

# Ryo Nakao

## List of Publications by Year in descending order

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122  
papers

2,190  
citations

304368

22  
h-index

301761

39  
g-index

126  
all docs

126  
docs citations

126  
times ranked

2301  
citing authors

#	ARTICLE	IF	CITATIONS
1	Revisiting the taxonomy and evolution of pathogenicity of the genus <i>Leptospira</i> through the prism of genomics. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007270.	1.3	417
2	A novel approach, based on BLSOMs (Batch Learning Self-Organizing Maps), to the microbiome analysis of ticks. <i>ISME Journal</i> , 2013, 7, 1003-1015.	4.4	132
3	Microbial Population Analysis of the Salivary Glands of Ticks; A Possible Strategy for the Surveillance of Bacterial Pathogens. <i>PLoS ONE</i> , 2014, 9, e103961.	1.1	95
4	Development of Loop-Mediated Isothermal Amplification (LAMP) Assays for Rapid Detection of <i>Ehrlichia ruminantium</i> . <i>BMC Microbiology</i> , 2010, 10, 296.	1.3	61
5	Emergence of the invasive malaria vector <i>Anopheles stephensi</i> in Khartoum State, Central Sudan. <i>Parasites and Vectors</i> , 2021, 14, 511.	1.0	45
6	Molecular detection of zoonotic tick-borne pathogens from ticks collected from ruminants in four South African provinces. <i>Journal of Veterinary Medical Science</i> , 2015, 77, 1573-1579.	0.3	44
7	Diversity of spotted fever group rickettsiae and their association with host ticks in Japan. <i>Scientific Reports</i> , 2019, 9, 1500.	1.6	43
8	Phylogenies from mitochondrial genomes of 120 species of ticks: Insights into the evolution of the families of ticks and of the genus <i>Amblyomma</i> . <i>Ticks and Tick-borne Diseases</i> , 2021, 12, 101577.	1.1	38
9	Nuclear (18S-28S rRNA) and mitochondrial genome markers of <i>Carios (Carios) vespertilionis</i> (Argasidae) support <i>Carios</i> Latreille, 1796 as a lineage embedded in the <i>Ornithodorinae</i> : re-classification of the <i>Carios sensu</i> Klompen and Oliver (1993) clade into its respective subgenera. <i>Ticks and Tick-borne Diseases</i> , 2021, 12, 101688.	1.1	37
10	The Unique Phylogenetic Position of a Novel Tick-Borne Phlebovirus Ensures an Ixodid Origin of the Genus <i>Phlebovirus</i> . <i>MSphere</i> , 2018, 3, .	1.3	36
11	Human Borreliosis Caused by a New World Relapsing Fever <i>Borrelia</i> -like Organism in the Old World. <i>Clinical Infectious Diseases</i> , 2019, 69, 107-112.	2.9	36
12	High prevalence of spotted fever group rickettsiae in <i>Amblyomma variegatum</i> from Uganda and their identification using sizes of intergenic spacers. <i>Ticks and Tick-borne Diseases</i> , 2013, 4, 506-512.	1.1	34
13	Ciliate <i>Paramecium</i> is a natural reservoir of <i>Legionella pneumophila</i> . <i>Scientific Reports</i> , 2016, 6, 24322.	1.6	34
14	Molecular detection of <i>Rickettsia felis</i> in dogs, rodents and cat fleas in Zambia. <i>Parasites and Vectors</i> , 2019, 12, 168.	1.0	32
15	Population genetic analysis and sub-structuring of <i>Theileria parva</i> in the northern and eastern parts of Zambia. <i>Parasites and Vectors</i> , 2012, 5, 255.	1.0	30
16	Viral population analysis of the taiga tick, <i>Ixodes persulcatus</i> , by using Batch Learning Self-Organizing Maps and BLAST search. <i>Journal of Veterinary Medical Science</i> , 2019, 81, 401-410.	0.3	30
17	A novel nairovirus associated with acute febrile illness in Hokkaido, Japan. <i>Nature Communications</i> , 2021, 12, 5539.	5.8	30
18	Detection and characterization of zoonotic pathogens of free-ranging non-human primates from Zambia. <i>Parasites and Vectors</i> , 2014, 7, 490.	1.0	29

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19	Evidence of multiple point mutations in <i>Theileria annulata</i> cytochrome b gene incriminated in buparvaquone treatment failure. <i>Acta Tropica</i> , 2019, 191, 128-132.	0.9	28
20	Occurrence of <i>Coxiella burnetii</i> , <i>Ehrlichia canis</i> , <i>Rickettsia</i> species and <i>Anaplasma phagocytophilum</i> -like bacterium in ticks collected from dogs and cats in South Africa. <i>Journal of the South African Veterinary Association</i> , 2017, 88, e1-e6.	0.2	27
21	Studies of trypanosomiasis in the Luangwa valley, north-eastern Zambia. <i>Parasites and Vectors</i> , 2015, 8, 497.	1.0	25
22	Anthropogenic interferences lead to gut microbiome dysbiosis in Asian elephants and may alter adaptation processes to surrounding environments. <i>Scientific Reports</i> , 2021, 11, 741.	1.6	24
23	Horizontally Transferred Genetic Elements in the Tsetse Fly Genome: An Alignment-Free Clustering Approach Using Batch Learning Self-Organising Map (BLSOM). <i>BioMed Research International</i> , 2016, 2016, 1-8.	0.9	23
24	Putative RNA viral sequences detected in an <i>Ixodes scapularis</i> -derived cell line. <i>Ticks and Tick-borne Diseases</i> , 2017, 8, 103-111.	1.1	23
25	Tick-borne haemoparasites and Anaplasmataceae in domestic dogs in Zambia. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 988-995.	1.1	23
26	Molecular detection and characterization of zoonotic <i>Anaplasma</i> species in domestic dogs in Lusaka, Zambia. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 39-43.	1.1	22
27	Molecular and phenotypic characterization of <i>Leptospira johnsoni</i> sp. nov., <i>Leptospira ellinghauseni</i> sp. nov. and <i>Leptospira ryugeni</i> sp. nov. isolated from soil and water in Japan. <i>Microbiology and Immunology</i> , 2019, 63, 89-99.	0.7	22
28	Evaluation of Efficacy of Bruceine A, a Natural Quassinoid Compound Extracted from a Medicinal Plant, <i>Brucea javanica</i> , for Canine Babesiosis. <i>Journal of Veterinary Medical Science</i> , 2009, 71, 33-41.	0.3	21
29	Molecular survey of <i>Babesia</i> infections in cattle from different areas of Myanmar. <i>Ticks and Tick-borne Diseases</i> , 2016, 7, 204-207.	1.1	21
30	Seroprevalence of Filovirus Infection of <i>Rousettus aegyptiacus</i> Bats in Zambia. <i>Journal of Infectious Diseases</i> , 2018, 218, S312-S317.	1.9	21
31	Molecular detection and genetic diversity of <i>Babesia gibsoni</i> in dogs in Bangladesh. <i>Infection, Genetics and Evolution</i> , 2015, 31, 53-60.	1.0	20
32	Isolation of <i>Candidatus Bartonella rousetti</i> and Other Bat-associated Bartonellae from Bats and Their Flies in Zambia. <i>Pathogens</i> , 2020, 9, 469.	1.2	20
33	Screening of tick-borne pathogens in argasid ticks in Zambia: Expansion of the geographic distribution of <i>Rickettsia lusitaniae</i> and <i>Rickettsia hoogstraalii</i> and detection of putative novel <i>Anaplasma</i> species. <i>Ticks and Tick-borne Diseases</i> , 2021, 12, 101720.	1.1	20
34	Genetic diversity of <i>Leishmania donovani</i> /infantum complex in China through microsatellite analysis. <i>Infection, Genetics and Evolution</i> , 2014, 22, 112-119.	1.0	18
35	Multi-locus sequence typing of <i>Ehrlichia ruminantium</i> strains from geographically diverse origins and collected in <i>Amblyomma variegatum</i> from Uganda. <i>Parasites and Vectors</i> , 2011, 4, 137.	1.0	17
36	Detection and molecular identification of <i>Leucocytozoon</i> and <i>Plasmodium</i> species from village chickens in different areas of Myanmar. <i>Acta Tropica</i> , 2020, 212, 105719.	0.9	17

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37	Molecular Detection of <i>Rickettsia africae</i> in <i>Amblyomma variegatum</i> Collected from Sudan. Vector-Borne and Zoonotic Diseases, 2015, 15, 323-325.	0.6	16
38	Exploring Prokaryotic and Eukaryotic Microbiomes Helps in Detecting Tick-Borne Infectious Agents in the Blood of Camels. Pathogens, 2021, 10, 351.	1.2	16
39	An outbreak of bovine trypanosomiasis in the Blue Nile State, Sudan. Parasites and Vectors, 2011, 4, 74.	1.0	15
40	Geographic strain differentiation of <i>Schistosoma japonicum</i> in the Philippines using microsatellite markers. PLoS Neglected Tropical Diseases, 2017, 11, e0005749.	1.3	15
41	First molecular detection and genetic characterization of <i>Coxiella burnetii</i> in Zambian dogs and rodents. Parasites and Vectors, 2018, 11, 40.	1.0	15
42	Detection of <i>Borrelia burgdorferi</i> Sensu Lato and Relapsing Fever <i>Borrelia</i> in Feeding Ixodes Ticks and Rodents in Sarawak, Malaysia: New Geographical Records of <i>Borrelia yangtzensis</i> and <i>Borrelia miyamotoi</i> . Pathogens, 2020, 9, 846.	1.2	15
43	Molecular and Serological Evidence of <i>Leishmania</i> Infection in Stray Dogs from Visceral Leishmaniasis-Endemic Areas of Bangladesh. American Journal of Tropical Medicine and Hygiene, 2016, 95, 795-799.	0.6	14
44	Infection of newly identified phleboviruses in ticks and wild animals in Hokkaido, Japan indicating tick-borne life cycles. Ticks and Tick-borne Diseases, 2019, 10, 328-335.	1.1	14
45	Isolation of the Thogoto virus from a <i>Haemaphysalis longicornis</i> in Kyoto City, Japan. Journal of General Virology, 2015, 96, 2099-2103.	1.3	13
46	Molecular characterization and specific detection of <i>Anaplasma</i> species (AP-sd) in sika deer and its first detection in wild brown bears and rodents in Hokkaido, Japan. Infection, Genetics and Evolution, 2015, 36, 268-274.	1.0	13
47	Genetic homogeneity of goat malaria parasites in Asia and Africa suggests their expansion with domestic goat host. Scientific Reports, 2018, 8, 5827.	1.6	13
48	Comparison of Database Search Methods for the Detection of <i>Legionella pneumophila</i> in Water Samples Using Metagenomic Analysis. Frontiers in Microbiology, 2018, 9, 1272.	1.5	13
49	Development and validation of direct dry loop mediated isothermal amplification for diagnosis of <i>Trypanosoma evansi</i> . Veterinary Parasitology, 2018, 260, 53-57.	0.7	13
50	Comparing the gut microbiome along the gastrointestinal tract of three sympatric species of wild rodents. Scientific Reports, 2021, 11, 19929.	1.6	13
51	Dynamics, co-infections and characteristics of zoonotic tick-borne pathogens in Hokkaido small mammals, Japan. Ticks and Tick-borne Diseases, 2016, 7, 922-928.	1.1	12
52	Molecular characterization of <i>Fasciola</i> flukes obtained from wild sika deer and domestic cattle in Hokkaido, Japan. Parasitology International, 2017, 66, 519-521.	0.6	12
53	&lt;i>Listeria monocytogenes</i> serotype 4b strains replicate in monocytes/macrophages more than the other serotypes. Journal of Veterinary Medical Science, 2017, 79, 962-969.	0.3	12
54	First Genetic Detection of <i>Coxiella burnetii</i> in Zambian Livestock. American Journal of Tropical Medicine and Hygiene, 2013, 89, 518-519.	0.6	11

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55	Molecular evidence of spotted fever group rickettsiae and Anaplasmataceae from ticks and stray dogs in Bangladesh. <i>Parasitology Research</i> , 2016, 115, 949-955.	0.6	11
56	Isolation of <i>Rickettsia</i> , <i>Rickettsiella</i> , and <i>Spiroplasma</i> from Questing Ticks in Japan Using Arthropod Cells. <i>Vector-Borne and Zoonotic Diseases</i> , 2019, 19, 474-485.	0.6	11
57	Serologic and molecular evidence for circulation of Crimean-Congo hemorrhagic fever virus in ticks and cattle in Zambia. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009452.	1.3	11
58	Identification of genetic loci affecting the establishment and development of <i>Echinococcus multilocularis</i> larvae in mice. <i>International Journal for Parasitology</i> , 2011, 41, 1121-1128.	1.3	10
59	First molecular detection of <i>Theileria luwenshuni</i> from goats in Myanmar. <i>Parasitology Research</i> , 2018, 117, 3361-3364.	0.6	10
60	Potential role of dogs as sentinels and reservoirs for piroplasms infecting equine and cattle in Riyadh City, Saudi Arabia. <i>Acta Tropica</i> , 2019, 193, 78-83.	0.9	10
61	Mutations in the TaPIN1 peptidyl prolyl isomerase gene in <i>Theileria annulata</i> parasites isolated in Sudan. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2019, 11, 101-105.	1.4	10
62	Development of a Multiplex Loop-Mediated Isothermal Amplification (LAMP) Method for Simultaneous Detection of Spotted Fever Group Rickettsiae and Malaria Parasites by Dipstick DNA Chromatography. <i>Diagnostics</i> , 2020, 10, 897.	1.3	10
63	Molecular identification and genetic characterization of tick-borne pathogens in sheep and goats at two farms in the central and southern regions of Malawi. <i>Ticks and Tick-borne Diseases</i> , 2021, 12, 101629.	1.1	10
64	Molecular identification and characterization of piroplasm species in Hokkaido sika deer ( <i>Cervus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.1	10
65	First detection of <i>Eimeria</i> species in Myanmar domestic goats with both microscopic and molecular methods. <i>Parasite</i> , 2020, 27, 38.	0.8	9
66	Genetic Diversity and Sequence Polymorphism of Two Genes Encoding <i>Theileria parva</i> Antigens Recognized by CD8+ T Cells among Vaccinated and Unvaccinated Cattle in Malawi. <i>Pathogens</i> , 2020, 9, 334.	1.2	9
67	Bacterial and protozoan pathogens/symbionts in ticks infecting wild grasscutters ( <i>Thryonomys</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.9	9
68	<i>Amblyomma testudinarium</i> infestation on a brown bear ( <i>Ursus arctos yesoensis</i> ) captured in Hokkaido, a northern island of Japan. <i>Parasitology International</i> , 2021, 80, 102209.	0.6	9
69	Evidence of <i>Borrelia theileri</i> in Wild and Domestic Animals in the Kafue Ecosystem of Zambia. <i>Microorganisms</i> , 2021, 9, 2405.	1.6	9
70	Cystic echinococcosis in humans and animals in Egypt: An epidemiological overview. <i>Current Research in Parasitology and Vector-borne Diseases</i> , 2021, 1, 100061.	0.7	9
71	Recombination and purifying and balancing selection determine the evolution of major antigenic protein 1 (map 1) family genes in <i>Ehrlichia ruminantium</i> . <i>Gene</i> , 2019, 683, 216-224.	1.0	8
72	BoLA-DRB3 gene haplotypes show divergence in native Sudanese cattle from taurine and indicine breeds. <i>Scientific Reports</i> , 2021, 11, 17202.	1.6	8

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73	Comparative mitogenomics elucidates the population genetic structure of <i>Amblyomma testudinarium</i> in Japan and a closely related <i>Amblyomma</i> species in Myanmar. <i>Evolutionary Applications</i> , 2022, 15, 1062-1078.	1.5	8
74	First molecular detection and characterization of Hepatozoon and Sarcocystis spp. in field mice and voles from Japan. <i>Parasitology Research</i> , 2017, 116, 2321-2325.	0.6	7
75	Potential of cell-free DNA as a screening marker for parasite infections in dog. <i>Genomics</i> , 2019, 111, 906-912.	1.3	7
76	Seroprevalence of <i>Toxoplasma gondii</i> in household cats in Myanmar and molecular identification of parasites using feline faecal oocysts. <i>Food and Waterborne Parasitology</i> , 2020, 20, e00094.	1.1	7
77	PCR detection and genetic characterization of piroplasms from dogs in Myanmar, and a possible role of dogs as reservoirs for <i>Theileria</i> parasites infecting cattle, water buffaloes, and goats. <i>Ticks and Tick-borne Diseases</i> , 2021, 12, 101729.	1.1	7
78	Distinct haplotypes and free movement of <i>Aedes aegypti</i> in Port Sudan, Sudan. <i>Journal of Applied Entomology</i> , 2020, 144, 817-823.	0.8	6
79	Molecular detection and characterization of tick-borne hemoparasites and Anaplasmataceae in dogs in major cities of Malawi. <i>Parasitology Research</i> , 2021, 120, 267-276.	0.6	6
80	Domestic dog demographics and estimates of canine vaccination coverage in a rural area of Zambia for the elimination of rabies. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009222.	1.3	6
81	Molecular Detection and Genotyping of Coxiella-Like Endosymbionts in Ticks Collected from Animals and Vegetation in Zambia. <i>Pathogens</i> , 2021, 10, 779.	1.2	6
82	Morphological and molecular identification of trematode cercariae related with humans and animal health in freshwater snails from a lake and a dam in Myanmar. <i>Parasitology Research</i> , 2022, 121, 653-665.	0.6	6
83	Development of multiple-locus variable-number tandem-repeat analysis for rapid genotyping of <i>Ehrlichia ruminantium</i> and its application to infected <i>Amblyomma variegatum</i> collected in heartwater endemic areas in Uganda. <i>Parasitology</i> , 2012, 139, 69-82.	0.7	5
84	Molecular identification of trypanosomes in cattle in Malawi using PCR methods and nanopore sequencing: epidemiological implications for the control of human and animal trypanosomiasis. <i>Parasite</i> , 2020, 27, 46.	0.8	5
85	<i>Spiroplasma</i> Infection among Ixodid Ticks Exhibits Species Dependence and Suggests a Vertical Pattern of Transmission. <i>Microorganisms</i> , 2021, 9, 333.	1.6	5
86	Diverse mosquito-specific flaviviruses in the Bolivian Amazon basin. <i>Journal of General Virology</i> , 2021, 102, .	1.3	5
87	Identification, genetic variation, and structural analysis of 18S rRNA of <i>Theileria orientalis</i> and <i>Theileria velifera</i> -like isolates from Myanmar. <i>Parasitology International</i> , 2021, 82, 102299.	0.6	5
88	Climatic requirements of the southern paralysis tick, <i>Ixodes cornuatus</i> , with a consideration of its host, <i>Vombatus ursinus</i> , and the possible geographic range of the tick up to 2090. <i>Ticks and Tick-borne Diseases</i> , 2021, 12, 101758.	1.1	5
89	High infection rate of tick-borne protozoan and rickettsial pathogens of cattle in Malawi and the development of a multiplex PCR for <i>Babesia</i> and <i>Theileria</i> species identification. <i>Acta Tropica</i> , 2022, 231, 106413.	0.9	5
90	Detection of Tick-Borne Bacterial and Protozoan Pathogens in Ticks from the Zambia–Angola Border. <i>Pathogens</i> , 2022, 11, 566.	1.2	5

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91	Draft Genome Sequences of Three Strains of Ehrlichia ruminantium, a Tick-Borne Pathogen of Ruminants, Isolated from Zimbabwe, The Gambia, and Ghana. Genome Announcements, 2016, 4, .	0.8	4
92	Molecular detection of apicomplexan protozoa in Hokkaido brown bears (Ursus arctos yesoensis) and Japanese black bears (Ursus thibetanus japonicus). Parasitology Research, 2020, 119, 3739-3753.	0.6	4
93	Morphological and molecular identification of cyathostomine gastrointestinal nematodes of Murshidia and Quilonia species from Asian elephants in Myanmar. International Journal for Parasitology: Parasites and Wildlife, 2020, 11, 294-301.	0.6	4
94	An African tick flavivirus forming an independent clade exhibits unique exoribonuclease-resistant RNA structures in the genomic 3' untranslated region. Scientific Reports, 2021, 11, 4883.	1.6	4
95	Molecular Survey of Babesia and Anaplasma Infection in Cattle in Bolivia. Veterinary Sciences, 2021, 8, 188.	0.6	4
96	Reconstruction of mitochondrial genomes from raw sequencing data provides insights on the phylogeny of Ixodes ticks and cautions for species misidentification. Ticks and Tick-borne Diseases, 2022, 13, 101832.	1.1	4
97	Description of the female, nymph and larva and mitochondrial genome, and redescription of the male of Ixodes barkeri Barker, 2019 (Acari: Ixodidae), from the short-beaked echidna, Tachyglossus aculeatus, with a consideration of the most suitable subgenus for this tick. Parasites and Vectors, 2022, 15, 117.	1.0	4
98	Novel symbionts and potential human pathogens excavated from argasid tick microbiomes that are shaped by dual or single symbiosis. Computational and Structural Biotechnology Journal, 2022, 20, 1979-1992.	1.9	4
99	Molecular characterization and phylogenetic analysis of Trypanosoma spp. detected from striped leaf-nosed bats (Hipposideros vittatus) in Zambia. International Journal for Parasitology: Parasites and Wildlife, 2019, 9, 234-238.	0.6	3
100	Complete Genome Sequence of Rickettsia asiatica Strain Maytaro1284, a Member of Spotted Fever Group Rickettsiae Isolated from an Ixodes ovatus Tick in Japan. Microbiology Resource Announcements, 2019, 8, .	0.3	3
101	Utilizing attached hard ticks as pointers to the risk of infection by Babesia and Theileria species in sika deer (Cervus nippon yesoensis), in Japan. Experimental and Applied Acarology, 2020, 82, 411-429.	0.7	3
102	Characterization of tick-borne encephalitis virus isolated from tick infesting dog in central Hokkaido in 2018. Ticks and Tick-borne Diseases, 2022, 13, 101900.	1.1	3
103	Draft Genome Sequences of Five Legionella pneumophila Strains Isolated from Environmental Water Samples. Genome Announcements, 2015, 3, .	0.8	2
104	First record and analysis of the COI gene of Cobboldia elephantis obtained from a captive Asian elephant from Myanmar. Parasitology International, 2020, 75, 102035.	0.6	2
105	Seroprevalence of fasciolosis in Hokkaido sika deer (Cervus nippon yesoensis) from Hokkaido Prefecture, Japan revealed by ELISA using recombinant cathepsin L1. Parasitology International, 2021, 80, 102222.	0.6	2
106	Metagenomic identification, sequencing, and genome analysis of porcine hepe-astroviruses (bastroviruses) in porcine feces in Japan. Infection, Genetics and Evolution, 2021, 88, 104664.	1.0	2
107	Microscopic and molecular detection of Eimeria maxima and Eimeria praecox naturally infected in free-range village chickens of Myanmar. Acta Parasitologica, 2021, 66, 1074-1078.	0.4	2
108	Characterization of microRNAs expressed in the cystic legion of the liver of Mus musculus perorally infected with Echinococcus multilocularis Nemuro strain. Parasitology International, 2021, 81, 102247.	0.6	2



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109	Applications of Blocker Nucleic Acids and Non-Metazoan PCR Improves the Discovery of the Eukaryotic Microbiome in Ticks. <i>Microorganisms</i> , 2021, 9, 1051.	1.6	2
110	Immunization Coverage and Antibody Retention against Rabies in Domestic Dogs in Lusaka District, Zambia. <i>Pathogens</i> , 2021, 10, 738.	1.2	2
111	Sensitivity comparison between Mini-FLOTAC and conventional techniques for the detection of <i>Echinococcus multilocularis</i> eggs. <i>Parasitology International</i> , 2022, 87, 102522.	0.6	2
112	Rediscovery of <i>Ixodes confusus</i> in Australia with the first description of the male from Australia, a redescription of the female and the mitochondrial (mt) genomes of five species of <i>Ixodes</i> . <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2022, 18, 1-11.	0.6	2
113	Gene expression profiles of the small intestinal mucosa of dogs repeatedly infected with the cestode <i>Echinococcus multilocularis</i> . <i>Data in Brief</i> , 2018, 17, 180-183.	0.5	1
114	Analysis for genetic loci controlling protoscolex development in the <i>Echinococcus multilocularis</i> infection using congenic mice. <i>Infection, Genetics and Evolution</i> , 2018, 65, 65-71.	1.0	1
115	Adult worm exclusion and histological data of dogs repeatedly infected with the cestode <i>Echinococcus multilocularis</i> . <i>Data in Brief</i> , 2020, 29, 105353.	0.5	1
116	SPECIFIC MOLECULAR DETECTION OF PIROPLASMS AND CHARACTERIZATION OF $\beta$ -TUBULIN FOR A NOVEL <i>BABESIA</i> SPECIES IN SIKA DEER ( <i>CERVUS NIPPON YESOENSIS</i> ). <i>Journal of Zoo and Wildlife Medicine</i> , 2021, 52, 200-205.	0.3	1
117	Demographic expansion and high level of matrilineal diversity in two populations of East African Baggara cattle. <i>Journal of Animal Breeding and Genetics</i> , 2022, 139, 161-169.	0.8	1
118	Early-phase migration dynamics of <i>Echinococcus multilocularis</i> in two mouse strains showing different infection susceptibilities. <i>International Journal for Parasitology</i> , 2021, 51, 893-898.	1.3	1
119	Complete Genome Sequence of <i>Leptospira kobayashii</i> Strain E30, Isolated from Soil in Japan. <i>Microbiology Resource Announcements</i> , 2021, 10, e0090721.	0.3	1
120	The strong influence of management factors on coccidian infections in smallholder pig farms and the first molecular identification of <i>Cystoisospora suis</i> in Myanmar. <i>Parasite</i> , 2022, 29, 1.	0.8	0
121	Scanning electron microscopy of <i>Quilonia renniei</i> from Asian elephants revealing variation in coronal leaflet number. <i>Parasitology</i> , 2022, 149, 529-533.	0.7	0
122	Genotyping of <i>Theileria parva</i> populations in vaccinated and non-vaccinated cattle in Malawi. <i>Parasitology</i> , 2022, , 1-28.	0.7	0