Biotechnology Advances*, **2015**, 33, 1744-54	17.8	12
47	Monoaminergic signaling as a target for anthelmintic drug discovery: receptor conservation among the free-living and parasitic nematodes. *Molecular and Biochemical Parasitology*, **2012**, 183, 1-7	1.9	12
46	Time-Dependent Transcriptional Changes in Axenic Giardia duodenalis Trophozoites. *PLoS Neglected Tropical Diseases*, **2015**, 9, e0004261	4.8	12
45	Recent advances in the genomic and molecular biology of Giardia. *Acta Tropica*, **2018**, 184, 67-72	3.2	11
44	The small RNA complement of adult Schistosoma haematobium. *PLoS Neglected Tropical Diseases*, **2018**, 12, e0006535	4.8	10
43	First report of anatoxin-a producing cyanobacteria in Australia illustrates need to regularly up-date monitoring strategies in a shifting global distribution. *Scientific Reports*, **2019**, 9, 10894	4.9	10
42	Bioinformatic exploration of RIO protein kinases of parasitic and free-living nematodes. *International Journal for Parasitology*, **2014**, 44, 827-36	4.3	10
41	The importance of host ecology in thelastomatoid (Nematoda: Oxyurida) host specificity. *Parasitology International*, **2006**, 55, 169-74	2.1	10
40	Proteomic diversity in a prevalent human-infective Giardia duodenalis sub-species. *International Journal for Parasitology*, **2018**, 48, 817-823	4.3	9
39	Diagnostic and analytical mutation scanning of Cryptosporidium: utility and advantages. *Expert Review of Molecular Diagnostics*, **2009**, 9, 179-85	3.8	9
38	Use of multiplexed tandem PCR to estimate the prevalence and intensity of Theileria orientalis infections in cattle. *Infection, Genetics and Evolution*, **2015**, 32, 68-73	4.5	8
37	Getting to the guts of the matter: the status and potential of RomicsR research of parasitic protists of the human gastrointestinal system. *International Journal for Parasitology*, **2013**, 43, 971-82	4.3	8
36	Analysis of genetic variation in Globocephaloides populations from macropodid marsupials using a mutation scanning-based approach. *Electrophoresis*, **2009**, 30, 2758-64	3.6	8
35	Direct Nanopore Sequencing of mRNA Reveals Landscape of Transcript Isoforms in Apicomplexan Parasites. *MSystems*, **2021**, 6,	7.6	8
34	Mutation scanning-coupled tools for the analysis of genetic variation in Taenia and diagnosis - status and prospects. *Infection, Genetics and Evolution*, **2009**, 9, 740-7	4.5	7
33	A real-time PCR assay for the diagnosis of gastrointestinal nematode infections of small ruminants. *Methods in Molecular Biology*, **2015**, 1247, 145-52	1.4	6
32	Flatworms have lost the right open reading frame kinase 3 gene during evolution. *Scientific Reports*, **2015**, 5, 9417	4.9	6

31	Is Cryptosporidium from the common wombat (Vombatus ursinus) a new species and distinct from Cryptosporidium ubiquitum?. *Infection, Genetics and Evolution*, **2016**, 44, 28-33	4.5	5
30	Thelastomatoidea (Nematoda: Oxyurida) of the Australian giant burrowing cockroach, Macropanesthia rhinoceros (Blaberidae: Geoscapheinae). *Nematology*, **2006**, 8, 347-357	0.9	5
29	Aoruroides queenslandensis n. sp. (Oxyurida: Thelastomatoidea), a new nematode from Australian Panesthiinae (Blattodea: Blaberidae). *Systematic Parasitology*, **2004**, 59, 65-9	1	5
28	Sequencing and annotation of mitochondrial genomes from individual parasitic helminths. *Methods in Molecular Biology*, **2015**, 1201, 51-63	1.4	5
27	Recent advances in functional research in Giardia intestinalis. *Advances in Parasitology*, **2020**, 107, 97-137	3.2	4
26	Asynchronous generation of oil droplets using a microfluidic flow focusing system. *Scientific Reports*, **2019**, 9, 10600	4.9	4
25	Analysis of the transcriptome of adult Dictyocaulus filaria and comparison with Dictyocaulus viviparus, with a focus on molecules involved in host-parasite interactions. *International Journal for Parasitology*, **2014**, 44, 251-61	4.3	4
24	New Thelastomatoidea (Nematoda: Oxyurida) from Australian burrowing cockroaches (Blaberidae: Geoscapheinae, Panesthiinae). *Nematology*, **2006**, 8, 443-454	0.9	4
23	Tunable Harmonic Flow Patterns in Microfluidic Systems through Simple Tube Oscillation. *Small*, **2020**, 16, e2003612	11	4
22	Eukaryote-Conserved Methylarginine Is Absent in Diplomonads and Functionally Compensated in Giardia. *Molecular Biology and Evolution*, **2020**, 37, 3525-3549	8.3	4
21	Comparative genomics revealed adaptive admixture in in Africa. *Microbial Genomics*, **2021**, 7,	4.4	4
20	New species of Cloacina von Linstow, 1898 (Nematoda: Strongyloidea) parasitic in the stomachs of wallaroos, Osphranter spp. (Marsupialia: Macropodidae) from northern Australia. *Systematic Parasitology*, **2018**, 95, 527-542	1	4
19	A theoretical study to establish the relationship between the three-dimensional structure of triose-phosphate isomerase of Giardia duodenalis and point mutations in the respective gene. *Molecular and Cellular Probes*, **2010**, 24, 281-5	3.3	3
18	Long-read assembly and comparative evidence-based reanalysis of genome sequences reveals expanded transporter repertoire and duplication of entire chromosome ends including subtelomeric regions. *Genome Research*, **2021**,	9.7	3
17	Cryptosporidiosis **2011**,		3
16	Eukaryote-conserved histone post-translational modification landscape in Giardia duodenalis revealed by mass spectrometry. *International Journal for Parasitology*, **2021**, 51, 225-239	4.3	3
15	Transcriptome and histone epigenome of Plasmodium vivax salivary-gland sporozoites point to tight regulatory control and potential mechanisms for liver-stage differentiation		2
14	Direct nanopore sequencing of mRNA reveals landscape of transcript isoforms in apicomplexan parasites		2

13	TriTOX: A novel Trichomonas vaginalis assay platform for high-throughput screening of compound libraries. *International Journal for Parasitology: Drugs and Drug Resistance*, **2021**, 15, 68-80	4	2
12	Long-read assembly and comparative evidence-based reanalysis of Cryptosporidium genome sequences reveal new biological insights		2
11	Effective low-cost preservation of human stools in field-based studies for helminth and microbiota analysis. *International Journal for Parasitology*, **2021**, 51, 741-748	4.3	2
10	Multimodal regulation of encystation in Giardia duodenalis revealed by deep proteomics. *International Journal for Parasitology*, **2021**, 51, 809-824	4.3	2
9	Single-cell RNA profiling of Plasmodium vivax liver stages reveals parasite- and host- specific transcriptomic signatures and drug targets		1
8	Single-cell RNA sequencing of Plasmodium vivax sporozoites reveals stage- and species-specific transcriptomic signatures		1
7	VIVID: a web application for variant interpretation and visualisation in multidimensional analyses		1
6	Cryptosporidium: Current State of Genomics and Systems Biological Research **2014**, 327-344		1
5	Field evaluation of the gut microbiome composition of pre-school and school-aged children in Tha Song Yang, Thailand, following oral MDA for STH infections. *PLoS Neglected Tropical Diseases*, **2021**, 15, e0009597	4.8	1
4	Recent Progress in Transcriptomics of Key Gastrointestinal Nematodes of Animals Fundamental Research Toward New Intervention Strategies61-72		1
3	Harnessing Genomic Technologies to Explore the Molecular Biology of Liver Flukes-Major Implications for Fundamental and Applied Research73-87		1
2	In vitro selection of Giardia duodenalis for Albendazole resistance identifies a tubulin mutation at amino acid E198K. *International Journal for Parasitology: Drugs and Drug Resistance*, **2021**, 16, 162-173	4	0
1	Decoding the Ascaris suum Genome using Massively Parallel Sequencing and Advanced Bioinformatic Methods Unprecedented Prospects for Fundamental and Applied Research **2013**, 287-314		