

# Makedonka Mitreva

## List of Publications by Year in descending order

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208  
papers

25,341  
citations

31949

53  
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7511

151  
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223  
all docs

223  
docs citations

223  
times ranked

32614  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , 2012, 486, 207-214.	13.7	9,614
2	A framework for human microbiome research. <i>Nature</i> , 2012, 486, 215-221.	13.7	2,249
3	Metabolic Reconstruction for Metagenomic Data and Its Application to the Human Microbiome. <i>PLoS Computational Biology</i> , 2012, 8, e1002358.	1.5	939
4	Genomic variation landscape of the human gut microbiome. <i>Nature</i> , 2013, 493, 45-50.	13.7	783
5	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008, 453, 175-183.	13.7	657
6	A Catalog of Reference Genomes from the Human Microbiome. <i>Science</i> , 2010, 328, 994-999.	6.0	621
7	A Systematic Analysis of Biosynthetic Gene Clusters in the Human Microbiome Reveals a Common Family of Antibiotics. <i>Cell</i> , 2014, 158, 1402-1414.	13.5	573
8	Draft Genome of the Filarial Nematode Parasite <i>Brugia malayi</i> . <i>Science</i> , 2007, 317, 1756-1760.	6.0	571
9	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	13.7	541
10	Alpha-gliadin genes from the A, B, and D genomes of wheat contain different sets of celiac disease epitopes. <i>BMC Genomics</i> , 2006, 7, 1.	1.2	445
11	Metabolic and metagenomic outcomes from early-life pulsed antibiotic treatment. <i>Nature Communications</i> , 2015, 6, 7486.	5.8	317
12	The <i>Pristionchus pacificus</i> genome provides a unique perspective on nematode lifestyle and parasitism. <i>Nature Genetics</i> , 2008, 40, 1193-1198.	9.4	310
13	The draft genome of the parasitic nematode <i>Trichinella spiralis</i> . <i>Nature Genetics</i> , 2011, 43, 228-235.	9.4	285
14	A transcriptomic analysis of the phylum Nematoda. <i>Nature Genetics</i> , 2004, 36, 1259-1267.	9.4	239
15	Microbiome Signatures Associated With Steatohepatitis and Moderate to Severe Fibrosis in Children With Nonalcoholic Fatty Liver Disease. <i>Gastroenterology</i> , 2019, 157, 1109-1122.	0.6	184
16	Widespread Colonization of the Lung by <i>Tropheryma whippelii</i> in HIV Infection. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2013, 187, 1110-1117.	2.5	175
17	Genome of the human hookworm <i>Necator americanus</i> . <i>Nature Genetics</i> , 2014, 46, 261-269.	9.4	166
18	Sepsis From the Gut: The Enteric Habitat of Bacteria That Cause Late-Onset Neonatal Bloodstream Infections. <i>Clinical Infectious Diseases</i> , 2014, 58, 1211-1218.	2.9	160

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19	Deep small RNA sequencing from the nematode <i>Ascaris</i> reveals conservation, functional diversification, and novel developmental profiles. <i>Genome Research</i> , 2011, 21, 1462-1477.	2.4	158
20	Responses to acute infection with SARS-CoV-2 in the lungs of rhesus macaques, baboons and marmosets. <i>Nature Microbiology</i> , 2021, 6, 73-86.	5.9	156
21	Impact of Experimental Hookworm Infection on the Human Gut Microbiota. <i>Journal of Infectious Diseases</i> , 2014, 210, 1431-1434.	1.9	153
22	Comparative genomics of nematodes. <i>Trends in Genetics</i> , 2005, 21, 573-581.	2.9	141
23	Dynamic Changes in the Subgingival Microbiome and Their Potential for Diagnosis and Prognosis of Periodontitis. <i>MBio</i> , 2015, 6, e01926-14.	1.8	139
24	Analysis and functional classification of transcripts from the nematode <i>Meloidogyne incognita</i> . <i>Genome Biology</i> , 2003, 4, R26.	13.9	133
25	RNAi Effector Diversity in Nematodes. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1176.	1.3	119
26	Exploration of bacterial community classes in major human habitats. <i>Genome Biology</i> , 2014, 15, R66.	13.9	109
27	Endosymbiont DNA in Endobacteria-Free Filarial Nematodes Indicates Ancient Horizontal Genetic Transfer. <i>PLoS ONE</i> , 2010, 5, e11029.	1.1	105
28	Differential human gut microbiome assemblages during soil-transmitted helminth infections in Indonesia and Liberia. <i>Microbiome</i> , 2018, 6, 33.	4.9	102
29	Silencing of Germline-Expressed Genes by DNA Elimination in Somatic Cells. <i>Developmental Cell</i> , 2012, 23, 1072-1080.	3.1	101
30	Genomes of <i>Fasciola hepatica</i> from the Americas Reveal Colonization with <i>Neorickettsia</i> Endobacteria Related to the Agents of Potomac Horse and Human Sennetsu Fevers. <i>PLoS Genetics</i> , 2017, 13, e1006537.	1.5	100
31	The Prevalence of Species and Strains in the Human Microbiome: A Resource for Experimental Efforts. <i>PLoS ONE</i> , 2014, 9, e97279.	1.1	93
32	<i>Mycobacterium tuberculosis</i> carrying a rifampicin drug resistance mutation reprograms macrophage metabolism through cell wall lipid changes. <i>Nature Microbiology</i> , 2018, 3, 1099-1108.	5.9	90
33	Secreted Proteomes of Different Developmental Stages of the Gastrointestinal Nematode <i>Nippostrongylus brasiliensis</i> . <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2736-2751.	2.5	88
34	Comparative Genomics of Gene Expression in the Parasitic and Free-Living Nematodes <i>Strongyloides stercoralis</i> and <i>Caenorhabditis elegans</i> . <i>Genome Research</i> , 2004, 14, 209-220.	2.4	87
35	Helminth-induced arginase-1 exacerbates lung inflammation and disease severity in tuberculosis. <i>Journal of Clinical Investigation</i> , 2015, 125, 4699-4713.	3.9	87
36	Helminth Genomics: The Implications for Human Health. <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e538.	1.3	86

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37	Experimental hookworm infection and escalating gluten challenges are associated with increased microbial richness in celiac subjects. <i>Scientific Reports</i> , 2015, 5, 13797.	1.6	86
38	Life Cycle Stage-resolved Proteomic Analysis of the Excretome/Secretome from <i>Strongyloides ratti</i> —Identification of Stage-specific Proteases. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.010157.	2.5	78
39	Nematode.net: a tool for navigating sequences from parasitic and free-living nematodes. <i>Nucleic Acids Research</i> , 2004, 32, 423D-426.	6.5	76
40	IFN signaling and neutrophil degranulation transcriptional signatures are induced during SARS-CoV-2 infection. <i>Communications Biology</i> , 2021, 4, 290.	2.0	74
41	Novel venom gene discovery in the platypus. <i>Genome Biology</i> , 2010, 11, R95.	13.9	72
42	A Symbiont-Independent Endo-1,4- $\beta$ -Xylanase from the Plant-Parasitic Nematode <i>Meloidogyne incognita</i> . <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 521-529.	1.4	71
43	Discovery of Anthelmintic Drug Targets and Drugs Using Chokeypoints in Nematode Metabolic Pathways. <i>PLoS Pathogens</i> , 2013, 9, e1003505.	2.1	69
44	Genomic introgression mapping of field-derived multiple-anthelmintic resistance in <i>Teladorsagia circumcincta</i> . <i>PLoS Genetics</i> , 2017, 13, e1006857.	1.5	67
45	Massively Parallel Sequencing and Analysis of the <i>Necator americanus</i> Transcriptome. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e684.	1.3	66
46	Mining the secretome of the root-knot nematode <i>Meloidogyne chitwoodi</i> for candidate parasitism genes. <i>Molecular Plant Pathology</i> , 2007, 9, 071031023555002-???	2.0	62
47	A practical, bioinformatic workflow system for large data sets generated by next-generation sequencing. <i>Nucleic Acids Research</i> , 2010, 38, e171-e171.	6.5	62
48	400,000 nematode ESTs on the Net. <i>Trends in Parasitology</i> , 2003, 19, 283-286.	1.5	61
49	Codon usage patterns in Nematoda: analysis based on over 25 million codons in thirty-two species. <i>Genome Biology</i> , 2006, 7, R75.	13.9	60
50	Changes in duodenal tissue-associated microbiota following hookworm infection and consecutive gluten challenges in humans with coeliac disease. <i>Scientific Reports</i> , 2016, 6, 36797.	1.6	59
51	Helminth.net: expansions to Nematode.net and an introduction to Trematode.net. <i>Nucleic Acids Research</i> , 2015, 43, D698-D706.	6.5	58
52	The Dynamic Genome and Transcriptome of the Human Fungal Pathogen <i>Blastomyces</i> and Close Relative <i>Emmonsia</i> . <i>PLoS Genetics</i> , 2015, 11, e1005493.	1.5	57
53	Gene discovery in the adenophorean nematode <i>Trichinella spiralis</i> : an analysis of transcription from three life cycle stages. <i>Molecular and Biochemical Parasitology</i> , 2004, 137, 277-291.	0.5	56
54	First transcriptomic analysis of the economically important parasitic nematode, <i>Trichostrongylus colubriformis</i> , using a next-generation sequencing approach. <i>Infection, Genetics and Evolution</i> , 2010, 10, 1199-1207.	1.0	55

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55	Role of Horizontal Gene Transfer in the Evolution of Plant Parasitism Among Nematodes. <i>Methods in Molecular Biology</i> , 2009, 532, 517-535.	0.4	54
56	Monocyte dysregulation and systemic inflammation during pediatric falciparum malaria. <i>JCI Insight</i> , 2017, 2, .	2.3	54
57	Exploring the transcriptome of the burrowing nematode <i>Radopholus similis</i> . <i>Molecular Genetics and Genomics</i> , 2008, 280, 1-17.	1.0	53
58	The effect of dietary resistant starch type 2 on the microbiota and markers of gut inflammation in rural Malawi children. <i>Microbiome</i> , 2015, 3, 37.	4.9	53
59	Genomic diversity in <i>Onchocerca volvulus</i> and its <i>Wolbachia</i> endosymbiont. <i>Nature Microbiology</i> , 2017, 2, 16207.	5.9	53
60	Immune correlates of tuberculosis disease and risk translate across species. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	52
61	mRNA sequences for <i>Haemonchus contortus</i> intestinal cathepsin B-like cysteine proteases display an extreme in abundance and diversity compared with other adult mammalian parasitic nematodes. <i>Molecular and Biochemical Parasitology</i> , 2004, 137, 297-305.	0.5	51
62	Expressed sequence tags of the peanut pod nematode <i>Ditylenchus africanus</i> : The first transcriptome analysis of an Anguinid nematode. <i>Molecular and Biochemical Parasitology</i> , 2009, 167, 32-40.	0.5	50
63	Genome-Wide Tissue-Specific Gene Expression, Co-expression and Regulation of Co-expressed Genes in Adult Nematode <i>Ascaris suum</i> . <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2678.	1.3	50
64	Characterizing <i>Ancylostoma caninum</i> transcriptome and exploring nematode parasitic adaptation. <i>BMC Genomics</i> , 2010, 11, 307.	1.2	48
65	Optimizing Read Mapping to Reference Genomes to Determine Composition and Species Prevalence in Microbial Communities. <i>PLoS ONE</i> , 2012, 7, e36427.	1.1	48
66	Investigating hookworm genomes by comparative analysis of two <i>Ancylostoma</i> species. <i>BMC Genomics</i> , 2005, 6, 58.	1.2	47
67	Targeting Lysine Deacetylases (KDACs) in Parasites. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0004026.	1.3	47
68	Detection of putative secreted proteins in the plant-parasitic nematode <i>Heterodera schachtii</i> . <i>Parasitology Research</i> , 2006, 98, 414-424.	0.6	46
69	Transcriptome Analysis of Female and Male <i>Xiphophorus maculatus</i> Jp 163 A. <i>PLoS ONE</i> , 2011, 6, e18379.	1.1	45
70	Gene expression analysis of ABC transporters in a resistant <i>Cooperia oncophora</i> isolate following <i>in vivo</i> and <i>in vitro</i> exposure to macrocyclic lactones. <i>Parasitology</i> , 2013, 140, 499-508.	0.7	45
71	Mining Novel Effector Proteins from the Esophageal Gland Cells of <i>Meloidogyne incognita</i> . <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 965-974.	1.4	45
72	Biology and genome of <i>Trichinella spiralis</i> . <i>WormBook</i> , 2006, , 1-21.	5.3	45

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73	Dynamic changes in human-gut microbiome in relation to a placebo-controlled anthelmintic trial in Indonesia. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006620.	1.3	44
74	Parasitic nematodes—From genomes to control. <i>Veterinary Parasitology</i> , 2007, 148, 31-42.	0.7	43
75	Sequence mining and transcript profiling to explore cyst nematode parasitism. <i>BMC Genomics</i> , 2009, 10, 58.	1.2	43
76	A novel role for C motif chemokine receptor 2 during infection with hypervirulent <i>Mycobacterium tuberculosis</i> . <i>Mucosal Immunology</i> , 2018, 11, 1727-1742.	2.7	43
77	Intestinal Transcriptomes of Nematodes: Comparison of the Parasites <i>Ascaris suum</i> and <i>Haemonchus contortus</i> with the Free-living <i>Caenorhabditis elegans</i> . <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e269.	1.3	42
78	Profiling of gender-regulated gene transcripts in the filarial nematode <i>Brugia malayi</i> by cDNA oligonucleotide array analysis. <i>Molecular and Biochemical Parasitology</i> , 2005, 143, 49-57.	0.5	41
79	Divergent evolution of arrested development in the dauer stage of <i>Caenorhabditis elegans</i> and the infective stage of <i>Heterodera glycines</i> . <i>Genome Biology</i> , 2007, 8, R211.	13.9	40
80	Nematode.net update 2011: addition of data sets and tools featuring next-generation sequencing data. <i>Nucleic Acids Research</i> , 2012, 40, D720-D728.	6.5	40
81	An expressed sequence tag analysis of the life-cycle of the parasitic nematode <i>Strongyloides ratti</i> . <i>Molecular and Biochemical Parasitology</i> , 2005, 142, 32-46.	0.5	39
82	Analysis of the <i>Trichuris suis</i> excretory/secretory proteins as a function of life cycle stage and their immunomodulatory properties. <i>Scientific Reports</i> , 2018, 8, 15921.	1.6	37
83	The canine hookworm genome: Analysis and classification of <i>Ancylostoma caninum</i> survey sequences. <i>Molecular and Biochemical Parasitology</i> , 2008, 157, 187-192.	0.5	36
84	Transcription profiling reveals stage- and function-dependent expression patterns in the filarial nematode <i>Brugia malayi</i> . <i>BMC Genomics</i> , 2012, 13, 184.	1.2	36
85	Using Existing Drugs as Leads for Broad Spectrum Anthelmintics Targeting Protein Kinases. <i>PLoS Pathogens</i> , 2013, 9, e1003149.	2.1	36
86	Transcriptomes and pathways associated with infectivity, survival and immunogenicity in <i>Brugia malayi</i> L3. <i>BMC Genomics</i> , 2009, 10, 267.	1.2	35
87	Transcripts analysis of the entomopathogenic nematode <i>Steinernema carpocapsae</i> induced in vitro with insect haemolymph. <i>Molecular and Biochemical Parasitology</i> , 2010, 169, 79-86.	0.5	35
88	Precise Dissection of an <i>Escherichia coli</i> O157:H7 Outbreak by Single Nucleotide Polymorphism Analysis. <i>Journal of Clinical Microbiology</i> , 2013, 51, 3950-3954.	1.8	35
89	Inter and intra-specific diversity of parasites that cause lymphatic filariasis. <i>Infection, Genetics and Evolution</i> , 2013, 14, 137-146.	1.0	34
90	Nematode.net update 2008: improvements enabling more efficient data mining and comparative nematode genomics. <i>Nucleic Acids Research</i> , 2009, 37, D571-D578.	6.5	33

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91	Coverage theories for metagenomic DNA sequencing based on a generalization of Stevens's theorem. <i>Journal of Mathematical Biology</i> , 2013, 67, 1141-1161.	0.8	33
92	Genome-Wide Analysis Reveals Novel Genes Essential for Heme Homeostasis in <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , 2010, 6, e1001044.	1.5	32
93	A vertebrate case study of the quality of assemblies derived from next-generation sequences. <i>Genome Biology</i> , 2011, 12, R31.	13.9	32
94	Targeting Protein-Protein Interactions for Parasite Control. <i>PLoS ONE</i> , 2011, 6, e18381.	1.1	31
95	Deep insights into <i>Dictyocaulus viviparus</i> transcriptomes provides unique prospects for new drug targets and disease intervention. <i>Biotechnology Advances</i> , 2011, 29, 261-271.	6.0	31
96	Transcriptome analyses reveal protein and domain families that delineate stage-related development in the economically important parasitic nematodes, <i>Ostertagia ostertagi</i> and <i>Cooperia oncophora</i> . <i>BMC Genomics</i> , 2013, 14, 118.	1.2	31
97	Gene diversity and genetic variation in lung flukes (genus <i>Paragonimus</i> ). <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2016, 110, 6-12.	0.7	31
98	Tackling Hypotheticals in Helminth Genomes. <i>Trends in Parasitology</i> , 2018, 34, 179-183.	1.5	29
99	Stage-specific excretory-secretory small heat shock proteins from the parasitic nematode <i>Strongyloides fratti</i> putative links to host's intestinal mucosal defense system. <i>FEBS Journal</i> , 2011, 278, 3319-3336.	2.2	28
100	Adaptive Radiation of the Flukes of the Family Fasciolidae Inferred from Genome-Wide Comparisons of Key Species. <i>Molecular Biology and Evolution</i> , 2020, 37, 84-99.	3.5	28
101	Downregulation of the Syk Signaling Pathway in Intestinal Dendritic Cells Is Sufficient To Induce Dendritic Cells That Inhibit Colitis. <i>Journal of Immunology</i> , 2016, 197, 2948-2957.	0.4	27
102	Conservation and global distribution of non-canonical antigens in Enterotoxigenic <i>Escherichia coli</i> . <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007825.	1.3	27
103	NemaPath: online exploration of KEGG-based metabolic pathways for nematodes. <i>BMC Genomics</i> , 2008, 9, 525.	1.2	26
104	Gender-Associated Genes in Filarial Nematodes Are Important for Reproduction and Potential Intervention Targets. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e947.	1.3	26
105	Pan-phylum Comparison of Nematode Metabolic Potential. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003788.	1.3	26
106	Skin Ecology during Sebaceous Drought—How Skin Microbes Respond to Isotretinoin. <i>Journal of Investigative Dermatology</i> , 2019, 139, 732-735.	0.3	26
107	Stunting Is Preceded by Intestinal Mucosal Damage and Microbiome Changes and Is Associated with Systemic Inflammation in a Cohort of Peruvian Infants. <i>American Journal of Tropical Medicine and Hygiene</i> , 2019, 101, 1009-1017.	0.6	26
108	Identification of small molecule enzyme inhibitors as broad-spectrum anthelmintics. <i>Scientific Reports</i> , 2019, 9, 9085.	1.6	25

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109	Comprehensive analysis of the secreted proteome of adult <i>Necator americanus</i> hookworms. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008237.	1.3	25
110	The bandit, a New DNA Transposon from a Hookworm—Possible Horizontal Genetic Transfer between Host and Parasite. <i>PLoS Neglected Tropical Diseases</i> , 2007, 1, e35.	1.3	24
111	Systematic analysis of insertions and deletions specific to nematode proteins and their proposed functional and evolutionary relevance. <i>BMC Evolutionary Biology</i> , 2009, 9, 23.	3.2	24
112	Systems Biology Studies of Adult <i>Paragonimus</i> Lung Flukes Facilitate the Identification of Immunodominant Parasite Antigens. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3242.	1.3	24
113	Variant in a common odorant-binding protein gene is associated with bitter sensitivity in people. <i>Behavioural Brain Research</i> , 2017, 329, 200-204.	1.2	24
114	The Effect of Gut Microbiome Composition on Human Immune Responses: An Exploration of Interference by Helminth Infections. <i>Frontiers in Genetics</i> , 2019, 10, 1028.	1.1	24
115	In-Depth Proteomic and Glycomic Analysis of the Adult-Stage <i>Cooperia oncophora</i> Excretome/Secretome. <i>Journal of Proteome Research</i> , 2013, 12, 3900-3911.	1.8	23
116	Functional and Phylogenetic Characterization of Proteins Detected in Various Nematode Intestinal Compartments*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 812-827.	2.5	23
117	<i>Dictyocaulus viviparus</i> genome, variome and transcriptome elucidate lungworm biology and support future intervention. <i>Scientific Reports</i> , 2016, 6, 20316.	1.6	23
118	Effects of Doxycycline on gene expression in <i>Wolbachia</i> and <i>Brugia malayi</i> adult female worms in vivo. <i>Journal of Biomedical Science</i> , 2012, 19, 21.	2.6	22
119	Expressed sequence tags from life cycle stages of <i>Trichinella spiralis</i> : Application to biology and parasite control. <i>Veterinary Parasitology</i> , 2005, 132, 13-17.	0.7	21
120	A nuclear single-nucleotide polymorphism (SNP) potentially useful for the separation of <i>Rhodnius prolixus</i> from members of the <i>Rhodnius robustus</i> cryptic species complex (Hemiptera: Reduviidae). <i>Infection, Genetics and Evolution</i> , 2013, 14, 426-433.	1.0	21
121	Cracking the nodule worm code advances knowledge of parasite biology and biotechnology to tackle major diseases of livestock. <i>Biotechnology Advances</i> , 2015, 33, 980-991.	6.0	21
122	Transcriptomic and Proteomic Analyses of a <i>Wolbachia</i> -Free Filarial Parasite Provide Evidence of Trans-Kingdom Horizontal Gene Transfer. <i>PLoS ONE</i> , 2012, 7, e45777.	1.1	20
123	Pan-Nematoda Transcriptomic Elucidation of Essential Intestinal Functions and Therapeutic Targets With Broad Potential. <i>EBioMedicine</i> , 2015, 2, 1079-1089.	2.7	20
124	The genome of a blood fluke associated with human cancer. <i>Nature Genetics</i> , 2012, 44, 116-118.	9.4	19
125	The hookworm <i>Ancylostoma ceylanicum</i> intestinal transcriptome provides a platform for selecting drug and vaccine candidates. <i>Parasites and Vectors</i> , 2016, 9, 518.	1.0	19
126	Genome Sequence of <i>Christensenella minuta</i> DSM 22607. <i>Genome Announcements</i> , 2017, 5,	0.8	19



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127	Strategies for Undertaking Expressed Sequence Tag (EST) Projects. <i>Methods in Molecular Biology</i> , 2009, 533, 13-32.	0.4	19
128	An analysis of the transcriptome of <i>Teladorsagia circumcincta</i> : its biological and biotechnological implications. <i>BMC Genomics</i> , 2012, 13, S10.	1.2	18
129	TIMPs of parasitic helminths – a large-scale analysis of high-throughput sequence datasets. <i>Parasites and Vectors</i> , 2013, 6, 156.	1.0	18
130	Small Molecule Inhibitors of Metabolic Enzymes Repurposed as a New Class of Anthelmintics. <i>ACS Infectious Diseases</i> , 2018, 4, 1130-1145.	1.8	18
131	Comparative genomics and transcriptomics of 4 <i>Paragonimus</i> species provide insights into lung fluke parasitism and pathogenesis. <i>GigaScience</i> , 2020, 9, .	3.3	18
132	Improving eukaryotic genome annotation using single molecule mRNA sequencing. <i>BMC Genomics</i> , 2018, 19, 172.	1.2	17
133	HelmCoP: An Online Resource for Helminth Functional Genomics and Drug and Vaccine Targets Prioritization. <i>PLoS ONE</i> , 2011, 6, e21832.	1.1	17
134	Identification of Hookworm DAF-16/FOXO Response Elements and Direct Gene Targets. <i>PLoS ONE</i> , 2010, 5, e12289.	1.1	16
135	Alteration of the fecal microbiota in Chinese patients with <i>Schistosoma japonicum</i> infection. <i>Parasite</i> , 2021, 28, 1.	0.8	16
136	An Integrated Approach to Identify New Anti-Filarial Leads to Treat River Blindness, a Neglected Tropical Disease. <i>Pathogens</i> , 2021, 10, 71.	1.2	16
137	Proteomic Analysis of <i>Oesophagostomum dentatum</i> (Nematoda) during Larval Transition, and the Effects of Hydrolase Inhibitors on Development. <i>PLoS ONE</i> , 2013, 8, e63955.	1.1	16
138	mBLAST: Keeping up with the Sequencing Explosion for (Meta) Genome Analysis. <i>Journal of Data Mining in Genomics &amp; Proteomics</i> , 2013, 04, .	0.5	16
139	Identification and analysis of genes expressed in the adult filarial parasitic nematode <i>Dirofilaria immitis</i> . <i>International Journal for Parasitology</i> , 2006, 36, 829-839.	1.3	15
140	The mixed model for the analysis of a repeated measurement multivariate count data. <i>Statistics in Medicine</i> , 2019, 38, 2248-2268.	0.8	15
141	<i>Mycobacterium tuberculosis</i> HN878 Infection Induces Human-Like B-Cell Follicles in Mice. <i>Journal of Infectious Diseases</i> , 2020, 221, 1636-1646.	1.9	15
142	The endosymbiont <i>Wolbachia</i> rebounds following antibiotic treatment. <i>PLoS Pathogens</i> , 2020, 16, e1008623.	2.1	15
143	Peptidases Compartmentalized to the <i>Ascaris suum</i> Intestinal Lumen and Apical Intestinal Membrane. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e3375.	1.3	14
144	<i>Trichinella spiralis</i> : Adaptation and parasitism. <i>Veterinary Parasitology</i> , 2016, 231, 8-21.	0.7	14

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