

# Anson V Koehler

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1595598/publications.pdf>

Version: 2024-02-01

113  
papers

4,657  
citations

172457

29  
h-index

123424

61  
g-index

113  
all docs

113  
docs citations

113  
times ranked

7297  
citing authors

#	ARTICLE	IF	CITATIONS
1	A multipronged next-generation sequencing metabarcoding approach unearths hyperdiverse and abundant dog pathogen communities in Cambodia. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 1933-1950.	3.0	15
2	A Perspective on the Molecular Identification, Classification, and Epidemiology of <i>Enterocytozoon bieneusi</i> of Animals. <i>Experientia Supplementum</i> (2012), 2022, 114, 389-415.	0.9	2
3	<i>Enterocytozoon bieneusi</i> of animals – With an “Australian twist”™. <i>Advances in Parasitology</i> , 2021, 111, 1-73.	3.2	26
4	Detection of <i>Breinlia</i> sp. (Nematoda) in the Leadbeater's possum ( <i>Gymnobelideus leadbeateri</i> ). <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2021, 15, 249-254.	1.5	3
5	Molecular detection of <i>Strongyloides</i> sp. in Australian Thoroughbred foals. <i>Parasites and Vectors</i> , 2021, 14, 444.	2.5	5
6	<i>Cryptosporidium</i> of birds in pet markets in Wuhan city, Hubei, China. <i>Current Research in Parasitology and Vector-borne Diseases</i> , 2021, 1, 100025.	1.9	3
7	Ocular Filariasis in Human Caused by <i>Breinlia</i> ( <i>Johnstonema</i> ) <i>annulipapillata</i> Nematode, Australia. <i>Emerging Infectious Diseases</i> , 2021, 27, 297-300.	4.3	4
8	Targeted Next-Generation Sequencing and Informatics as an Effective Tool to Establish the Composition of Bovine Piroplasm Populations in Endemic Regions. <i>Microorganisms</i> , 2021, 9, 21.	3.6	10
9	Phylogenetic relationships of the nematode subfamily Phascolostrongylinae from macropodid and vombatid marsupials inferred using mitochondrial protein sequence data. <i>Parasites and Vectors</i> , 2021, 14, 523.	2.5	2
10	Disseminated protozoal infection in a wild feathertail glider ( <i>Acrobates pygmaeus</i> ) in Australia. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2020, 13, 46-50.	1.5	1
11	<i>Cryptosporidium</i> cf. <i>avium</i> in an inland-bearded dragon ( <i>Pogona vitticeps</i> ) – A case report and review of the literature. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2020, 13, 150-159.	1.5	2
12	Natural Compounds from the Marine Brown Alga <i>Caulocystis cephalornithos</i> with Potent In Vitro-Activity against the Parasitic Nematode <i>Haemonchus contortus</i> . <i>Pathogens</i> , 2020, 9, 550.	2.8	17
13	Marked mitochondrial genetic variation in individuals and populations of the carcinogenic liver fluke <i>Clonorchis sinensis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008480.	3.0	6
14	Phylogenetic Analysis of Mitogenomic Data Sets Resolves the Relationship of Seven <i>Macropostrongyloides</i> Species from Australian Macropodid and Vombatid Marsupials. <i>Pathogens</i> , 2020, 9, 1042.	2.8	5
15	Age of first infection across a range of parasite taxa in a wild mammalian population. <i>Biology Letters</i> , 2020, 16, 20190811.	2.3	16
16	Multiplex PCRs for the specific identification of marsupial and deer species from faecal samples as a basis for non-invasive epidemiological studies of parasites. <i>Parasites and Vectors</i> , 2020, 13, 144.	2.5	3
17	A Targeted “Next-Generation” Sequencing-Informatic Approach to Define Genetic Diversity in <i>Theileria orientalis</i> Populations within Individual Cattle: Proof-of-Principle. <i>Pathogens</i> , 2020, 9, 448.	2.8	6
18	Elucidating cryptic dynamics of <i>Theileria</i> communities in African buffalo using a high-throughput sequencing informatics approach. <i>Ecology and Evolution</i> , 2020, 10, 70-80.	1.9	19

#	ARTICLE	IF	CITATIONS
19	A Host-Specific Blocking Primer Combined with Optimal DNA Extraction Improves the Detection Capability of a Metabarcoding Protocol for Canine Vector-Borne Bacteria. <i>Pathogens</i> , 2020, 9, 258.	2.8	14
20	Use of Markers to Determine <i>Cryptosporidium</i> Genotypes for Epidemiology Tracking and Detection. <i>Methods in Molecular Biology</i> , 2020, 2052, 117-127.	0.9	2
21	<i>Enterocytozoon bienersi</i> genotypes in cats and dogs in Victoria, Australia. <i>BMC Microbiology</i> , 2019, 19, 183.	3.3	22
22	Human toxocarasis – A look at a neglected disease through an epidemiological “prism”. <i>Infection, Genetics and Evolution</i> , 2019, 74, 104002.	2.3	76
23	Assessment of a metabarcoding approach for the characterisation of vector-borne bacteria in canines from Bangkok, Thailand. <i>Parasites and Vectors</i> , 2019, 12, 394.	2.5	29
24	A novel metabarcoding diagnostic tool to explore protozoan haemoparasite diversity in mammals: a proof-of-concept study using canines from the tropics. <i>Scientific Reports</i> , 2019, 9, 12644.	3.3	29
25	High throughput LC-MS/MS-based proteomic analysis of excretory-secretory products from short-term in vitro culture of <i>Haemonchus contortus</i> . <i>Journal of Proteomics</i> , 2019, 204, 103375.	2.4	44
26	Phenotypic screening of the “Kurz-box” of chemicals identifies two compounds (BLK127 and HBK4) with anthelmintic activity in vitro against parasitic larval stages of <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , 2019, 12, 191.	2.5	10
27	Selected Î±-pyrones from the plants <i>Cryptocarya novoguineensis</i> (Lauraceae) and <i>Piper methysticum</i> (Piperaceae) with activity against <i>Haemonchus contortus</i> in vitro. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2019, 9, 72-79.	3.4	10
28	Somatic proteome of <i>Haemonchus contortus</i> . <i>International Journal for Parasitology</i> , 2019, 49, 311-320.	3.1	38
29	Comparative bioinformatic analysis suggests that specific dauer-like signalling pathway components regulate <i>Toxocara canis</i> development and migration in the mammalian host. <i>Parasites and Vectors</i> , 2019, 12, 32.	2.5	15
30	Tetrahydroquinoxalines induce a lethal evisceration phenotype in <i>Haemonchus contortus</i> in vitro. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2019, 9, 59-71.	3.4	15
31	<i>Enterocytozoon bienersi</i> Genotypes in Cattle on Farms Located within a Water Catchment Area. <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 553-559.	1.7	26
32	Phylogenetic relationships of three tribes of cloacinine nematodes (Strongylida: Chabertiidae) from macropodid marsupials. <i>Journal of Helminthology</i> , 2019, 93, 486-493.	1.0	3
33	An improved method for PCR-based detection and routine monitoring of geosmin-producing cyanobacterial blooms. <i>Water Research</i> , 2018, 136, 34-40.	11.3	20
34	First detection and genetic characterisation of <i>Enterocytozoon bienersi</i> in wild deer in Melbourne’s water catchments in Australia. <i>Parasites and Vectors</i> , 2018, 11, 2.	2.5	41
35	Parasites of the Giant Panda: A Risk Factor in the Conservation of a Species. <i>Advances in Parasitology</i> , 2018, 99, 1-33.	3.2	28
36	<i>Cryptosporidium viatorum</i> from the native Australian swamp rat <i>Rattus lutreolus</i> - An emerging zoonotic pathogen?. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2018, 7, 18-26.	1.5	33

#	ARTICLE	IF	CITATIONS
37	Using PCR-Based Sequencing to Diagnose <i>Haycocknema perplexum</i> Infection in Human Myositis Case, Australia. <i>Emerging Infectious Diseases</i> , 2018, 24, 2368-2370.	4.3	5
38	PCR-coupled sequencing achieves specific diagnosis of onchocerciasis in a challenging clinical case, to underpin effective treatment and clinical management. <i>Infection, Genetics and Evolution</i> , 2018, 66, 192-194.	2.3	4
39	Molecular investigation of <i>Cryptosporidium</i> in farmed chickens in Hubei Province, China, identifies zoonotic subtypes of <i>C. meleagridis</i> . <i>Parasites and Vectors</i> , 2018, 11, 484.	2.5	31
40	First cross-sectional, molecular epidemiological survey of <i>Cryptosporidium</i> , <i>Giardia</i> and <i>Enterocytozoon</i> in alpaca ( <i>Vicugna pacos</i> ) in Australia. <i>Parasites and Vectors</i> , 2018, 11, 498.	2.5	25
41	The developmental lipidome of <i>Haemonchus contortus</i> . <i>International Journal for Parasitology</i> , 2018, 48, 887-895.	3.1	30
42	Molecular alterations during larval development of <i>Haemonchus contortus</i> in vitro are under tight post-transcriptional control. <i>International Journal for Parasitology</i> , 2018, 48, 763-772.	3.1	30
43	Arylpyrrole and fipronil analogues that inhibit the motility and/or development of <i>Haemonchus contortus</i> in vitro. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2018, 8, 379-385.	3.4	9
44	New operational taxonomic units of <i>Enterocytozoon</i> in three marsupial species. <i>Parasites and Vectors</i> , 2018, 11, 371.	2.5	20
45	<i>Enterocytozoon bienewisi</i> genotypes in people with gastrointestinal disorders in Queensland and Western Australia. <i>Infection, Genetics and Evolution</i> , 2018, 65, 293-299.	2.3	22
46	Mitochondrial genomic comparison of <i>Clonorchis sinensis</i> from South Korea with other isolates of this species. <i>Infection, Genetics and Evolution</i> , 2017, 51, 160-166.	2.3	13
47	Mitochondrial genomes of two <i>Babesia</i> taxa from sheep in China as a foundation for population genetic and epidemiological investigations. <i>Infection, Genetics and Evolution</i> , 2017, 47, 51-55.	2.3	6
48	Screening of the Open Scaffolds collection from Compounds Australia identifies a new chemical entity with anthelmintic activities against different developmental stages of the barber's pole worm and other parasitic nematodes. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2017, 7, 286-294.	3.4	33
49	First survey of <i>Cryptosporidium</i> , <i>Giardia</i> and <i>Enterocytozoon</i> in diarrhoeic children from Wuhan, China. <i>Infection, Genetics and Evolution</i> , 2017, 51, 127-131.	2.3	51
50	The apicoplast genomes of two taxonomic units of <i>Babesia</i> from sheep. <i>Veterinary Parasitology</i> , 2017, 233, 123-128.	1.8	10
51	The Beringian Coevolution Project: holistic collections of mammals and associated parasites reveal novel perspectives on evolutionary and environmental change in the North. <i>Arctic Science</i> , 2017, 3, 585-617.	2.3	50
52	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	27.8	1,942
53	Speciation in the genus <i>Cloacina</i> (Nematoda: Strongylida): species flocks and intra-host speciation. <i>Parasitology</i> , 2017, 144, 1828-1840.	1.5	8
54	Genetic diversity in the C-terminus of merozoite surface protein 1 among <i>Plasmodium knowlesi</i> isolates from Selangor and Sabah Borneo, Malaysia. <i>Infection, Genetics and Evolution</i> , 2017, 54, 39-46.	2.3	15

#	ARTICLE	IF	CITATIONS
55	Screening of a small, well-curated natural product-based library identifies two rotenoids with potent nematocidal activity against <i>Haemonchus contortus</i> . <i>Veterinary Parasitology</i> , 2017, 244, 172-175.	1.8	19
56	Phylogenetic analysis of the Australasian paralysis ticks and their relatives (Ixodidae: Ixodes: Ixodes) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702 T	2.5	17
57	Assessing the anthelmintic activity of pyrazole-5-carboxamide derivatives against <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , 2017, 10, 272.	2.5	25
58	Application of PCR-Based Tools to Explore <i>Strongyloides</i> Infection in People in Parts of Northern Australia. <i>Tropical Medicine and Infectious Disease</i> , 2017, 2, 62.	2.3	15
59	Screening of the "Stasis Box"™ identifies two kinase inhibitors under pharmaceutical development with activity against <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , 2017, 10, 323.	2.5	22
60	Use of a bioinformatic-assisted primer design strategy to establish a new nested PCR-based method for <i>Cryptosporidium</i> . <i>Parasites and Vectors</i> , 2017, 10, 509.	2.5	18
61	Molecular investigation of <i>Cryptosporidium</i> and <i>Giardia</i> in pre- and post-weaned calves in Hubei Province, China. <i>Parasites and Vectors</i> , 2017, 10, 519.	2.5	37
62	<i>Pharyngostromylus thylogale</i> n. sp. (Nematoda: Strongylida) from the stomachs of macropodid marsupials defined by morphological and molecular criteria. <i>Systematic Parasitology</i> , 2016, 93, 749-760.	1.1	4
63	Molecular characterization of species of <i>Cloacina</i> (Strongyloidea: Cloacininae) from the common wallaroo, <i>Macropus robustus</i> (Marsupialia: Macropodidae) in Australia. <i>Infection, Genetics and Evolution</i> , 2016, 44, 245-253.	2.3	3
64	Is <i>Cryptosporidium</i> from the common wombat ( <i>Vombatus ursinus</i> ) a new species and distinct from <i>Cryptosporidium ubiquitum</i> ?. <i>Infection, Genetics and Evolution</i> , 2016, 44, 28-33.	2.3	6
65	Genomic resources for a unique, low-virulence <i>Babesia</i> taxon from China. <i>Parasites and Vectors</i> , 2016, 9, 564.	2.5	17
66	More parasitic myositis cases in humans in Australia, and the definition of genetic markers for the causative agents as a basis for molecular diagnosis. <i>Infection, Genetics and Evolution</i> , 2016, 44, 69-75.	2.3	4
67	<i>Cryptosporidium</i> and <i>Giardia</i> taxa in faecal samples from animals in catchments supplying the city of Melbourne with drinking water (2011 to 2015). <i>Parasites and Vectors</i> , 2016, 9, 315.	2.5	48
68	Phylogenetic relationships of species of the oesophageal parasitic nematode genera <i>Cyclostrongylus</i> and <i>Spirostrongylus</i> (Strongyloidea: Chabertiidae: Cloacininae) with their wallaby hosts (Marsupialia: Tj ETQq0 0 0 rgBT /Overlock 10 Tf		
69	Detection of cryptic species of <i>Rugopharynx</i> (Nematoda: Strongylida) from the stomachs of Australian macropodid marsupials. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2016, 5, 124-133.	1.5	12
70	Molecular analysis of <i>Cryptosporidium</i> from cattle from five states of Peninsular Malaysia. <i>Molecular and Cellular Probes</i> , 2016, 30, 39-43.	2.1	7
71	Genetic characterisation of <i>Taenia multiceps</i> cysts from ruminants in Greece. <i>Infection, Genetics and Evolution</i> , 2016, 38, 110-116.	2.3	18
72	Phylogenomic and biogeographic reconstruction of the <i>Trichinella</i> complex. <i>Nature Communications</i> , 2016, 7, 10513.	12.8	107

#	ARTICLE	IF	CITATIONS
73	The complement of family M1 aminopeptidases of <i>Haemonchus contortus</i> – Biotechnological implications. <i>Biotechnology Advances</i> , 2016, 34, 65-76.	11.7	8
74	Exploring molecular variation in <i>Schistosoma japonicum</i> in China. <i>Scientific Reports</i> , 2015, 5, 17345.	3.3	33
75	Detection of <i>Cyclospora</i> in captive chimpanzees and macaques by a quantitative PCR-based mutation scanning approach. <i>Parasites and Vectors</i> , 2015, 8, 274.	2.5	22
76	First Human Case of Fatal <i>Halicephalobus gingivalis</i> Meningoencephalitis in Australia. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1768-1774.	3.9	19
77	The barber's pole worm CAP protein superfamily – A basis for fundamental discovery and biotechnology advances. <i>Biotechnology Advances</i> , 2015, 33, 1744-1754.	11.7	16
78	Molecular detection of <i>Cyclospora</i> in water, soil, vegetables and humans in southern Italy signals a need for improved monitoring by health authorities. <i>International Journal of Food Microbiology</i> , 2015, 211, 95-100.	4.7	41
79	Mitochondrial genome of <i>Hypoderaeum conoideum</i> – comparison with selected trematodes. <i>Parasites and Vectors</i> , 2015, 8, 97.	2.5	30
80	Genetic analysis of <i>Giardia</i> and <i>Cryptosporidium</i> from people in Northern Australia using PCR-based tools. <i>Infection, Genetics and Evolution</i> , 2015, 36, 389-395.	2.3	25
81	The phylogenetic relationships of endemic Australasian trichostrongylin families (Nematoda: Tj ETQq1 1 0.784314 <sub>rgBT</sub> / Overlock 10 <sub>1.8</sub> / 6		
82	<i>Cryptosporidium cuniculus</i> - new records in human and kangaroo in Australia. <i>Parasites and Vectors</i> , 2014, 7, 492.	2.5	44
83	First genetic analysis of <i>Cryptosporidium</i> from humans from Tasmania, and identification of a new genotype from a traveller to Bali. <i>Electrophoresis</i> , 2014, 35, 2600-2607.	2.4	26
84	<i>Giardia/giardiasis</i> – A perspective on diagnostic and analytical tools. <i>Biotechnology Advances</i> , 2014, 32, 280-289.	11.7	73
85	<i>Cryptosporidium parvum</i> genotype IIa and <i>Giardia duodenalis</i> assemblage A in <i>Mytilus galloprovincialis</i> on sale at local food markets. <i>International Journal of Food Microbiology</i> , 2014, 171, 62-67.	4.7	33
86	Genetic variation within and among species of <i>Cloacina</i> (Strongyloidea: Cloacinine) from the swamp wallaby, <i>Wallabia bicolor</i> (Marsupialia: Macropodidae). <i>Infection, Genetics and Evolution</i> , 2014, 28, 261-269.	2.3	8
87	Mitochondrial genomes of <i>Trichinella</i> species and genotypes – a basis for diagnosis, and systematic and epidemiological explorations. <i>International Journal for Parasitology</i> , 2014, 44, 1073-1080.	3.1	40
88	Genetic identification of an oxyurid from a captive, black-handed spider monkey – implications for treatment and control. <i>Parasitology Research</i> , 2014, 113, 3445-3448.	1.6	5
89	Description of <i>Cloacina atthis</i> sp. nov. from the stomach of the euro ( <i>Macropus robustus</i> ) (Marsupialia: Macropodidae) from Western Australia based on morphological and molecular criteria. <i>Parasitology Research</i> , 2014, 113, 3485-3493.	1.6	11
90	First molecular characterization of <i>Cryptosporidium</i> and <i>Giardia</i> from bovines ( <i>Bos taurus</i> and) Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 60 Vectors, 2014, 7, 75.	2.5	34

#	ARTICLE	IF	CITATIONS
91	Unexpected occurrence of <i>Haemonchus placei</i> in cattle in southern Western Australia. <i>Infection, Genetics and Evolution</i> , 2014, 21, 252-258.	2.3	11
92	Molecular-based investigation of <i>Cryptosporidium</i> and <i>Giardia</i> from animals in water catchments in southeastern Australia. <i>Water Research</i> , 2013, 47, 1726-1740.	11.3	65
93	Getting to the guts of the matter: The status and potential of "omics" research of parasitic protists of the human gastrointestinal system. <i>International Journal for Parasitology</i> , 2013, 43, 971-982.	3.1	11
94	Genetic characterization of selected parasites from people with histories of gastrointestinal disorders using a mutation scanning-coupled approach. <i>Electrophoresis</i> , 2013, 34, 1720-1728.	2.4	47
95	Assessing calves as carriers of <i>Cryptosporidium</i> and <i>Giardia</i> with zoonotic potential on dairy and beef farms within a water catchment area by mutation scanning. <i>Electrophoresis</i> , 2013, 34, 2259-2267.	2.4	21
96	Upstream-downstream gradient in infection levels by fish parasites: a common river pattern?. <i>Parasitology</i> , 2013, 140, 266-274.	1.5	33
97	Clone-specific immune reactions in a trematode-crustacean system. <i>Parasitology</i> , 2012, 139, 128-136.	1.5	9
98	Disentangling phylogenetic constraints from selective forces in the evolution of trematode transmission stages. <i>Evolutionary Ecology</i> , 2012, 26, 1497-1512.	1.2	30
99	Genetic and phenotypic influences on clone-level success and host specialization in a generalist parasite. <i>Journal of Evolutionary Biology</i> , 2012, 25, 66-79.	1.7	15
100	Effects of wetland vs. landscape variables on parasite communities of <i>Rana pipiens</i> : links to anthropogenic factors. , 2011, 21, 1257-1271.		49
101	Genetic and environmental determinants of host use in the trematode <i>Maritrema novaezealandensis</i> (Microphallidae). <i>Parasitology</i> , 2011, 138, 100-106.	1.5	10
102	Intra- and interclonal phenotypic and genetic variability of the trematode <i>Maritrema novaezealandensis</i> . <i>Biological Journal of the Linnean Society</i> , 2011, 103, 106-116.	1.6	24
103	Variation of parasite load and immune parameters in two species of New Zealand shore crabs. <i>Parasitology Research</i> , 2011, 109, 759-767.	1.6	9
104	Host Partitioning by Parasites in an Intertidal Crustacean Community. <i>Journal of Parasitology</i> , 2010, 96, 862-868.	0.7	43
105	Avian influenza at both ends of a migratory flyway: characterizing viral genomic diversity to optimize surveillance plans for North America. <i>Evolutionary Applications</i> , 2009, 2, 457-468.	3.1	61
106	Trematode parasites of Otago Harbour (New Zealand) soft-sediment intertidal ecosystems: Life cycles, ecological roles and DNA barcodes. <i>New Zealand Journal of Marine and Freshwater Research</i> , 2009, 43, 857-865.	2.0	67
107	A Molecular View of the Superfamily Dioctophymatoidea (Nematoda). <i>Comparative Parasitology</i> , 2009, 76, 100-104.	0.4	12
108	Permanent Genetic Resources added to Molecular Ecology Resources database 1 January 2009-30 April 2009. <i>Molecular Ecology Resources</i> , 2009, 9, 1375-1379.	4.8	64

#	ARTICLE	IF	CITATIONS
109	Genetic evidence of intercontinental movement of avian influenza in a migratory bird: the northern pintail ( <i>Anas acuta</i> ). <i>Molecular Ecology</i> , 2008, 17, 4754-4762.	3.9	135
110	Beringia: Intercontinental exchange and diversification of high latitude mammals and their parasites during the Pliocene and Quaternary. <i>Mammal Study</i> , 2005, 30, S33-S44.	0.6	81
111	Influence of <i>Ribeiroia ondatrae</i> (Trematoda: Digenea) infection on limb development and survival of northern leopard frogs ( <i>Rana pipiens</i> ): effects of host stage and parasite-exposure level. <i>Canadian Journal of Zoology</i> , 2003, 81, 1144-1153.	1.0	73
112	Phylogeography of a Holarctic nematode, <i>Soboliphyme baturini</i> , among mustelids: climate change, episodic colonization, and diversification in a complex host-parasite system. <i>Biological Journal of the Linnean Society</i> , 0, 96, 651-663.	1.6	26
113	<i>Citellinema</i> (Nematoda: Heligmosomidae) from North America with descriptions of two new species from the red squirrel <i>Tamiasciurus hudsonicus</i> and one from the Canadian Woodchuck, <i>Marmota monax</i> . <i>Parasitology</i> , 0, , 1-51.	1.5	0