Andrea Paparini

List of Publications by Year
in descending order

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43 papers	1,780 citations	249298 26 h-index	299063 42 g-index
43 all docs	43 docs citations	43 times ranked	2426 citing authors

#	Article	IF	Citations
1	Population structure and genetic diversity of Trichomonas vaginalis clinical isolates in Australia and Ghana. Infection, Genetics and Evolution, 2020, 82, 104318.	1.0	5
2	Establishment of Coral-Bacteria Symbioses Reveal Changes in the Core Bacterial Community With Host Ontogeny. Frontiers in Microbiology, 2019, 10, 1529.	1.5	50
3	No evidence for widespread Babesia microti transmission in Australia. Transfusion, 2019, 59, 2368-2374.	0.8	8
4	Identification of eukaryotic microorganisms with 18S rRNA next-generation sequencing in wastewater treatment plants, with a more targeted NGS approach required for Cryptosporidium detection. Water Research, 2019, 158, 301-312.	5.3	41
5	Evaluation of 16S next-generation sequencing of hypervariable region 4 in wastewater samples: An unsuitable approach for bacterial enteric pathogen identification. Science of the Total Environment, 2019, 670, 1111-1124.	3.9	44
6	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.	1.1	6
7	A novel Ehrlichia species in blood and Ixodes ornithorhynchi ticks from platypuses (Ornithorhynchus) Tj ETQq1 1 0.784314 rgBT /Ove	1.1	23
8	Direct oxygen uptake from air by novel glycogen accumulating organism dominated biofilm minimizes excess sludge production. Science of the Total Environment, 2018, 640-641, 80-88.	3.9	11
9	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.	1.3	10
10	Recent insights into the tick microbiome gained through next-generation sequencing. Parasites and Vectors, 2018, 11, 12.	1.0	146
11	Prevalence, genetic diversity and potential clinical impact of blood-borne and enteric protozoan parasites in native mammals from northern Australia. Veterinary Parasitology, 2017, 238, 94-105.	0.7	18
12	Next Generation Sequencing uncovers within-host differences in the genetic diversity of Cryptosporidium gp60 subtypes. International Journal for Parasitology, 2017, 47, 601-607.	1.3	38
13	Rapid adaptation of activated sludge bacteria into a glycogen accumulating biofilm enabling anaerobic BOD uptake. Bioresource Technology, 2017, 228, 1-8.	4.8	24
14	New Technologies for Detection of Enteric Parasites. Trends in Parasitology, 2017, 33, 532-546.	1.5	94
15	Cryptosporidium in fish: alternative sequencing approaches and analyses at multiple loci to resolve mixed infections. Parasitology, 2017, 144, 1811-1820.	0.7	21
16	Novel Primer Sets for Next Generation Sequencing-Based Analyses of Water Quality. PLoS ONE, 2017, 12, e0170008.	1.1	8
17	Increased genetic diversity and prevalence of co-infection with Trypanosoma spp. in koalas (Phascolarctos cinereus) and their ticks identified using next-generation sequencing (NGS). PLoS ONE, 2017, 12, e0181279.	1.1	41
18	It's official â€“ Cryptosporidium is a gregarine: What are the implications for the water industry?. Water Research, 2016, 105, 305-313.	5.3	110

#	Article	IF	Citations
19	Public health significance of zoonotic Cryptosporidium species in wildlife: Critical insights into better drinking water management. International Journal for Parasitology: Parasites and Wildlife, 2016, 5, 88-109.	0.6	142
20	Molecular characterization of native Australian trypanosomes in quokka (Setonix brachyurus) populations from Western Australia. Parasitology International, 2016, 65, 205-208.	0.6	4
21	First report of Trypanosoma vegrandis in koalas (Phascolarctos cinereus). Parasitology International, 2016, 65, 316-318.	0.6	10
22	Zoonotic Cryptosporidium Species in Animals Inhabiting Sydney Water Catchments. PLoS ONE, 2016, 11, e0168169.	1.1	47
23	A simple method to test the reproducibility of the phylogenetic reconstructions: the molecular systematics of cyanobacteria as a case study. Fottea, 2016, 16, 209-217.	0.4	0
24	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.	1.0	95
25	Theileria annae (syn. Babesia microti-like) infection in dogs in NW Spain detected using direct and indirect diagnostic techniques: clinical report of 75 cases. Parasites and Vectors, 2015, 8, 217.	1.0	48
26	First Molecular Characterization of Theileria ornithorhynchi Mackerras, 1959: yet Another Challenge to the Systematics of the Piroplasms. Protist, 2015, 166, 609-620.	0.6	18
27	Cryptosporidium huwi n. sp. (Apicomplexa: Eimeriidae) from the guppy (Poecilia reticulata). Experimental Parasitology, 2015, 150, 31-35.	0.5	64
28	Comparison of Sanger and next generation sequencing performance for genotyping Cryptosporidium isolates at the 18S rRNA and actin loci. Experimental Parasitology, 2015, 151-152, 21-27.	0.5	32
29	Genetic diversity of Cryptosporidium in fish at the 18S and actin loci and high levels of mixed infections. Veterinary Parasitology, 2015, 214, 255-263.	0.7	29
30	Bacterial Profiling Reveals Novel â€œCa. Neoehrlichiaâ€; Ehrlichia, and Anaplasma Species in Australian Human-Biting Ticks. PLoS ONE, 2015, 10, e0145449.	1.1	58
31	Comparison of next-generation droplet digital PCR (ddPCR) with quantitative PCR (qPCR) for enumeration of Cryptosporidium oocysts in faecal samples. International Journal for Parasitology, 2014, 44, 1105-1113.	1.3	152
32	Novel genotypes of Trypanosoma binneyi from wild platypuses (Ornithorhynchus anatinus) and identification of a leech as a potential vector. Experimental Parasitology, 2014, 145, 42-50.	0.5	26
33	Piroplasms of New Zealand seabirds. Parasitology Research, 2014, 113, 4407-4414.	0.6	20
34	Molecular confirmation of the first autochthonous case of human babesiosis in Australia using a novel primer set for the beta-tubulin gene. Experimental Parasitology, 2014, 141, 93-97.	0.5	19
35	Polyphasic identification of cyanobacterial isolates from Australia. Water Research, 2014, 59, 248-261.	5.3	27
36	Multiple Cryptosporidium genotypes detected in wild black rats (Rattus rattus) from northern Australia. Experimental Parasitology, 2012, 131, 404-412.	0.5	31

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37	First report of human babesiosis in Australia. Medical Journal of Australia, 2012, 196, 350-352.	0.8	61
38	Identification of novel Babesia and Theileria genotypes in the endangered marsupials, the woylie (Bettongia penicillata ogilbyi) and boodie (Bettongia lesueur). Experimental Parasitology, 2012, 131, 25-30.	0.5	38
39	Identification of novel trypanosome genotypes in native Australian marsupials. Veterinary Parasitology, 2011, 183, 21-30.	0.7	36
40	ACTN3 Genotyping by Real-Time PCR in the Italian Population and Athletes. Medicine and Science in Sports and Exercise, 2007, 39, 810-815.	0.2	46
41	Swimming pools and fungi: An environmental epidemiology survey in Italian indoor swimming facilities. International Journal of Environmental Health Research, 2007, 17, 197-206.	1.3	40
42	Gene Transfer and Cauliflower Mosaic Virus Promoter 35S Activity in Mammalian Cells. Journal of Environmental Science and Health - Part B Pesticides, Food Contaminants, and Agricultural Wastes, 2006, 41, 437-449.	0.7	8
43	Public health issues related with the consumption of food obtained from genetically modified organisms. Biotechnology Annual Review, 2004, 10, 85-122.	2.1	31