

Anson V Koehler

List of Publications by Year in descending order

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Version: 2024-02-01

113
papers

4,657
citations

172207

29
h-index

123241

61
g-index

113
all docs

113
docs citations

113
times ranked

7297
citing authors

#	ARTICLE	IF	CITATIONS
1	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	13.7	1,942
2	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.	2.0	135
3	Phylogenomic and biogeographic reconstruction of the <i>Trichinella</i> complex. <i>Nature Communications</i> , 2016, 7, 10513.	5.8	107
4	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.	0.2	81
5	Human toxocariasis – A look at a neglected disease through an epidemiological prism. <i>Infection, Genetics and Evolution</i> , 2019, 74, 104002.	1.0	76
6	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.	0.4	73
7	<i>Giardia/giardiasis</i> – A perspective on diagnostic and analytical tools. <i>Biotechnology Advances</i> , 2014, 32, 280-289.	6.0	73
8	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.	0.8	67
9	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.	5.3	65
10	Permanent Genetic Resources added to Molecular Ecology Resources database 1 January 2009–30 April 2009. <i>Molecular Ecology Resources</i> , 2009, 9, 1375-1379.	2.2	64
11	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.	1.5	61
12	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.	1.0	51
13	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.	0.9	50
14	Effects of wetland vs. landscape variables on parasite communities of <i>Rana pipiens</i> : links to anthropogenic factors. , 2011, 21, 1257-1271.		49
15	<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.	1.0	48
16	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.	1.3	47
17	<i>Cryptosporidium cuniculus</i> - new records in human and kangaroo in Australia. <i>Parasites and Vectors</i> , 2014, 7, 492.	1.0	44
18	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.	1.2	44

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19	Host Partitioning by Parasites in an Intertidal Crustacean Community. <i>Journal of Parasitology</i> , 2010, 96, 862-868.	0.3	43
20	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.	2.1	41
21	First detection and genetic characterisation of <i>Enterocytozoon bieneusi</i> in wild deer in Melbourne's water catchments in Australia. <i>Parasites and Vectors</i> , 2018, 11, 2.	1.0	41
22	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.	1.3	40
23	Somatic proteome of <i>Haemonchus contortus</i> . <i>International Journal for Parasitology</i> , 2019, 49, 311-320.	1.3	38
24	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.	1.0	37
25	First molecular characterization of <i>Cryptosporidium</i> and <i>Giardia</i> from bovines (<i>Bos taurus</i> and <i>Bos indicus</i>) in the Overlock 1000 water catchment in Australia. <i>Parasites and Vectors</i> , 2014, 7, 75.	1.0	34
26	Upstream-downstream gradient in infection levels by fish parasites: a common river pattern?. <i>Parasitology</i> , 2013, 140, 266-274.	0.7	33
27	<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.	2.1	33
28	Exploring molecular variation in <i>Schistosoma japonicum</i> in China. <i>Scientific Reports</i> , 2015, 5, 17345.	1.6	33
29	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.	1.4	33
30	<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.	0.6	33
31	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.	1.0	31
32	Disentangling phylogenetic constraints from selective forces in the evolution of trematode transmission stages. <i>Evolutionary Ecology</i> , 2012, 26, 1497-1512.	0.5	30
33	Mitochondrial genome of <i>Hypoderaeum conoideum</i> – comparison with selected trematodes. <i>Parasites and Vectors</i> , 2015, 8, 97.	1.0	30
34	The developmental lipidome of <i>Haemonchus contortus</i> . <i>International Journal for Parasitology</i> , 2018, 48, 887-895.	1.3	30
35	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.	1.3	30
36	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.	1.0	29

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37	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.	1.6	29
38	Parasites of the Giant Panda: A Risk Factor in the Conservation of a Species. <i>Advances in Parasitology</i> , 2018, 99, 1-33.	1.4	28
39	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.	0.7	26
40	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.	1.3	26
41	<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.	0.8	26
42	<i>Enterocytozoon bienersi</i> of animals – With an “Australian twist”. <i>Advances in Parasitology</i> , 2021, 111, 1-73.	1.4	26
43	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.	1.0	25
44	Assessing the anthelmintic activity of pyrazole-5-carboxamide derivatives against <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , 2017, 10, 272.	1.0	25
45	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.	1.0	25
46	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.	0.7	24
47	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.	1.0	22
48	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.	1.0	22
49	<i>Enterocytozoon bienersi</i> genotypes in people with gastrointestinal disorders in Queensland and Western Australia. <i>Infection, Genetics and Evolution</i> , 2018, 65, 293-299.	1.0	22
50	<i>Enterocytozoon bienersi</i> genotypes in cats and dogs in Victoria, Australia. <i>BMC Microbiology</i> , 2019, 19, 183.	1.3	22
51	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.	1.3	21
52	An improved method for PCR-based detection and routine monitoring of geosmin-producing cyanobacterial blooms. <i>Water Research</i> , 2018, 136, 34-40.	5.3	20
53	New operational taxonomic units of <i>Enterocytozoon</i> in three marsupial species. <i>Parasites and Vectors</i> , 2018, 11, 371.	1.0	20
54	First Human Case of Fatal <i>Halicephalobus gingivalis</i> Meningoencephalitis in Australia. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1768-1774.	1.8	19

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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.	0.7	19
56	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.	0.8	19
57	Genetic characterisation of <i>Taenia multiceps</i> cysts from ruminants in Greece. <i>Infection, Genetics and Evolution</i> , 2016, 38, 110-116.	1.0	18
58	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.	1.0	18
59	Genomic resources for a unique, low-virulence <i>Babesia</i> taxon from China. <i>Parasites and Vectors</i> , 2016, 9, 564.	1.0	17
60	Phylogenetic analysis of the Australasian paralysis ticks and their relatives (Ixodidae: Ixodes:). <i>Trends in Parasitology</i> , 2017, 32, 542-547.	1.0	17
61	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.	1.2	17
62	The barber's pole worm CAP protein superfamily: A basis for fundamental discovery and biotechnology advances. <i>Biotechnology Advances</i> , 2015, 33, 1744-1754.	6.0	16
63	Age of first infection across a range of parasite taxa in a wild mammalian population. <i>Biology Letters</i> , 2020, 16, 20190811.	1.0	16
64	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.	0.8	15
65	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.	1.0	15
66	Application of PCR-Based Tools to Explore Strongyloides Infection in People in Parts of Northern Australia. <i>Tropical Medicine and Infectious Disease</i> , 2017, 2, 62.	0.9	15
67	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.	1.0	15
68	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.	1.4	15
69	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.	1.3	15
70	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.	1.2	14
71	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.	1.0	13
72	A Molecular View of the Superfamily Dioctophymatoidea (Nematoda). <i>Comparative Parasitology</i> , 2009, 76, 100-104.	0.0	12

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73	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.	0.6	12
74	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.	1.3	11
75	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.	0.6	11
76	Unexpected occurrence of <i>Haemonchus placei</i> in cattle in southern Western Australia. <i>Infection, Genetics and Evolution</i> , 2014, 21, 252-258.	1.0	11
77	Genetic and environmental determinants of host use in the trematode <i>Maritrema novaezealandensis</i> (Microphallidae). <i>Parasitology</i> , 2011, 138, 100-106.	0.7	10
78	The apicoplast genomes of two taxonomic units of <i>Babesia</i> from sheep. <i>Veterinary Parasitology</i> , 2017, 233, 123-128.	0.7	10
79	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.	1.0	10
80	Selected ß-pyrone 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.	1.4	10
81	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.	1.6	10
82	Variation of parasite load and immune parameters in two species of New Zealand shore crabs. <i>Parasitology Research</i> , 2011, 109, 759-767.	0.6	9
83	Clone-specific immune reactions in a trematode-crustacean system. <i>Parasitology</i> , 2012, 139, 128-136.	0.7	9
84	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.	1.4	9
85	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.	1.0	8
86	The complement of family M1 aminopeptidases of <i>Haemonchus contortus</i> – Biotechnological implications. <i>Biotechnology Advances</i> , 2016, 34, 65-76.	6.0	8
87	Speciation in the genus <i>Cloacina</i> (Nematoda: Strongylida): species flocks and intra-host speciation. <i>Parasitology</i> , 2017, 144, 1828-1840.	0.7	8
88	Molecular analysis of <i>Cryptosporidium</i> from cattle from five states of Peninsular Malaysia. <i>Molecular and Cellular Probes</i> , 2016, 30, 39-43.	0.9	7
89	The phylogenetic relationships of endemic Australasian trichostrongylin families (Nematoda: Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.8	6
90	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.	1.0	6

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91	Mitochondrial genomes of two Babesia taxa from sheep in China as a foundation for population genetic and epidemiological investigations. Infection, Genetics and Evolution, 2017, 47, 51-55.	1.0	6
92	Marked mitochondrial genetic variation in individuals and populations of the carcinogenic liver fluke Clonorchis sinensis. PLoS Neglected Tropical Diseases, 2020, 14, e0008480.	1.3	6
93	A Targeted "Next-Generation" Sequencing-Informatic Approach to Define Genetic Diversity in Theileria orientalis Populations within Individual Cattle: Proof-of-Principle. Pathogens, 2020, 9, 448.	1.2	6
94	Genetic identification of an oxyurid from a captive, black-handed spider monkey" implications for treatment and control. Parasitology Research, 2014, 113, 3445-3448.	0.6	5
95	Using PCR-Based Sequencing to Diagnose Haycocknema perplexum Infection in Human Myositis Case, Australia. Emerging Infectious Diseases, 2018, 24, 2368-2370.	2.0	5
96	Phylogenetic Analysis of Mitogenomic Data Sets Resolves the Relationship of Seven Macropostrongyloides Species from Australian Macropodid and Vombatid Marsupials. Pathogens, 2020, 9, 1042.	1.2	5
97	Molecular detection of Strongyloides sp. in Australian Thoroughbred foals. Parasites and Vectors, 2021, 14, 444.	1.0	5
98	Pharyngostrongylus thylogale n. sp. (Nematoda: Strongylida) from the stomachs of macropodid marsupials defined by morphological and molecular criteria. Systematic Parasitology, 2016, 93, 749-760.	0.5	4
99	More parasitic myositis cases in humans in Australia, and the definition of genetic markers for the causative agents as a basis for molecular diagnosis. Infection, Genetics and Evolution, 2016, 44, 69-75.	1.0	4
100	Phylogenetic relationships of species of the oesophageal parasitic nematode genera Cyclostrongylus and Spirostrongylus (Strongyloidea: Chabertiidae: Cloacininae) with their wallaby hosts (Marsupialia: Tj ETQq0 0 0 0gBT /Overlock 10 Tf	0.5	4
101	PCR-coupled sequencing achieves specific diagnosis of onchocerciasis in a challenging clinical case, to underpin effective treatment and clinical management. Infection, Genetics and Evolution, 2018, 66, 192-194.	1.0	4
102	Ocular Filariasis in Human Caused by Breinlia (Johnstonema) annulipapillata Nematode, Australia. Emerging Infectious Diseases, 2021, 27, 297-300.	2.0	4
103	Molecular characterization of species of Cloacina (Strongyloidea: Cloacininae) from the common wallaroo, Macropus robustus (Marsupialia: Macropodidae) in Australia. Infection, Genetics and Evolution, 2016, 44, 245-253.	1.0	3
104	Phylogenetic relationships of three tribes of cloacinine nematodes (Strongylida: Chabertiidae) from macropodid marsupials. Journal of Helminthology, 2019, 93, 486-493.	0.4	3
105	Multiplex PCRs for the specific identification of marsupial and deer species from faecal samples as a basis for non-invasive epidemiological studies of parasites. Parasites and Vectors, 2020, 13, 144.	1.0	3
106	Detection of Breinlia sp. (Nematoda) in the Leadbeater's possum (Gymnobelideus leadbeateri). International Journal for Parasitology: Parasites and Wildlife, 2021, 15, 249-254.	0.6	3
107	Cryptosporidium of birds in pet markets in Wuhan city, Hubei, China. Current Research in Parasitology and Vector-borne Diseases, 2021, 1, 100025.	0.7	3
108	Cryptosporidium cf. avium in an inland-bearded dragon (Pogona vitticeps) " A case report and review of the literature. International Journal for Parasitology: Parasites and Wildlife, 2020, 13, 150-159.	0.6	2

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109	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.	1.0	2
110	Use of Markers to Determine <i>Cryptosporidium</i> Genotypes for Epidemiology Tracking and Detection. <i>Methods in Molecular Biology</i> , 2020, 2052, 117-127.	0.4	2
111	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.	0.5	2
112	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.	0.6	1
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.	0.7	0