Ryo Nakao

List of Publications by Year in descending order

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	304368	301761
2,190	22	39
citations	h-index	g-index
126	126	2301
		citing authors
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	2,190 citations 126 docs citations	2,190 22 citations h-index 126 126

#	Article	IF	CITATIONS
1	Demographic expansion and high level of matrilineal diversity in two populations of East African Baggara cattle. Journal of Animal Breeding and Genetics, 2022, 139, 161-169.	0.8	1
2	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
3	Sensitivity comparison between Mini-FLOTAC and conventional techniques for the detection of Echinococcus multilocularis eggs. Parasitology International, 2022, 87, 102522.	0.6	2
4	The strong influence of management factors on coccidian infections in smallholder pig farms and the first molecular identification of Cystoisospora suis in Myanmar. Parasite, 2022, 29, 1.	0.8	O
5	Morphological and molecular identification of trematode cercariae related with humans and animal health in freshwater snails from a lake and a dam in Myanmar. Parasitology Research, 2022, 121, 653-665.	0.6	6
6	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
7	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
8	High infection rate of tick-borne protozoan and rickettsial pathogens of cattle in Malawi and the development of a multiplex PCR for Babesia and Theileria species identification. Acta Tropica, 2022, 231, 106413.	0.9	5
9	Rediscovery of Ixodes confusus 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 Ixodes. International Journal for Parasitology: Parasites and Wildlife, 2022, 18, 1-11.	0.6	2
10	Scanning electron microscopy of <i>Quilonia renniei</i> from Asian elephants revealing variation in coronal leaflet number. Parasitology, 2022, 149, 529-533.	0.7	0
11	Genotyping of <i>Theileria parva</i> populations in vaccinated and non-vaccinated cattle in Malawi. Parasitology, 2022, , 1-28.	0.7	O
12	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
13	Detection of Tick-Borne Bacterial and Protozoan Pathogens in Ticks from the Zambia–Angola Border. Pathogens, 2022, 11, 566.	1.2	5
14	Comparative mitogenomics elucidates the population genetic structure of <i>Amblyomma testudinarium</i> in Japan and a closely related <i>Amblyomma</i> species in Myanmar. Evolutionary Applications, 2022, 15, 1062-1078.	1.5	8
15	Phylogenies from mitochondrial genomes of 120 species of ticks: Insights into the evolution of the families of ticks and of the genus Amblyomma. Ticks and Tick-borne Diseases, 2021, 12, 101577.	1.1	38
16	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
17	Molecular detection and characterization of tick-borne hemoparasites and Anaplasmataceae in dogs in major cities of Malawi. Parasitology Research, 2021, 120, 267-276.	0.6	6
18	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

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19	Molecular identification and genetic characterization of tick-borne pathogens in sheep and goats at two farms in the central and southern regions of Malawi. Ticks and Tick-borne Diseases, 2021, 12, 101629.	1.1	10
20	Amblyomma testudinarium infestation on a brown bear (Ursus arctos yesoensis) captured in Hokkaido, a northern island of Japan. Parasitology International, 2021, 80, 102209.	0.6	9
21	Anthropogenic interferences lead to gut microbiome dysbiosis in Asian elephants and may alter adaptation processes to surrounding environments. Scientific Reports, 2021, 11, 741.	1.6	24
22	Spiroplasma Infection among Ixodid Ticks Exhibits Species Dependence and Suggests a Vertical Pattern of Transmission. Microorganisms, 2021, 9, 333.	1.6	5
23	Exploring Prokaryotic and Eukaryotic Microbiomes Helps in Detecting Tick-Borne Infectious Agents in the Blood of Camels. Pathogens, 2021, 10, 351.	1.2	16
24	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
25	Diverse mosquito-specific flaviviruses in the Bolivian Amazon basin. Journal of General Virology, 2021, 102, .	1.3	5
26	An African tick flavivirus forming an independent clade exhibits unique exoribonuclease-resistant RNA structures in the genomic $3\hat{a} \in \mathbb{Z}^2$ -untranslated region. Scientific Reports, 2021, 11, 4883.	1.6	4
27	SPECIFIC MOLECULAR DETECTION OF PIROPLASMS AND CHARACTERIZATION OF Î ² -TUBULIN FOR A NOVEL BABESIA SPECIES IN SIKA DEER (CERVUS NIPPON YESOENSIS). Journal of Zoo and Wildlife Medicine, 2021, 52, 200-205.	0.3	1
28	Domestic dog demographics and estimates of canine vaccination coverage in a rural area of Zambia for the elimination of rabies. PLoS Neglected Tropical Diseases, 2021, 15, e0009222.	1.3	6
29	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
30	Applications of Blocker Nucleic Acids and Non-Metazoan PCR Improves the Discovery of the Eukaryotic Microbiome in Ticks. Microorganisms, 2021, 9, 1051.	1.6	2
31	Molecular Detection and Genotyping of Coxiella-Like Endosymbionts in Ticks Collected from Animals and Vegetation in Zambia. Pathogens, 2021, 10, 779.	1.2	6
32	Immunization Coverage and Antibody Retention against Rabies in Domestic Dogs in Lusaka District, Zambia. Pathogens, 2021, 10, 738.	1.2	2
33	Identification, genetic variation, and structural analysis of 18S rRNA of Theileria orientalis and Theileria velifera-like isolates from Myanmar. Parasitology International, 2021, 82, 102299.	0.6	5
34	Serologic and molecular evidence for circulation of Crimean-Congo hemorrhagic fever virus in ticks and cattle in Zambia. PLoS Neglected Tropical Diseases, 2021, 15, e0009452.	1.3	11
35	PCR detection and genetic characterization of piroplasms from dogs in Myanmar, and a possible role of dogs as reservoirs for Theileria parasites infecting cattle, water buffaloes, and goats. Ticks and Tick-borne Diseases, 2021, 12, 101729.	1.1	7
36	Screening of tick-borne pathogens in argasid ticks in Zambia: Expansion of the geographic distribution of Rickettsia lusitaniae and Rickettsia hoogstraalii and detection of putative novel Anaplasma species. Ticks and Tick-borne Diseases, 2021, 12, 101720.	1.1	20

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37	Nuclear (18S-28S rRNA) and mitochondrial genome markers of Carios (Carios) vespertilionis (Argasidae) support Carios Latreille, 1796 as a lineage embedded in the Ornithodorinae: re-classification of the Carios sensu Klompen and Oliver (1993) clade into its respective subgenera. Ticks and Tick-borne Diseases, 2021, 12, 101688.	1.1	37
38	BoLA-DRB3 gene haplotypes show divergence in native Sudanese cattle from taurine and indicine breeds. Scientific Reports, 2021, 11, 17202.	1.6	8
39	A novel nairovirus associated with acute febrile illness in Hokkaido, Japan. Nature Communications, 2021, 12, 5539.	5.8	30
40	Molecular Survey of Babesia and Anaplasma Infection in Cattle in Bolivia. Veterinary Sciences, 2021, 8, 188.	0.6	4
41	Climatic requirements of the southern paralysis tick, Ixodes cornuatus, with a consideration of its host, Vombatus ursinus, and the possible geographic range of the tick up to 2090. Ticks and Tick-borne Diseases, 2021, 12, 101758.	1.1	5
42	Early-phase migration dynamics of Echinococcus multilocularis in two mouse strains showing different infection susceptibilities. International Journal for Parasitology, 2021, 51, 893-898.	1.3	1
43	Emergence of the invasive malaria vector Anopheles stephensi in Khartoum State, Central Sudan. Parasites and Vectors, 2021, 14, 511.	1.0	45
44	Comparing the gut microbiome along the gastrointestinal tract of three sympatric species of wild rodents. Scientific Reports, 2021, 11, 19929.	1.6	13
45	Evidence of Borrelia theileri in Wild and Domestic Animals in the Kafue Ecosystem of Zambia. Microorganisms, 2021, 9, 2405.	1.6	9
46	Complete Genome Sequence of Leptospira kobayashii Strain E30, Isolated from Soil in Japan. Microbiology Resource Announcements, 2021, 10, e0090721.	0.3	1
47	Cystic echinococcosis in humans and animals in Egypt: An epidemiological overview. Current Research in Parasitology and Vector-borne Diseases, 2021, 1, 100061.	0.7	9
48	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
49	Detection of Borrelia burgdorferi Sensu Lato and Relapsing Fever Borrelia in Feeding Ixodes Ticks and Rodents in Sarawak, Malaysia: New Geographical Records of Borrelia yangtzensis and Borrelia miyamotoi. Pathogens, 2020, 9, 846.	1.2	15
50	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
51	Molecular identification of trypanosomes in cattle in Malawi using PCR methods and nanopore sequencing: epidemiological implications for the control of human and animal trypanosomiases. Parasite, 2020, 27, 46.	0.8	5
52	Seroprevalence of Toxoplasma gondii in household cats in Myanmar and molecular identification of parasites using feline faecal oocysts. Food and Waterborne Parasitology, 2020, 20, e00094.	1.1	7
53	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
54	Detection and molecular identification of Leucocytozoon and Plasmodium species from village chickens in different areas of Myanmar. Acta Tropica, 2020, 212, 105719.	0.9	17

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55	Distinct haplotypes and free movement of <i>Aedes aegypti</i> in Port Sudan, Sudan. Journal of Applied Entomology, 2020, 144, 817-823.	0.8	6
56	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. Diagnostics, 2020, 10, 897.	1.3	10
57	First detection of <i>Eimeria </i> species in Myanmar domestic goats with both microscopic and molecular methods. Parasite, 2020, 27, 38.	0.8	9
58	Genetic Diversity and Sequence Polymorphism of Two Genes Encoding Theileria parva Antigens Recognized by CD8+ T Cells among Vaccinated and Unvaccinated Cattle in Malawi. Pathogens, 2020, 9, 334.	1.2	9
59	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
60	Adult worm exclusion and histological data of dogs repeatedly infected with the cestode Echinococcus multilocularis. Data in Brief, 2020, 29, 105353.	0.5	1
61	Isolation of Candidatus Bartonella rousetti and Other Bat-associated Bartonellae from Bats and Their Flies in Zambia. Pathogens, 2020, 9, 469.	1.2	20
62	Bacterial and protozoan pathogens/symbionts in ticks infecting wild grasscutters (Thryonomys) Tj ETQq0 0 0 rg	BT /Oyerlo	ock JO Tf 50 4
63	Potential of cell-free DNA as a screening marker for parasite infections in dog. Genomics, 2019, 111, 906-912.	1.3	7
64	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
65	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
66	Revisiting the taxonomy and evolution of pathogenicity of the genus Leptospira through the prism of genomics. PLoS Neglected Tropical Diseases, 2019, 13, e0007270.	1.3	417
67	Viral population analysis of the taiga tick, <i>lxodes persulcatus,</i> by using Batch Learning Self-Organizing Maps and BLAST search. Journal of Veterinary Medical Science, 2019, 81, 401-410.	0.3	30
68	Molecular and phenotypic characterization ofLeptospira johnsoniisp. nov.,Leptospira ellinghauseniisp. nov. andLeptospira ryugeniisp. nov. isolated from soil and water in Japan. Microbiology and Immunology, 2019, 63, 89-99.	0.7	22
69	Potential role of dogs as sentinels and reservoirs for piroplasms infecting equine and cattle in Riyadh City, Saudi Arabia. Acta Tropica, 2019, 193, 78-83.	0.9	10
70	Molecular detection of Rickettsia felis in dogs, rodents and cat fleas in Zambia. Parasites and Vectors, 2019, 12, 168.	1.0	32
71	Diversity of spotted fever group rickettsiae and their association with host ticks in Japan. Scientific Reports, 2019, 9, 1500.	1.6	43
72	Isolation of <i>Rickettsia </i> , <i>Rickettsiella </i> , and <i>Spiroplasma </i> from Questing Ticks in Japan Using Arthropod Cells. Vector-Borne and Zoonotic Diseases, 2019, 19, 474-485.	0.6	11

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73	Mutations in the TaPIN1 peptidyl prolyl isomerase gene in Theileria annulata parasites isolated in Sudan. International Journal for Parasitology: Drugs and Drug Resistance, 2019, 11, 101-105.	1.4	10
74	Evidence of multiple point mutations in Theileria annulata cytochrome b gene incriminated in buparvaquone treatment failure. Acta Tropica, 2019, 191, 128-132.	0.9	28
75	Human Borreliosis Caused by a New World Relapsing Fever Borrelia–like Organism in the Old World. Clinical Infectious Diseases, 2019, 69, 107-112.	2.9	36
76	Recombination and purifying and balancing selection determine the evolution of major antigenic protein 1 (map 1) family genes in Ehrlichia ruminantium. Gene, 2019, 683, 216-224.	1.0	8
77	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
78	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
79	Gene expression profiles of the small intestinal mucosa of dogs repeatedly infected with the cestode Echinococcus multilocularis. Data in Brief, 2018, 17, 180-183.	0.5	1
80	Tick-borne haemoparasites and Anaplasmataceae in domestic dogs in Zambia. Ticks and Tick-borne Diseases, 2018, 9, 988-995.	1.1	23
81	Molecular detection and characterization of zoonotic Anaplasma species in domestic dogs in Lusaka, Zambia. Ticks and Tick-borne Diseases, 2018, 9, 39-43.	1.1	22
82	The Unique Phylogenetic Position of a Novel Tick-Borne Phlebovirus Ensures an Ixodid Origin of the Genus $\langle i \rangle$ Phlebovirus $\langle i \rangle$. MSphere, 2018, 3, .	1.3	36
83	First molecular detection of Theileria luwenshuni from goats in Myanmar. Parasitology Research, 2018, 117, 3361-3364.	0.6	10
84	Comparison of Database Search Methods for the Detection of Legionella pneumophila in Water Samples Using Metagenomic Analysis. Frontiers in Microbiology, 2018, 9, 1272.	1.5	13
85	First molecular detection and genetic characterization of Coxiella burnetii in Zambian dogs and rodents. Parasites and Vectors, 2018, 11, 40.	1.0	15
86	Analysis for genetic loci controlling protoscolex development in the Echinococcus multilocularis infection using congenic mice. Infection, Genetics and Evolution, 2018, 65, 65-71.	1.0	1
87	Development and validation of direct dry loop mediated isothermal amplification for diagnosis of Trypanosoma evansi. Veterinary Parasitology, 2018, 260, 53-57.	0.7	13
88	Seroprevalence of Filovirus Infection of Rousettus aegyptiacus Bats in Zambia. Journal of Infectious Diseases, 2018, 218, S312-S317.	1.9	21
89	Molecular characterization of Fasciola flukes obtained from wild sika deer and domestic cattle in Hokkaido, Japan. Parasitology International, 2017, 66, 519-521.	0.6	12
90	First molecular detection and characterization of Hepatozoon and Sarcocystis spp. in field mice and voles from Japan. Parasitology Research, 2017, 116, 2321-2325.	0.6	7

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91	Molecular identification and characterization of piroplasm species in Hokkaido sika deer (Cervus) Tj ETQq1 1	0.784314 rgB	Г _у Overlock
92	Putative RNA viral sequences detected in an Ixodes scapularis-derived cell line. Ticks and Tick-borne Diseases, 2017, 8, 103-111.	1.1	23
93	Occurrence of <i>Coxiella burnetii</i> , <i>Ehrlichia canis</i> , <i>, <i>Rickettsia</i>-like bacterium in ticks collected from dogs and cats in South Africa. Journal of the South African Veterinary Association. 2017. 88. e1-e6.</i>	0.2	27
94	Geographic strain differentiation of Schistosoma japonicum in the Philippines using microsatellite markers. PLoS Neglected Tropical Diseases, 2017, 11, e0005749.	1.3	15
95	<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
96	Horizontally Transferred Genetic Elements in the Tsetse Fly Genome: An Alignment-Free Clustering Approach Using Batch Learning Self-Organising Map (BLSOM). BioMed Research International, 2016, 2016, 1-8.	0.9	23
97	Ciliate Paramecium is a natural reservoir of Legionella pneumophila. Scientific Reports, 2016, 6, 24322.	1.6	34
98	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
99	Molecular and Serological Evidence of Leishmania 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
100	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
101	Molecular survey of Babesia infections in cattle from different areas of Myanmar. Ticks and Tick-borne Diseases, 2016, 7, 204-207.	1.1	21
102	Molecular evidence of spotted fever group rickettsiae and Anaplasmataceae from ticks and stray dogs in Bangladesh. Parasitology Research, 2016, 115, 949-955.	0.6	11
103	Molecular detection of zoonotic tick-borne pathogens from ticks collected from ruminants in four South African provinces. Journal of Veterinary Medical Science, 2015, 77, 1573-1579.	0.3	44
104	Studies of trypanosomiasis in the Luangwa valley, north-eastern Zambia. Parasites and Vectors, 2015, 8, 497.	1.0	25
105	Isolation of the Thogoto virus from a Haemaphysalis longicornis in Kyoto City, Japan. Journal of General Virology, 2015, 96, 2099-2103.	1.3	13
106	Draft Genome Sequences of Five Legionella pneumophila Strains Isolated from Environmental Water Samples. Genome Announcements, 2015, 3, .	0.8	2
107	Molecular detection and genetic diversity of Babesia gibsoni in dogs in Bangladesh. Infection, Genetics and Evolution, 2015, 31, 53-60.	1.0	20
108	Molecular Detection of <i>Rickettsia africae </i> ii>in <i>Amblyomma variegatum </i> Collected from Sudan. Vector-Borne and Zoonotic Diseases, 2015, 15, 323-325.	0.6	16

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109	Molecular characterization and specific detection of Anaplasma 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
110	Detection and characterization of zoonotic pathogens of free-ranging non-human primates from Zambia. Parasites and Vectors, 2014, 7, 490.	1.0	29
111	Genetic diversity of Leishmania donovani/infantum complex in China through microsatellite analysis. Infection, Genetics and Evolution, 2014, 22, 112-119.	1.0	18
112	Microbial Population Analysis of the Salivary Glands of Ticks; A Possible Strategy for the Surveillance of Bacterial Pathogens. PLoS ONE, 2014, 9, e103961.	1.1	95
113	A novel approach, based on BLSOMs (Batch Learning Self-Organizing Maps), to the microbiome analysis of ticks. ISME Journal, 2013, 7, 1003-1015.	4.4	132
114	High prevalence of spotted fever group rickettsiae in Amblyomma variegatum from Uganda and their identification using sizes of intergenic spacers. Ticks and Tick-borne Diseases, 2013, 4, 506-512.	1.1	34
115	First Genetic Detection of Coxiella burnetii in Zambian Livestock. American Journal of Tropical Medicine and Hygiene, 2013, 89, 518-519.	0.6	11
116	Development of multiple-locus variable-number tandem-repeat analysis for rapid genotyping of Ehrlichia ruminantiumand its application to infected Amblyomma variegatum collected in heartwater endemic areas in Uganda. Parasitology, 2012, 139, 69-82.	0.7	5
117	Population genetic analysis and sub-structuring of Theileria parva in the northern and eastern parts of Zambia. Parasites and Vectors, 2012, 5, 255.	1.0	30
118	An outbreak of bovine trypanosomiasis in the Blue Nile State, Sudan. Parasites and Vectors, 2011, 4, 74.	1.0	15
119	Identification of genetic loci affecting the establishment and development of Echinococcus multilocularis larvae in mice. International Journal for Parasitology, 2011, 41, 1121-1128.	1.3	10
120	Multi-locus sequence typing of Ehrlichia ruminantium strains from geographically diverse origins and collected in Amblyomma variegatum from Uganda. Parasites and Vectors, 2011, 4, 137.	1.0	17
121	Development of Loop-Mediated Isothermal Amplification (LAMP) Assays for Rapid Detection of Ehrlichia ruminantium. BMC Microbiology, 2010, 10, 296.	1.3	61
122	Evaluation of Efficacy of Bruceine A, a Natural Quassinoid Compound Extracted from a Medicinal Plant, Bruced javanica, for Canine Babesiosis. Journal of Veterinary Medical Science, 2009, 71, 33-41.	0.3	21