Charlotte L Oskam

List of Publications by Year
in descending order

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60	2,367	236925 25	214800 47
papers	citations	h-index	g-index

63	63	63	3125
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	First record of the stump-tailed lizard tick, Amblyomma albolimbatum (Ixodida, Ixodidae) parasitising a human.. Ticks and Tick-borne Diseases, 2022, 13, 101873.	2.7	3
2	Cryptosporidium abrahamseni n. sp. (Apicomplexa: Cryptosporidiidae) from red-eye tetra (Moenkhausia) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.2	27
3	Molecular analysis of cryptosporidiosis cases in Western Australia in 2019 and 2020 supports the occurrence of two swimming pool associated outbreaks and reveals the emergence of a rare C. hominis IbA12G3 subtype. Infection, Genetics and Evolution, 2021, 92, 104859.	2.3	12
4	Haemoprotozoan surveillance in peri-urban native and introduced wildlife from Australia. Current Research in Parasitology and Vector-borne Diseases, 2021, 1, 100052.	1.9	8
5	Illuminating the bacterial microbiome of Australian ticks with 16S and Rickettsia-specific next-generation sequencing. Current Research in Parasitology and Vector-borne Diseases, 2021, 1, 100037.	1.9	9
6	Zoonotic infection by Cryptosporidium fayeri IVgA10G1T1R1 in a Western Australian human. Zoonoses and Public Health, 2021, 68, 358-360.	2.2	7
7	Knowledge, Attitude and Practices Towards Cryptosporidium Among Public Swimming Pool Patrons and Staff in Western Australia. Acta Parasitologica, 2021, , 1.	1.1	1
8	The bacterial biome of ticks and their wildlife hosts at the urbanâ€“wildland interface. Microbial Genomics, 2021, 7, .	2.0	8
9	Comment on: Gupta, 2019, distinction between Borrelia and Borreliella is more robustly supported by molecular and phenotypic characteristics than all other neighbouring prokaryotic genera: Response to Margosâ€™ et al. â€œThe genus Borrelia reloadedâ€•(PLoS One 13(12): e0208432). PLoS One 14(8):e0221397. Ticks and Tick-borne Diseases, 2020, 11, 101320.	2.7	6
10	Cryptosporidium bollandi n. sp. (Apicomplexa: Cryptosporidiidae) from angelfish (Pterophyllum scalare) and Oscar fish (Astronotus ocellatus). Experimental Parasitology, 2020, 217, 107956.	1.2	25
11	Blood Parasites in Endangered Wildlife-Trypanosomes Discovered during a Survey of Haemoprotozoa from the Tasmanian Devil. Pathogens, 2020, 9, 873.	2.8	8
12	Molecular identification of the Trypanosoma (Herpetosoma) lewisi clade in black rats (Rattus rattus) from Australia. Parasitology Research, 2020, 119, 1691-1696.	1.6	11
13	First glimpse into the origin and spread of the Asian longhorned tick, Haemaphysalis longicornis, in the United States. Zoonoses and Public Health, 2020, 67, 637-650.	2.2	61
14	Bacterial community profiling highlights complex diversity and novel organisms in wildlife ticks. Ticks and Tick-borne Diseases, 2020, 11, 101407.	2.7	13
15	Molecular Characterization of Haemaphysalis Species and a Molecular Genetic Key for the Identification of Haemaphysalis of North America. Frontiers in Veterinary Science, 2020, 7, 141.	2.2	20
16	Rejection of the name Borreliella and all proposed species comb. nov. placed therein. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3577-3581.	1.7	43
17	Comparison of morphological and molecular methods to identify the diet of a generalist omnivore. Wildlife Research, 2020, , .	1.4	2
18	Automatic Barcode Gap Discovery reveals large COI intraspecific divergence in Australian Ixodidae . Zootaxa, 2019, 4656, 393-396.	0.5	6

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19	Retrospective analysis of Cryptosporidium species in Western Australian human populations (2015â€“2018), and emergence of the C. hominis IfA12G1R5 subtype. Infection, Genetics and Evolution, 2019, 73, 306-313.	2.3	28
20	Response to the Letter to the Editor by Harris. Parasites and Vectors, 2019, 12, 178.	2.5	6
21	Sequence analyses at mitochondrial and nuclear loci reveal a novel Theileria sp. and aid in the phylogenetic resolution of piroplasms from Australian marsupials and ticks. PLoS ONE, 2019, 14, e0225822.	2.5	19
22	Detecting respiratory bacterial communities of wild dolphins: implications for animal health. Marine Ecology - Progress Series, 2019, 622, 203-217.	1.9	15
23	Identification of Theileria fuliginosa-like species in Ixodes australiensis ticks from western grey kangaroos (Macropus fuliginosus) in Western Australia. Ticks and Tick-borne Diseases, 2018, 9, 632-637.	2.7	6
24	Cryptosporidium species and subtypes in animals inhabiting drinking water catchments in three states across Australia. Water Research, 2018, 134, 327-340.	11.3	54
25	Australian penguin ticks screened for novel Borrelia species. Ticks and Tick-borne Diseases, 2018, 9, 410-414.	2.7	2
26	A novel Ehrlichia species in blood and Ixodes ornithorhynchi ticks from platypuses (Ornithorhynchus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.7	23
27	Endemic, exotic and novel apicomplexan parasites detected during a national study of ticks from companion animals in Australia. Parasites and Vectors, 2018, 11, 197.	2.5	49
28	The genus Borrelia reloaded. PLoS ONE, 2018, 13, e0208432.	2.5	88
29	Genome-wide analysis of Borrelia turcica and â€˜Candidatus Borrelia tachyglossiâ€™ shows relapsing fever-like genomes with unique genomic links to Lyme disease Borrelia. Infection, Genetics and Evolution, 2018, 66, 72-81.	2.3	28
30	Molecular surveillance of piroplasms in ticks from small and medium-sized urban and peri-urban mammals in Australia. International Journal for Parasitology: Parasites and Wildlife, 2018, 7, 197-203.	1.5	12
31	An Australian dog diagnosed with an exotic tick-borne infection: should Australia still be considered free from Hepatozoon canis?. International Journal for Parasitology, 2018, 48, 805-815.	3.1	10
32	Profiling the diversity of Cryptosporidium species and genotypes in wastewater treatment plants in Australia using next generation sequencing. Science of the Total Environment, 2018, 644, 635-648.	8.0	45
33	Recent insights into the tick microbiome gained through next-generation sequencing. Parasites and Vectors, 2018, 11, 12.	2.5	146
34	Bacterial tick-associated infections in Australia: current studies and future directions. Microbiology Australia, 2018, 39, 200.	0.4	3
35	Rethinking Coxiella infections in Australia. Microbiology Australia, 2018, 39, 223.	0.4	3
36	Molecular investigation into the presence of a Coxiella sp. in Rhipicephalus sanguineus ticks in Australia. Veterinary Microbiology, 2017, 201, 141-145.	1.9	15

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37	Characterization of two complete Isospora mitochondrial genomes from passerine birds: Isospora serinuse in a domestic canary and Isospora manorinae in a yellow-throated miner. Veterinary Parasitology, 2017, 237, 137-142.	1.8	8
38	Next Generation Sequencing uncovers within-host differences in the genetic diversity of Cryptosporidium gp60 subtypes. International Journal for Parasitology, 2017, 47, 601-607.	3.1	38
39	New Technologies for Detection of Enteric Parasites. Trends in Parasitology, 2017, 33, 532-546.	3.3	94
40	New host records for ticks (Acari : Ixodidae) from the echidna (Tachyglossus aculeatus) revealed in Australian museum survey. Australian Journal of Zoology, 2017, 65, 379.	1.0	2
41	Molecular characterization of â€˜Candidatus Borrelia tachyglossiâ€™ (family Spirochaetaceae) in echidna ticks, Bothriocroton concolor. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 1075-1080.	1.7	39
42	Novel Borrelia species detected in echidna ticks, Bothriocroton concolor, in Australia. Parasites and Vectors, 2016, 9, 339.	2.5	63
43	A survey of ticks (Acari: Ixodidae) of companion animals in Australia. Parasites and Vectors, 2016, 9, 207.	2.5	42
44	Zoonotic Cryptosporidium Species in Animals Inhabiting Sydney Water Catchments. PLoS ONE, 2016, 11, e0168169.	2.5	47
45	Inhibition of the endosymbiont â€œCandidatus Midichloria mitochondriiâ€•during 16S rRNA gene profiling reveals potential pathogens in Ixodes ticks from Australia. Parasites and Vectors, 2015, 8, 345.	2.5	95
46	Utilising Mobile-Augmented Reality for Learning Human Anatomy. Procedia, Social and Behavioral Sciences, 2015, 197, 659-668.	0.5	99
47	Bacterial Profiling Reveals Novel â€œCa. Neoehrlichiaâ€, Ehrlichia, and Anaplasma Species in Australian Human-Biting Ticks. PLoS ONE, 2015, 10, e0145449.	2.5	58
48	Extinct New Zealand megafauna were not in decline before human colonization. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4922-4927.	7.1	109
49	An extremely low-density human population exterminated New Zealand moa. Nature Communications, 2014, 5, 5436.	12.8	42
50	High-precision dating and ancient DNA profiling of moa (Aves: Dinornithiformes) eggshell documents a complex feature at Wairau Bar and refines the chronology of New Zealand settlement by Polynesians. Journal of Archaeological Science, 2014, 50, 24-30.	2.4	38
51	Ancient DNA analyses of early archaeological sites in New Zealand reveal extreme exploitation of moa (Aves: Dinornithiformes) at all life stages. Quaternary Science Reviews, 2012, 52, 41-48.	3.0	20
52	The half-life of DNA in bone: measuring decay kinetics in 158 dated fossils. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 4724-4733.	2.6	478
53	A molecular characterization of a newly discovered megafaunal fossil site in North Canterbury, South Island, New Zealand. Journal of the Royal Society of New Zealand, 2012, 42, 241-256.	1.9	6
54	DNA Extraction from Fossil Eggshell. Methods in Molecular Biology, 2012, 840, 65-70.	0.9	5

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55	Quantitative Real-Time PCR in aDNA Research. Methods in Molecular Biology, 2012, 840, 121-132.	0.9	13
56	Profiling the Dead: Generating Microsatellite Data from Fossil Bones of Extinct Megafaunaâ€"Protocols, Problems, and Prospects. PLoS ONE, 2011, 6, e16670.	2.5	39
57	Molecular and morphological analyses of avian eggshell excavated from a late thirteenth century earth oven. Journal of Archaeological Science, 2011, , .	2.4	12
58	Bizygomatic breadth determination in damaged skulls. International Journal of Osteoarchaeology, 2010, 20, 540-548.	1.2	1
59	Fossil avian eggshell preserves ancient DNA. Proceedings of the Royal Society B: Biological Sciences, 2010, 277, 1991-2000.	2.6	103
60	Identification of microsatellites from an extinct moa species using high-throughput (454) sequence data. BioTechniques, 2009, 46, 195-200.	1.8	94