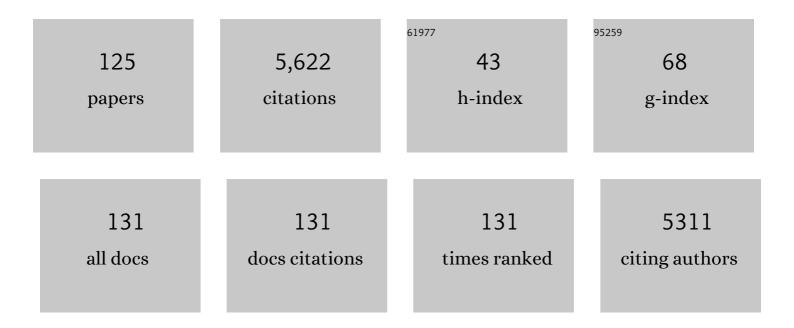
## Cinzia Cantacessi

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Whole-genome sequence of Schistosoma haematobium. Nature Genetics, 2012, 44, 221-225.	21.4	383
2	Ascaris suum draft genome. Nature, 2011, 479, 529-533.	27.8	246
3	Impact of Experimental Hookworm Infection on the Human Gut Microbiota. Journal of Infectious Diseases, 2014, 210, 1431-1434.	4.0	153
4	Unlocking the Transcriptomes of Two Carcinogenic Parasites, Clonorchis sinensis and Opisthorchis viverrini. PLoS Neglected Tropical Diseases, 2010, 4, e719.	3.0	141
5	Carcinogenic Liver Fluke Secretes Extracellular Vesicles That Promote Cholangiocytes to Adopt a Tumorigenic Phenotype. Journal of Infectious Diseases, 2015, 212, 1636-1645.	4.0	141
6	A portrait of the "SCP/TAPS―proteins of eukaryotes — Developing a framework for fundamental research and biotechnological outcomes. Biotechnology Advances, 2009, 27, 376-388.	11.7	139
7	The role of wild canids and felids in spreading parasites to dogs and cats in Europe. Part II: Helminths and arthropods. Veterinary Parasitology, 2015, 213, 24-37.	1.8	139
8	Elucidating the transcriptome of Fasciola hepatica — A key to fundamental and biotechnological discoveries for a neglected parasite. Biotechnology Advances, 2010, 28, 222-231.	11.7	119
9	Phortica variegata as an intermediate host of Thelazia callipaeda under natural conditions: Evidence for pathogen transmission by a male arthropod vector. International Journal for Parasitology, 2006, 36, 1167-1173.	3.1	113
10	Lungworms and gastrointestinal parasites of domestic cats: a European perspective. International Journal for Parasitology, 2017, 47, 517-528.	3.1	113
11	Schistosoma mansoni infection is associated with quantitative and qualitative modifications of the mammalian intestinal microbiota. Scientific Reports, 2018, 8, 12072.	3.3	112
12	This Gut Ain't Big Enough for Both of Us. Or Is It? Helminth–Microbiota Interactions in Veterinary Species. Trends in Parasitology, 2017, 33, 619-632.	3.3	105
13	Infections by human gastrointestinal helminths are associated with changes in faecal microbiota diversity and composition. PLoS ONE, 2017, 12, e0184719.	2.5	100
14	Nematode biology and larval development of Thelazia callipaeda (Spirurida, Thelaziidae) in the drosophilid intermediate host in Europe and China. Parasitology, 2005, 131, 847.	1.5	96
15	Human Thelaziosis—A Neglected Parasitic Disease of the Eye. Journal of Parasitology, 2006, 92, 872-876.	0.7	95
16	The past, present, and future of Leishmania genomics and transcriptomics. Trends in Parasitology, 2015, 31, 100-108.	3.3	90
17	Secreted Proteomes of Different Developmental Stages of the Gastrointestinal Nematode Nippostrongylus brasiliensis. Molecular and Cellular Proteomics, 2014, 13, 2736-2751.	3.8	88
18	Experimental hookworm infection and escalating gluten challenges are associated with increased microbial richness in celiac subjects. Scientific Reports, 2015, 5, 13797.	3.3	86

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19	The role of wild canids and felids in spreading parasites to dogs and cats in Europe. Veterinary Parasitology, 2015, 213, 12-23.	1.8	86
20	A Portrait of the Transcriptome of the Neglected Trematode, Fasciola gigantica—Biological and Biotechnological Implications. PLoS Neglected Tropical Diseases, 2011, 5, e1004.	3.0	84
21	The zoophilic fruitfly Phortica variegata: morphology, ecology and biological niche. Medical and Veterinary Entomology, 2006, 20, 358-364.	1.5	83
22	Suppression of inflammation by helminths: a role for the gut microbiota?. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140296.	4.0	78
23	Efficacy of a combination of 10% imidacloprid/50% permethrin for the prevention of leishmaniasis in kennelled dogs in an endemic area. Veterinary Parasitology, 2007, 144, 270-278.	1.8	77
24	First reports of autochthonous eyeworm infection by Thelazia callipaeda (Spirurida, Thelaziidae) in dogs and cat from France. Veterinary Parasitology, 2007, 149, 294-297.	1.8	73
25	Heterochronic faecal transplantation boosts gut germinal centres in aged mice. Nature Communications, 2019, 10, 2443.	12.8	72
26	Massively Parallel Sequencing and Analysis of the Necator americanus Transcriptome. PLoS Neglected Tropical Diseases, 2010, 4, e684.	3.0	66
27	A practical, bioinformatic workflow system for large data sets generated by next-generation sequencing. Nucleic Acids Research, 2010, 38, e171-e171.	14.5	62
28	Morphological and molecular differentiation between Dicrocoelium dendriticum (Rudolphi, 1819) and Dicrocoelium chinensis (Sudarikov and Ryjikov, 1951) Tang and Tang, 1978 (Platyhelminthes: Digenea). Acta Tropica, 2007, 104, 91-98.	2.0	61
29	Changes in duodenal tissue-associated microbiota following hookworm infection and consecutive gluten challenges in humans with coeliac disease. Scientific Reports, 2016, 6, 36797.	3.3	59
30	First transcriptomic analysis of the economically important parasitic nematode, Trichostrongylus colubriformis, using a next-generation sequencing approach. Infection, Genetics and Evolution, 2010, 10, 1199-1207.	2.3	55
31	Helminth infections and gut microbiota – a feline perspective. Parasites and Vectors, 2016, 9, 625.	2.5	54
32	Bovine theileriosis – An emerging problem in south-eastern Australia?. Infection, Genetics and Evolution, 2011, 11, 2095-2097.	2.3	52
33	Prevention of Canine Leishmaniosis in a Hyper-Endemic Area Using a Combination of 10% Imidacloprid/4.5% Flumethrin. PLoS ONE, 2013, 8, e56374.	2.5	52
34	A comprehensive analysis of the faecal microbiome and metabolome of Strongyloides stercoralis infected volunteers from a non-endemic area. Scientific Reports, 2018, 8, 15651.	3.3	51
35	The specific identification of anisakid larvae from fishes from the Yellow Sea, China, using mutation scanning-coupled sequence analysis of nuclear ribosomal DNA. Molecular and Cellular Probes, 2007, 21, 386-390.	2.1	49
36	Helminth-microbiota cross-talk – A journey through the vertebrate digestive system. Molecular and Biochemical Parasitology, 2019, 233, 111222.	1.1	49

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37	Genetic characterization of three unique operational taxonomic units of Eimeria from chickens in Australia based on nuclear spacer ribosomal DNA. Veterinary Parasitology, 2008, 152, 226-234.	1.8	47
38	Differences in transcription between free-living and CO2-activated third-stage larvae of Haemonchus contortus. BMC Genomics, 2010, 11, 266.	2.8	47
39	Probing of a Human Proteome Microarray With a Recombinant Pathogen Protein Reveals a Novel Mechanism by Which Hookworms Suppress B-Cell Receptor Signaling. Journal of Infectious Diseases, 2015, 211, 416-425.	4.0	47
40	Efficacy of a combination of imidacloprid 10%/permethrin 50% versus fipronil 10%/(S)-methoprene 12%, against ticks in naturally infected dogs. Veterinary Parasitology, 2005, 130, 293-304.	1.8	46
41	Efficacy of an imidacloprid/flumethrin collar against fleas, ticks and tick-borne pathogens in dogs. Parasites and Vectors, 2013, 6, 245.	2.5	46
42	Tissue-specific transcriptomes of Anisakis simplex (sensu stricto) and Anisakis pegreffii reveal potential molecular mechanisms involved in pathogenicity. Parasites and Vectors, 2018, 11, 31.	2.5	46
43	SCP/TAPS proteins in helminths $\hat{a}$ €" Where to from now?. Molecular and Cellular Probes, 2012, 26, 54-59.	2.1	44
44	The Transcriptome of Trichuris suis – First Molecular Insights into a Parasite with Curative Properties for Key Immune Diseases of Humans. PLoS ONE, 2011, 6, e23590.	2.5	43
45	The Anisakis Transcriptome Provides a Resource for Fundamental and Applied Studies on Allergy-Causing Parasites. PLoS Neglected Tropical Diseases, 2016, 10, e0004845.	3.0	41
46	Occurrence of strongyloidiasis in privately owned and sheltered dogs: clinical presentation and treatment outcome. Parasites and Vectors, 2017, 10, 345.	2.5	40
47	Helminths and microbes within the vertebrate gut – not all studies are created equal. Parasitology, 2019, 146, 1371-1378.	1.5	40
48	Infection with the sheep gastrointestinal nematode Teladorsagia circumcincta increases luminal pathobionts. Microbiome, 2020, 8, 60.	11.1	40
49	The relationships between faecal egg counts and gut microbial composition in UK Thoroughbreds infected by cyathostomins. International Journal for Parasitology, 2018, 48, 403-412.	3.1	39
50	Hookworm Treatment for Relapsing Multiple Sclerosis. JAMA Neurology, 2020, 77, 1089.	9.0	39
51	Feline lungworms unlock a novel mode of parasite transmission. Scientific Reports, 2015, 5, 13105.	3.3	38
52	Key strongylid nematodes of animals — Impact of next-generation transcriptomics on systems biology and biotechnology. Biotechnology Advances, 2012, 30, 469-488.	11.7	37
53	Application of 10% imidacloprid/50% permethrin to prevent Ehrlichia canis exposure in dogs under natural conditions. Veterinary Parasitology, 2008, 153, 320-328.	1.8	36
54	Gastropod-Borne Helminths: A Look at the Snail–Parasite Interplay. Trends in Parasitology, 2016, 32, 255-264.	3.3	36

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55	Helminth Microbiomes â $\in$ " A Hidden Treasure Trove?. Trends in Parasitology, 2019, 35, 13-22.	3.3	36
56	A Deep Exploration of the Transcriptome and "Excretory/Secretory―Proteome of Adult Fascioloides magna. Molecular and Cellular Proteomics, 2012, 11, 1340-1353.	3.8	35
57	First Report of Thelazia callipaeda (Spirurida, Thelaziidae) in Wolves in Italy. Journal of Wildlife Diseases, 2007, 43, 508-511.	0.8	34
58	Molecular mechanisms of hookworm disease: Stealth, virulence, and vaccines. Journal of Allergy and Clinical Immunology, 2012, 130, 13-21.	2.9	34
59	Comparative analyses of mitochondrial and nuclear genetic markers for the molecular identification of Rhipicephalus spp Infection, Genetics and Evolution, 2013, 20, 422-427.	2.3	34
60	Deep insights into Dictyocaulus viviparus transcriptomes provides unique prospects for new drug targets and disease intervention. Biotechnology Advances, 2011, 29, 261-271.	11.7	31
61	A genome-wide analysis of annexins from parasitic organisms and their vectors. Scientific Reports, 2013, 3, 2893.	3.3	31
62	DNA technological progress toward advanced diagnostic tools to support human hookworm control. Biotechnology Advances, 2008, 26, 35-45.	11.7	30
63	Classic Models for New Perspectives: Delving into Helminth–Microbiota–Immune System Interactions. Trends in Parasitology, 2018, 34, 640-654.	3.3	29
64	Atypical (RIO) protein kinases from Haemonchus contortus — Promise as new targets for nematocidal drugs. Biotechnology Advances, 2011, 29, 338-350.	11.7	28
65	Risk factors for canine neosporosis in farm and kennel dogs in southern Italy. Veterinary Parasitology, 2007, 145, 240-244.	1.8	27
66	Genomic-Bioinformatic Analysis of Transcripts Enriched in the Third-Stage Larva of the Parasitic Nematode Ascaris suum. PLoS Neglected Tropical Diseases, 2008, 2, e246.	3.0	27
67	Dollfustrema durum n. sp. and Heterobucephalopsis perardua n. sp. (Digenea: Bucephalidae) from the giant moray eel, Gymnothorax javanicus (Bleeker) (Anguilliformes: Muraenidae), and proposal of the Heterobucephalopsinae n. subfam. Parasitology International, 2015, 64, 559-570.	1.3	27
68	Dysbiosis associated with acute helminth infections in herbivorous youngstock – observations and implications. Scientific Reports, 2019, 9, 11121.	3.3	27
69	MICHELINdb: a web-based tool for mining of helminth-microbiota interaction datasets, and a meta-analysis of current research. Microbiome, 2020, 8, 10.	11.1	27
70	Progress on the transcriptomics of carcinogenic liver flukes of humans—Unique biological and biotechnological prospects. Biotechnology Advances, 2010, 28, 859-870.	11.7	26
71	Tick vectors of Cercopithifilaria bainae in dogs: Rhipicephalus sanguineus sensu lato versus Ixodes ricinus. Parasitology Research, 2013, 112, 3013-3017.	1.6	26
72	Chronic polyarthritis associated to Cercopithifilaria bainae infection in a dog. Veterinary Parasitology, 2014, 205, 401-404.	1.8	25

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73	Evaluation of blood and bone marrow in selected canine vector-borne diseases. Parasites and Vectors, 2014, 7, 534.	2.5	25
74	Angiostrongylus chabaudi in felids: New findings and a review of the literature. Veterinary Parasitology, 2016, 228, 188-192.	1.8	25
75	Molecular characterization of selected dermatophytes and their identification by electrophoretic mutation scanning. Electrophoresis, 2009, 30, 3555-3564.	2.4	24
76	Exclusive dependence of IL-10R $\hat{l}$ ± signalling on intestinal microbiota homeostasis and control of whipworm infection. PLoS Pathogens, 2019, 15, e1007265.	4.7	24
77	Comparative Transcriptomics Reveals Clues for Differences in Pathogenicity between Hysterothylacium aduncum, Anisakis simplex sensu stricto and Anisakis pegreffii. Genes, 2020, 11, 321.	2.4	24
78	Insights into SCP/TAPS Proteins of Liver Flukes Based on Large-Scale Bioinformatic Analyses of Sequence Datasets. PLoS ONE, 2012, 7, e31164.	2.5	24
79	Bioinformatics meets parasitology. Parasite Immunology, 2012, 34, 265-275.	1.5	23
80	Getting the most out of parasitic helminth transcriptomes using HelmDB: Implications for biology and biotechnology. Biotechnology Advances, 2013, 31, 1109-1119.	11.7	23
81	Vertical transmission of Anaplasma platys and Leishmania infantum in dogs during the first half of gestation. Parasites and Vectors, 2016, 9, 269.	2.5	23
82	Molecular characterization and phylogenesis of Steganinae (Diptera, Drosophilidae) inferred by the mitochondrial cytochrome c oxidase subunit 1. Medical and Veterinary Entomology, 2008, 22, 37-47.	1.5	21
83	Cryptic Parasite Revealed. Advances in Parasitology, 2011, 77, 141-173.	3.2	21
84	Baseline Gut Microbiota Composition Is Associated With Schistosoma mansoni Infection Burden in Rodent Models. Frontiers in Immunology, 2020, 11, 593838.	4.8	21
85	Cyathostomine egg reappearance period following ivermectin treatment in a cohort of UK Thoroughbreds. Parasites and Vectors, 2018, 11, 61.	2.5	20
86	Helminths, hosts, and their microbiota: new avenues for managing gastrointestinal helminthiases in ruminants. Expert Review of Anti-Infective Therapy, 2020, 18, 977-985.	4.4	20
87	A preliminary investigation of serological tools for the detection of Onchocerca lupi infection in dogs. Parasitology Research, 2014, 113, 1989-1991.	1.6	19
88	Cardicola beveridgei n. sp. (Digenea: Aporocotylidae) from the mangrove jack, Lutjanus argentimaculatus (Perciformes: Lutjanidae), and C. bullardi n. sp. from the Australian spotted mackerel, Scomberomorus munroi (Perciformes: Scombridae), from the northern Great Barrier Reef. Parasitology International, 2014, 63, 735-745.	1.3	19
89	Improved molecular diagnostic tools for human hookworms. Expert Review of Molecular Diagnostics, 2009, 9, 17-21.	3.1	18
90	TIMPs of parasitic helminths – a large-scale analysis of high-throughput sequence datasets. Parasites and Vectors, 2013, 6, 156.	2.5	18

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91	Proteomic profile of Bithynia siamensis goniomphalos snails upon infection with the carcinogenic liver fluke Opisthorchis viverrini. Journal of Proteomics, 2015, 113, 281-291.	2.4	17
92	Experimental infection with the hookworm, Necator americanus, is associated with stable gut microbial diversity in human volunteers with relapsing multiple sclerosis. BMC Biology, 2021, 19, 74.	3.8	17
93	Bioinformatic analysis of abundant, gender-enriched transcripts of adult Ascaris suum (Nematoda) using a semi-automated workflow platform. Molecular and Cellular Probes, 2009, 23, 205-217.	2.1	16
94	Novel Inhibitor Cystine Knot Peptides from Momordica charantia. PLoS ONE, 2013, 8, e75334.	2.5	16
95	Coming out of the Shell: Building the Molecular Infrastructure for Research on Parasite-Harbouring Snails. PLoS Neglected Tropical Diseases, 2013, 7, e2284.	3.0	15
96	RNA-Seq Reveals Infection-Induced Gene Expression Changes in the Snail Intermediate Host of the Carcinogenic Liver Fluke, Opisthorchis viverrini. PLoS Neglected Tropical Diseases, 2014, 8, e2765.	3.0	14
97	RORÎ <sup>3</sup> t+ Treg to Th17 ratios correlate with susceptibility to Giardia infection. Scientific Reports, 2019, 9, 20328.	3.3	14
98	Investigation of the regulation of transcriptional changes in Ancylostoma caninum larvae following serum activation, with a focus on the insulin-like signalling pathway. Veterinary Parasitology, 2009, 159, 139-148.	1.8	13
99	Differential Protein Expression in the Hemolymph of Bithynia siamensis goniomphalos Infected with Opisthorchis viverrini. PLoS Neglected Tropical Diseases, 2016, 10, e0005104.	3.0	12
100	Parasitic helminths and the host microbiome – a missing â€~extracellular vesicle-sized' link?. Trends in Parasitology, 2022, 38, 737-747.	3.3	12
101	Exploring transcriptional conservation between Ancylostoma caninum and Haemonchus contortus by oligonucleotide microarray and bioinformatic analyses. Molecular and Cellular Probes, 2009, 23, 1-9.	2.1	11
102	Filaria martis Gmelin 1790 (Spirurida, Filariidae) affecting beech marten (Martes foina): morphological description and molecular characterisation of the cytochrome oxidase c subunit I. Parasitology Research, 2007, 101, 877-883.	1.6	10
103	Parasite transmission by insects: a female affair?. Trends in Parasitology, 2008, 24, 116-120.	3.3	10
104	High-intensity cardiac infections of Phthinomita heinigerae n. sp. (Digenea: Aporocotylidae) in the orangelined cardinalfish, Taeniamia fucata (Cantor), off Heron Island on the Great Barrier Reef. Parasitology International, 2016, 65, 371-377.	1.3	10
105	A new PCR assay for the detection and differentiation of Babesia canis and Babesia vogeli. Ticks and Tick-borne Diseases, 2017, 8, 862-865.	2.7	10
106	<i>Oestrus ovis</i> causing human ocular myiasis: from countryside to town centre. Clinical and Experimental Ophthalmology, 2009, 37, 327-328.	2.6	9
107	Molecular characterization and phylogenetic inferences of <i>Dermanyssus gallinae</i> isolates in <scp>I</scp> taly within an <scp>E</scp> uropean framework. Medical and Veterinary Entomology, 2014, 28, 447-452.	1.5	9
108	A bug's life: Delving into the challenges of helminth microbiome studies. PLoS Neglected Tropical Diseases, 2020, 14, e0008446.	3.0	9

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109	The best type of inoculum for testing the antifungal drug susceptibility of <i>Microsporum canis</i> : In vivo and in vitro results. Mycoses, 2020, 63, 711-716.	4.0	9
110	Impact of Next-Generation Technologies on Exploring Socioeconomically Important Parasites and Developing New Interventions. Methods in Molecular Biology, 2015, 1247, 437-474.	0.9	9
111	Filarial infection caused by Onchocerca boehmi (Supperer, 1953) in a horse from Italy. Parasitology Research, 2017, 116, 191-198.	1.6	8
112	First laboratory culture ofPhortica variegata(Diptera, Steganinae), a vector ofThelazia callipaeda. Journal of Vector Ecology, 2012, 37, 458-461.	1.0	7
113	Worms and bugs of the gut: the search for diagnostic signatures using barcoding, and metagenomics–metabolomics. Parasites and Vectors, 2022, 15, 118.	2.5	7
114	Molecular identification of Phortica variegata and Phortica semivirgo (Drosophilidae, Steganinae) by PCR-RFLP of the mitochondrial cytochrome oxidase c subunit I gene. Parasitology Research, 2008, 103, 727-730.	1.6	6
115	Data set from the proteomic analysis of Bithynia siamensis goniomphalos snails upon infection with the carcinogenic liver fluke Opisthorchis viverrini. Data in Brief, 2015, 2, 16-20.	1.0	6
116	Virulence and in vitro antifungal susceptibility of Candida albicans and Candida catenulata from laying hens. International Microbiology, 2021, 24, 57-63.	2.4	6
117	Vaccination against the brown stomach worm, Teladorsagia circumcincta, followed by parasite challenge, induces inconsistent modifications in gut microbiota composition of lambs. Parasites and Vectors, 2021, 14, 189.	2.5	6
118	Investigation of Host–Microbe–Parasite Interactions in an In Vitro 3D Model of the Vertebrate Gut. Advanced Biology, 2022, 6, .	2.5	6
119	Heartworm Genomics: Unprecedented Opportunities for Fundamental Molecular Insights and New Intervention Strategies. Topics in Companion Animal Medicine, 2011, 26, 193-199.	0.9	5
120	Gut-microbiota-derived extracellular vesicles: Overlooked mediators in host–helminth interactions?. Trends in Parasitology, 2021, 37, 690-693.	3.3	5
121	Serum amyloid A levels and alpha 2 and gamma globulins on serum protein electrophoresis in cats exposed to and infected with Leishmania infantum. Parasites and Vectors, 2021, 14, 217.	2.5	4
122	MIxS-SA: a MIxS extension defining the minimum information standard for sequence data from symbiont-associated micro-organisms. ISME Communications, 2022, 2, .	4.2	3
123	Major prospects for exploring canine vector borne diseases and novel intervention methods using 'omic technologies. Parasites and Vectors, 2011, 4, 53.	2.5	2
124	Helminth Microbiota Profiling Using Bacterial 16S rRNA Gene Amplicon Sequencing: From Sampling to Sequence Data Mining. Methods in Molecular Biology, 2021, 2369, 263-298.	0.9	1
125	Editorial: Systems Biology of Hosts, Parasites and Vectors. Frontiers in Cellular and Infection Microbiology, 2021, 11, 796475.	3.9	0