

# Andrea Papparini

## List of Publications by Year in descending order

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Version: 2024-02-01

43  
papers

1,780  
citations

218677

26  
h-index

265206

42  
g-index

43  
all docs

43  
docs citations

43  
times ranked

2239  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparison of next-generation droplet digital PCR (ddPCR) with quantitative PCR (qPCR) for enumeration of <i>Cryptosporidium</i> oocysts in faecal samples. <i>International Journal for Parasitology</i> , 2014, 44, 1105-1113.	3.1	152
2	Recent insights into the tick microbiome gained through next-generation sequencing. <i>Parasites and Vectors</i> , 2018, 11, 12.	2.5	146
3	Public health significance of zoonotic <i>Cryptosporidium</i> species in wildlife: Critical insights into better drinking water management. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2016, 5, 88-109.	1.5	142
4	It's official "Cryptosporidium is a gregarine: What are the implications for the water industry?". <i>Water Research</i> , 2016, 105, 305-313.	11.3	110
5	Inhibition of the endosymbiont "Candidatus <i>Midichloria mitochondrii</i> " during 16S rRNA gene profiling reveals potential pathogens in <i>Ixodes</i> ticks from Australia. <i>Parasites and Vectors</i> , 2015, 8, 345.	2.5	95
6	New Technologies for Detection of Enteric Parasites. <i>Trends in Parasitology</i> , 2017, 33, 532-546.	3.3	94
7	<i>Cryptosporidium huwi</i> n. sp. (Apicomplexa: Eimeriidae) from the guppy ( <i>Poecilia reticulata</i> ). <i>Experimental Parasitology</i> , 2015, 150, 31-35.	1.2	64
8	First report of human babesiosis in Australia. <i>Medical Journal of Australia</i> , 2012, 196, 350-352.	1.7	61
9	Bacterial Profiling Reveals Novel "Ca. <i>Neoehrlichia</i> ", Ehrlichia, and Anaplasma Species in Australian Human-Biting Ticks. <i>PLoS ONE</i> , 2015, 10, e0145449.	2.5	58
10	Establishment of Coral-Bacteria Symbioses Reveal Changes in the Core Bacterial Community With Host Ontogeny. <i>Frontiers in Microbiology</i> , 2019, 10, 1529.	3.5	50
11	<i>Theileria annae</i> (syn. <i>Babesia microti</i> -like) infection in dogs in NW Spain detected using direct and indirect diagnostic techniques: clinical report of 75 cases. <i>Parasites and Vectors</i> , 2015, 8, 217.	2.5	48
12	Zoonotic <i>Cryptosporidium</i> Species in Animals Inhabiting Sydney Water Catchments. <i>PLoS ONE</i> , 2016, 11, e0168169.	2.5	47
13	ACTN3 Genotyping by Real-Time PCR in the Italian Population and Athletes. <i>Medicine and Science in Sports and Exercise</i> , 2007, 39, 810-815.	0.4	46
14	Evaluation of 16S next-generation sequencing of hypervariable region 4 in wastewater samples: An unsuitable approach for bacterial enteric pathogen identification. <i>Science of the Total Environment</i> , 2019, 670, 1111-1124.	8.0	44
15	Increased genetic diversity and prevalence of co-infection with <i>Trypanosoma</i> spp. in koalas ( <i>Phascolarctos cinereus</i> ) and their ticks identified using next-generation sequencing (NGS). <i>PLoS ONE</i> , 2017, 12, e0181279.	2.5	41
16	Identification of eukaryotic microorganisms with 18S rRNA next-generation sequencing in wastewater treatment plants, with a more targeted NGS approach required for <i>Cryptosporidium</i> detection. <i>Water Research</i> , 2019, 158, 301-312.	11.3	41
17	Swimming pools and fungi: An environmental epidemiology survey in Italian indoor swimming facilities. <i>International Journal of Environmental Health Research</i> , 2007, 17, 197-206.	2.7	40
18	Identification of novel <i>Babesia</i> and <i>Theileria</i> genotypes in the endangered marsupials, the woylie ( <i>Bettongia penicillata ogilbyi</i> ) and boodie ( <i>Bettongia lesueur</i> ). <i>Experimental Parasitology</i> , 2012, 131, 25-30.	1.2	38

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19	Next Generation Sequencing uncovers within-host differences in the genetic diversity of <i>Cryptosporidium</i> gp60 subtypes. <i>International Journal for Parasitology</i> , 2017, 47, 601-607.	3.1	38
20	Identification of novel trypanosome genotypes in native Australian marsupials. <i>Veterinary Parasitology</i> , 2011, 183, 21-30.	1.8	36
21	Comparison of Sanger and next generation sequencing performance for genotyping <i>Cryptosporidium</i> isolates at the 18S rRNA and actin loci. <i>Experimental Parasitology</i> , 2015, 151-152, 21-27.	1.2	32
22	Public health issues related with the consumption of food obtained from genetically modified organisms. <i>Biotechnology Annual Review</i> , 2004, 10, 85-122.	2.1	31
23	Multiple <i>Cryptosporidium</i> genotypes detected in wild black rats ( <i>Rattus rattus</i> ) from northern Australia. <i>Experimental Parasitology</i> , 2012, 131, 404-412.	1.2	31
24	Genetic diversity of <i>Cryptosporidium</i> in fish at the 18S and actin loci and high levels of mixed infections. <i>Veterinary Parasitology</i> , 2015, 214, 255-263.	1.8	29
25	Polyphasic identification of cyanobacterial isolates from Australia. <i>Water Research</i> , 2014, 59, 248-261.	11.3	27
26	Novel genotypes of <i>Trypanosoma binneyi</i> from wild platypuses ( <i>Ornithorhynchus anatinus</i> ) and identification of a leech as a potential vector. <i>Experimental Parasitology</i> , 2014, 145, 42-50.	1.2	26
27	Rapid adaptation of activated sludge bacteria into a glycogen accumulating biofilm enabling anaerobic BOD uptake. <i>Bioresource Technology</i> , 2017, 228, 1-8.	9.6	24
28	A novel Ehrlichia species in blood and Ixodes ornithorhynchi ticks from platypuses ( <i>Ornithorhynchus</i> ) Tj ETQq0 0 0 ggBT /Overlock 10 Tf	2.7	23
29	<i>Cryptosporidium</i> in fish: alternative sequencing approaches and analyses at multiple loci to resolve mixed infections. <i>Parasitology</i> , 2017, 144, 1811-1820.	1.5	21
30	Piroplasms of New Zealand seabirds. <i>Parasitology Research</i> , 2014, 113, 4407-4414.	1.6	20
31	Molecular confirmation of the first autochthonous case of human babesiosis in Australia using a novel primer set for the beta-tubulin gene. <i>Experimental Parasitology</i> , 2014, 141, 93-97.	1.2	19
32	First Molecular Characterization of <i>Theileria ornithorhynchi</i> Mackerras, 1959: yet Another Challenge to the Systematics of the Piroplasms. <i>Protist</i> , 2015, 166, 609-620.	1.5	18
33	Prevalence, genetic diversity and potential clinical impact of blood-borne and enteric protozoan parasites in native mammals from northern Australia. <i>Veterinary Parasitology</i> , 2017, 238, 94-105.	1.8	18
34	Direct oxygen uptake from air by novel glycogen accumulating organism dominated biofilm minimizes excess sludge production. <i>Science of the Total Environment</i> , 2018, 640-641, 80-88.	8.0	11
35	First report of <i>Trypanosoma vegrandis</i> in koalas ( <i>Phascolarctos cinereus</i> ). <i>Parasitology International</i> , 2016, 65, 316-318.	1.3	10
36	An Australian dog diagnosed with an exotic tick-borne infection: should Australia still be considered free from <i>Hepatozoon canis</i> ?. <i>International Journal for Parasitology</i> , 2018, 48, 805-815.	3.1	10

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37	Gene Transfer and Cauliflower Mosaic Virus Promoter 35S Activity in Mammalian Cells. <i>Journal of Environmental Science and Health - Part B Pesticides, Food Contaminants, and Agricultural Wastes</i> , 2006, 41, 437-449.	1.5	8
38	Novel Primer Sets for Next Generation Sequencing-Based Analyses of Water Quality. <i>PLoS ONE</i> , 2017, 12, e0170008.	2.5	8
39	No evidence for widespread <i>Babesia microti</i> transmission in Australia. <i>Transfusion</i> , 2019, 59, 2368-2374.	1.6	8
40	Identification of <i>Theileria fuliginosa</i> -like species in <i>Ixodes australiensis</i> ticks from western grey kangaroos ( <i>Macropus fuliginosus</i> ) in Western Australia. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 632-637.	2.7	6
41	Population structure and genetic diversity of <i>Trichomonas vaginalis</i> clinical isolates in Australia and Ghana. <i>Infection, Genetics and Evolution</i> , 2020, 82, 104318.	2.3	5
42	Molecular characterization of native Australian trypanosomes in quokka ( <i>Setonix brachyurus</i> ) populations from Western Australia. <i>Parasitology International</i> , 2016, 65, 205-208.	1.3	4
43	A simple method to test the reproducibility of the phylogenetic reconstructions: the molecular systematics of cyanobacteria as a case study. <i>Fottea</i> , 2016, 16, 209-217.	0.9	0