

# Makedonka Mitreva

## List of Publications by Citations

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195  
papers

19,133  
citations

49  
h-index

137  
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223  
ext. papers

23,163  
ext. citations

8.7  
avg, IF

7.87  
L-index

#	Paper	IF	Citations
195	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , <b>2012</b> , 486, 207-14	50.4	6938
194	A framework for human microbiome research. <i>Nature</i> , <b>2012</b> , 486, 215-21	50.4	1722
193	Metabolic reconstruction for metagenomic data and its application to the human microbiome. <i>PLoS Computational Biology</i> , <b>2012</b> , 8, e1002358	5	730
192	Genomic variation landscape of the human gut microbiome. <i>Nature</i> , <b>2013</b> , 493, 45-50	50.4	571
191	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , <b>2008</b> , 453, 175-83	50.4	545
190	Draft genome of the filarial nematode parasite <i>Brugia malayi</i> . <i>Science</i> , <b>2007</b> , 317, 1756-60	33.3	513
189	A catalog of reference genomes from the human microbiome. <i>Science</i> , <b>2010</b> , 328, 994-9	33.3	508
188	A systematic analysis of biosynthetic gene clusters in the human microbiome reveals a common family of antibiotics. <i>Cell</i> , <b>2014</b> , 158, 1402-1414	56.2	433
187	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , <b>2011</b> , 469, 529-33	50.4	431
186	Alpha-gliadin genes from the A, B, and D genomes of wheat contain different sets of celiac disease epitopes. <i>BMC Genomics</i> , <b>2006</b> , 7, 1	4.5	301
185	The <i>Pristionchus pacificus</i> genome provides a unique perspective on nematode lifestyle and parasitism. <i>Nature Genetics</i> , <b>2008</b> , 40, 1193-8	36.3	280
184	Metabolic and metagenomic outcomes from early-life pulsed antibiotic treatment. <i>Nature Communications</i> , <b>2015</b> , 6, 7486	17.4	232
183	The draft genome of the parasitic nematode <i>Trichinella spiralis</i> . <i>Nature Genetics</i> , <b>2011</b> , 43, 228-35	36.3	230
182	A transcriptomic analysis of the phylum Nematoda. <i>Nature Genetics</i> , <b>2004</b> , 36, 1259-67	36.3	209
181	Widespread colonization of the lung by <i>Tropheryma whipplei</i> in HIV infection. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2013</b> , 187, 1110-7	10.2	140
180	Genome of the human hookworm <i>Necator americanus</i> . <i>Nature Genetics</i> , <b>2014</b> , 46, 261-269	36.3	139
179	Deep small RNA sequencing from the nematode <i>Ascaris</i> reveals conservation, functional diversification, and novel developmental profiles. <i>Genome Research</i> , <b>2011</b> , 21, 1462-77	9.7	133

178	Sepsis from the gut: the enteric habitat of bacteria that cause late-onset neonatal bloodstream infections. <i>Clinical Infectious Diseases</i> , <b>2014</b> , 58, 1211-8	11.6	124
177	Analysis and functional classification of transcripts from the nematode <i>Meloidogyne incognita</i> . <i>Genome Biology</i> , <b>2003</b> , 4, R26	18.3	116
176	Comparative genomics of nematodes. <i>Trends in Genetics</i> , <b>2005</b> , 21, 573-81	8.5	115
175	RNAi effector diversity in nematodes. <i>PLoS Neglected Tropical Diseases</i> , <b>2011</b> , 5, e1176	4.8	104
174	Impact of experimental hookworm infection on the human gut microbiota. <i>Journal of Infectious Diseases</i> , <b>2014</b> , 210, 1431-4	7	100
173	Dynamic changes in the subgingival microbiome and their potential for diagnosis and prognosis of periodontitis. <i>MBio</i> , <b>2015</b> , 6, e01926-14	7.8	95
172	Responses to acute infection with SARS-CoV-2 in the lungs of rhesus macaques, baboons and marmosets. <i>Nature Microbiology</i> , <b>2021</b> , 6, 73-86	26.6	95
171	Microbiome Signatures Associated With Steatohepatitis and Moderate to Severe Fibrosis in Children With Nonalcoholic Fatty Liver Disease. <i>Gastroenterology</i> , <b>2019</b> , 157, 1109-1122	13.3	92
170	Endosymbiont DNA in endobacteria-free filarial nematodes indicates ancient horizontal genetic transfer. <i>PLoS ONE</i> , <b>2010</b> , 5, e11029	3.7	92
169	Exploration of bacterial community classes in major human habitats. <i>Genome Biology</i> , <b>2014</b> , 15, R66	18.3	83
168	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> , <b>2004</b> , 14, 209-20	9.7	81
167	Silencing of germline-expressed genes by DNA elimination in somatic cells. <i>Developmental Cell</i> , <b>2012</b> , 23, 1072-80	10.2	79
166	Helminth genomics: The implications for human health. <i>PLoS Neglected Tropical Diseases</i> , <b>2009</b> , 3, e538	4.8	79
165	3559 Mechanisms of sebaceous skin microbial community remodeling through microenvironment modulation.. <i>Journal of Clinical and Translational Science</i> , <b>2019</b> , 3, 109-109	0.4	78
164	Nematode.net: a tool for navigating sequences from parasitic and free-living nematodes. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D423-6	20.1	72
163	Experimental hookworm infection and escalating gluten challenges are associated with increased microbial richness in celiac subjects. <i>Scientific Reports</i> , <b>2015</b> , 5, 13797	4.9	70
162	Massively parallel sequencing and analysis of the <i>Necator americanus</i> transcriptome. <i>PLoS Neglected Tropical Diseases</i> , <b>2010</b> , 4, e684	4.8	66
161	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> , <b>2011</b> , 10, M111.010157	7.6	66

160	Genomes of <i>Fasciola hepatica</i> from the Americas Reveal Colonization with Neorickettsia Endobacteria Related to the Agents of Potomac Horse and Human Sennetsu Fevers. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006537	6	65
159	Secreted proteomes of different developmental stages of the gastrointestinal nematode <i>Nippostrongylus brasiliensis</i> . <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 2736-51	7.6	63
158	The prevalence of species and strains in the human microbiome: a resource for experimental efforts. <i>PLoS ONE</i> , <b>2014</b> , 9, e97279	3.7	62
157	A practical, bioinformatic workflow system for large data sets generated by next-generation sequencing. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, e171	20.1	60
156	Helminth-induced arginase-1 exacerbates lung inflammation and disease severity in tuberculosis. <i>Journal of Clinical Investigation</i> , <b>2015</b> , 125, 4699-713	15.9	60
155	Differential human gut microbiome assemblages during soil-transmitted helminth infections in Indonesia and Liberia. <i>Microbiome</i> , <b>2018</b> , 6, 33	16.6	59
154	Discovery of anthelmintic drug targets and drugs using chokepoints in nematode metabolic pathways. <i>PLoS Pathogens</i> , <b>2013</b> , 9, e1003505	7.6	57
153	A symbiont-independent endo-1,4-beta-xylanase from the plant-parasitic nematode <i>Meloidogyne incognita</i> . <i>Molecular Plant-Microbe Interactions</i> , <b>2006</b> , 19, 521-9	3.6	57
152	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> , <b>2004</b> , 137, 277-91	1.9	53
151	400000 nematode ESTs on the Net. <i>Trends in Parasitology</i> , <b>2003</b> , 19, 283-6	6.4	53
150	The Dynamic Genome and Transcriptome of the Human Fungal Pathogen <i>Blastomyces</i> and Close Relative <i>Emmonsia</i> . <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005493	6	51
149	<i>Mycobacterium tuberculosis</i> carrying a rifampicin drug resistance mutation reprograms macrophage metabolism through cell wall lipid changes. <i>Nature Microbiology</i> , <b>2018</b> , 3, 1099-1108	26.6	51
148	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> , <b>2010</b> , 10, 1199-207	4.5	50
147	Mining the secretome of the root-knot nematode <i>Meloidogyne chitwoodi</i> for candidate parasitism genes. <i>Molecular Plant Pathology</i> , <b>2008</b> , 9, 1-10	5.7	50
146	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> , <b>2004</b> , 137, 297-305	1.9	49
145	Helminth.net: expansions to Nematode.net and an introduction to Trematode.net. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D698-706	20.1	48
144	Characterizing <i>Ancylostoma caninum</i> transcriptome and exploring nematode parasitic adaptation. <i>BMC Genomics</i> , <b>2010</b> , 11, 307	4.5	48
143	Role of horizontal gene transfer in the evolution of plant parasitism among nematodes. <i>Methods in Molecular Biology</i> , <b>2009</b> , 532, 517-35	1.4	47

142	Exploring the transcriptome of the burrowing nematode <i>Radopholus similis</i> . <i>Molecular Genetics and Genomics</i> , <b>2008</b> , 280, 1-17	3.1	47
141	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> , <b>2009</b> , 167, 32-40	1.9	46
140	Detection of putative secreted proteins in the plant-parasitic nematode <i>Heterodera schachtii</i> . <i>Parasitology Research</i> , <b>2006</b> , 98, 414-24	2.4	46
139	Investigating hookworm genomes by comparative analysis of two <i>Ancylostoma</i> species. <i>BMC Genomics</i> , <b>2005</b> , 6, 58	4.5	46
138	Novel venom gene discovery in the platypus. <i>Genome Biology</i> , <b>2010</b> , 11, R95	18.3	45
137	Changes in duodenal tissue-associated microbiota following hookworm infection and consecutive gluten challenges in humans with coeliac disease. <i>Scientific Reports</i> , <b>2016</b> , 6, 36797	4.9	44
136	The effect of dietary resistant starch type 2 on the microbiota and markers of gut inflammation in rural Malawi children. <i>Microbiome</i> , <b>2015</b> , 3, 37	16.6	42
135	Optimizing read mapping to reference genomes to determine composition and species prevalence in microbial communities. <i>PLoS ONE</i> , <b>2012</b> , 7, e36427	3.7	42
134	Parasitic nematodes - from genomes to control. <i>Veterinary Parasitology</i> , <b>2007</b> , 148, 31-42	2.8	42
133	Codon usage patterns in Nematoda: analysis based on over 25 million codons in thirty-two species. <i>Genome Biology</i> , <b>2006</b> , 7, R75	18.3	42
132	Gene expression analysis of ABC transporters in a resistant <i>Cooperia oncophora</i> isolate following in vivo and in vitro exposure to macrocyclic lactones. <i>Parasitology</i> , <b>2013</b> , 140, 499-508	2.7	40
131	Genomic introgression mapping of field-derived multiple-anthelmintic resistance in <i>Teladorsagia circumcincta</i> . <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006857	6	38
130	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> , <b>2014</b> , 8, e2678	4.8	38
129	Nematode.net update 2011: addition of data sets and tools featuring next-generation sequencing data. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D720-8	20.1	38
128	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> , <b>2005</b> , 143, 49-57	1.9	38
127	Targeting Lysine Deacetylases (KDACS) in Parasites. <i>PLoS Neglected Tropical Diseases</i> , <b>2015</b> , 9, e0004026	4.8	36
126	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> , <b>2007</b> , 8, R211	18.3	36
125	An expressed sequence tag analysis of the life-cycle of the parasitic nematode <i>Strongyloides ratti</i> . <i>Molecular and Biochemical Parasitology</i> , <b>2005</b> , 142, 32-46	1.9	36

124	Monocyte dysregulation and systemic inflammation during pediatric falciparum malaria. <i>JCI Insight</i> , <b>2017</b> , 2,	9.9	36
123	Genomic diversity in <i>Onchocerca volvulus</i> and its <i>Wolbachia</i> endosymbiont. <i>Nature Microbiology</i> , <b>2016</b> , 2, 16207	26.6	35
122	The canine hookworm genome: analysis and classification of <i>Ancylostoma caninum</i> survey sequences. <i>Molecular and Biochemical Parasitology</i> , <b>2008</b> , 157, 187-92	1.9	35
121	Sequence mining and transcript profiling to explore cyst nematode parasitism. <i>BMC Genomics</i> , <b>2009</b> , 10, 58	4.5	34
120	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> , <b>2008</b> , 2, e269	4.8	34
119	Biology and genome of <i>Trichinella spiralis</i> . <i>WormBook</i> , <b>2006</b> , 1-21		34
118	Nematode.net update 2008: improvements enabling more efficient data mining and comparative nematode genomics. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D571-8	20.1	33
117	Transcription profiling reveals stage- and function-dependent expression patterns in the filarial nematode <i>Brugia malayi</i> . <i>BMC Genomics</i> , <b>2012</b> , 13, 184	4.5	32
116	Using existing drugs as leads for broad spectrum anthelmintics targeting protein kinases. <i>PLoS Pathogens</i> , <b>2013</b> , 9, e1003149	7.6	32
115	Precise dissection of an <i>Escherichia coli</i> O157:H7 outbreak by single nucleotide polymorphism analysis. <i>Journal of Clinical Microbiology</i> , <b>2013</b> , 51, 3950-4	9.7	32
114	Transcriptome analysis of female and male <i>Xiphophorus maculatus</i> Jp 163 A. <i>PLoS ONE</i> , <b>2011</b> , 6, e18379	3.7	31
113	Transcriptomes and pathways associated with infectivity, survival and immunogenicity in <i>Brugia malayi</i> L3. <i>BMC Genomics</i> , <b>2009</b> , 10, 267	4.5	31
112	Transcripts analysis of the entomopathogenic nematode <i>Steinernema carpocapsae</i> induced in vitro with insect haemolymph. <i>Molecular and Biochemical Parasitology</i> , <b>2010</b> , 169, 79-86	1.9	30
111	Mining novel effector proteins from the esophageal gland cells of <i>Meloidogyne incognita</i> . <i>Molecular Plant-Microbe Interactions</i> , <b>2014</b> , 27, 965-74	3.6	29
110	Genome-wide analysis reveals novel genes essential for heme homeostasis in <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , <b>2010</b> , 6, e1001044	6	28
109	IFN signaling and neutrophil degranulation transcriptional signatures are induced during SARS-CoV-2 infection. <i>Communications Biology</i> , <b>2021</b> , 4, 290	6.7	28
108	A vertebrate case study of the quality of assemblies derived from next-generation sequences. <i>Genome Biology</i> , <b>2011</b> , 12, R31	18.3	27
107	Deep insights into <i>Dictyocaulus viviparus</i> transcriptomes provides unique prospects for new drug targets and disease intervention. <i>Biotechnology Advances</i> , <b>2011</b> , 29, 261-71	17.8	27

106	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> , <b>2018</b> , 8, 15921	4.9	26
105	NemaPath: online exploration of KEGG-based metabolic pathways for nematodes. <i>BMC Genomics</i> , <b>2008</b> , 9, 525	4.5	25
104	Gene diversity and genetic variation in lung flukes (genus <i>Paragonimus</i> ). <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , <b>2016</b> , 110, 6-12	2	25
103	Immune correlates of tuberculosis disease and risk translate across species. <i>Science Translational Medicine</i> , <b>2020</b> , 12,	17.5	24
102	Coverage theories for metagenomic DNA sequencing based on a generalization of StevensU theorem. <i>Journal of Mathematical Biology</i> , <b>2013</b> , 67, 1141-61	2	24
101	Inter and intra-specific diversity of parasites that cause lymphatic filariasis. <i>Infection, Genetics and Evolution</i> , <b>2013</b> , 14, 137-46	4.5	24
100	Dynamic changes in human-gut microbiome in relation to a placebo-controlled anthelmintic trial in Indonesia. <i>PLoS Neglected Tropical Diseases</i> , <b>2018</b> , 12, e0006620	4.8	23
99	Stage-specific excretory-secretory small heat shock proteins from the parasitic nematode <i>Strongyloides ratti</i> —putative links to host's intestinal mucosal defense system. <i>FEBS Journal</i> , <b>2011</b> , 278, 3319-36	5.7	23
98	Systematic analysis of insertions and deletions specific to nematode proteins and their proposed functional and evolutionary relevance. <i>BMC Evolutionary Biology</i> , <b>2009</b> , 9, 23	3	23
97	Gender-associated genes in filarial nematodes are important for reproduction and potential intervention targets. <i>PLoS Neglected Tropical Diseases</i> , <b>2011</b> , 5, e947	4.8	23
96	Pan-phyllum Comparison of Nematode Metabolic Potential. <i>PLoS Neglected Tropical Diseases</i> , <b>2015</b> , 9, e0003788	4.8	22
95	The bandit, a new DNA transposon from a hookworm—possible horizontal genetic transfer between host and parasite. <i>PLoS Neglected Tropical Diseases</i> , <b>2007</b> , 1, e35	4.8	22
94	Variant in a common odorant-binding protein gene is associated with bitter sensitivity in people. <i>Behavioural Brain Research</i> , <b>2017</b> , 329, 200-204	3.4	21
93	In-depth proteomic and glycomic analysis of the adult-stage <i>Cooperia oncophora</i> excretome/secretome. <i>Journal of Proteome Research</i> , <b>2013</b> , 12, 3900-11	5.6	21
92	SARS-CoV-2 infection leads to acute infection with dynamic cellular and inflammatory flux in the lung that varies across nonhuman primate species		21
91	Tackling Hypotheticals in Helminth Genomes. <i>Trends in Parasitology</i> , <b>2018</b> , 34, 179-183	6.4	20
90	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> , <b>2013</b> , 14, 118	4.5	20
89	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> , <b>2013</b> , 14, 426-33	4.5	20



88	Systems biology studies of adult paragonimus lung flukes facilitate the identification of immunodominant parasite antigens. <i>PLoS Neglected Tropical Diseases</i> , <b>2014</b> , 8, e3242	4.8	20
87	Transcriptomic and proteomic analyses of a Wolbachia-free filarial parasite provide evidence of trans-kingdom horizontal gene transfer. <i>PLoS ONE</i> , <b>2012</b> , 7, e45777	3.7	20
86	A novel role for C-C motif chemokine receptor 2 during infection with hypervirulent Mycobacterium tuberculosis. <i>Mucosal Immunology</i> , <b>2018</b> , 11, 1727-1742	9.2	19
85	Targeting protein-protein interactions for parasite control. <i>PLoS ONE</i> , <b>2011</b> , 6, e18381	3.7	19
84	Expressed sequence tags from life cycle stages of Trichinella spiralis: application to biology and parasite control. <i>Veterinary Parasitology</i> , <b>2005</b> , 132, 13-7	2.8	19
83	Cracking the nodule worm code advances knowledge of parasite biology and biotechnology to tackle major diseases of livestock. <i>Biotechnology Advances</i> , <b>2015</b> , 33, 980-91	17.8	18
82	Effects of doxycycline on gene expression in Wolbachia and Brugia malayi adult female worms in vivo. <i>Journal of Biomedical Science</i> , <b>2012</b> , 19, 21	13.3	18
81	Dictyocaulus viviparus genome, variome and transcriptome elucidate lungworm biology and support future intervention. <i>Scientific Reports</i> , <b>2016</b> , 6, 20316	4.9	17
80	An analysis of the transcriptome of Teladorsagia circumcincta: its biological and biotechnological implications. <i>BMC Genomics</i> , <b>2012</b> , 13 Suppl 7, S10	4.5	16
79	HelmCoP: an online resource for helminth functional genomics and drug and vaccine targets prioritization. <i>PLoS ONE</i> , <b>2011</b> , 6, e21832	3.7	16
78	Skin Ecology during Sebaceous Drought-How Skin Microbes Respond to Isotretinoin. <i>Journal of Investigative Dermatology</i> , <b>2019</b> , 139, 732-735	4.3	16
77	TIMPs of parasitic helminths - a large-scale analysis of high-throughput sequence datasets. <i>Parasites and Vectors</i> , <b>2013</b> , 6, 156	4	15
76	Functional and phylogenetic characterization of proteins detected in various nematode intestinal compartments. <i>Molecular and Cellular Proteomics</i> , <b>2015</b> , 14, 812-27	7.6	15
75	Identification and analysis of genes expressed in the adult filarial parasitic nematode Dirofilaria immitis. <i>International Journal for Parasitology</i> , <b>2006</b> , 36, 829-39	4.3	15
74	mBLAST: Keeping up with the sequencing explosion for (meta)genome analysis. <i>Journal of Data Mining in Genomics &amp; Proteomics</i> , <b>2015</b> , 4,		15
73	The hookworm Ancylostoma ceylanicum intestinal transcriptome provides a platform for selecting drug and vaccine candidates. <i>Parasites and Vectors</i> , <b>2016</b> , 9, 518	4	15
72	Downregulation of the Syk Signaling Pathway in Intestinal Dendritic Cells Is Sufficient To Induce Dendritic Cells That Inhibit Colitis. <i>Journal of Immunology</i> , <b>2016</b> , 197, 2948-57	5.3	14
71	Strategies for undertaking expressed sequence tag (EST) projects. <i>Methods in Molecular Biology</i> , <b>2009</b> , 533, 13-32	1.4	14



70	The Effect of Gut Microbiome Composition on Human Immune Responses: An Exploration of Interference by Helminth Infections. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 1028	4.5	14
69	Pan-Nematoda Transcriptomic Elucidation of Essential Intestinal Functions and Therapeutic Targets With Broad Potential. <i>EBioMedicine</i> , <b>2015</b> , 2, 1079-89	8.8	12
68	Identification of hookworm DAF-16/FOXO response elements and direct gene targets. <i>PLoS ONE</i> , <b>2010</b> , 5, e12289	3.7	12
67	Proteomic analysis of Oesophagostomum dentatum (Nematoda) during larval transition, and the effects of hydrolase inhibitors on development. <i>PLoS ONE</i> , <b>2013</b> , 8, e63955	3.7	12
66	Nematode gene sequences: update for december 2005. <i>Journal of Nematology</i> , <b>2005</b> , 37, 417-21	1.1	12
65	Adaptive Radiation of the Flukes of the Family Fasciolidae Inferred from Genome-Wide Comparisons of Key Species. <i>Molecular Biology and Evolution</i> , <b>2020</b> , 37, 84-99	8.3	12
64	Comparative genomics and transcriptomics of 4 Paragonimus species provide insights into lung fluke parasitism and pathogenesis. <i>GigaScience</i> , <b>2020</b> , 9,	7.6	12
63	Genome Sequence of Christensenella minuta DSM 22607T. <i>Genome Announcements</i> , <b>2017</b> , 5,		11
62	Comprehensive analysis of the secreted proteome of adult Necator americanus hookworms. <i>PLoS Neglected Tropical Diseases</i> , <b>2020</b> , 14, e0008237	4.8	11
61	Small Molecule Inhibitors of Metabolic Enzymes Repurposed as a New Class of Anthelmintics. <i>ACS Infectious Diseases</i> , <b>2018</b> , 4, 1130-1145	5.5	11
60	Identification of small molecule enzyme inhibitors as broad-spectrum anthelmintics. <i>Scientific Reports</i> , <b>2019</b> , 9, 9085	4.9	11
59	Large-scale sequencing and analytical processing of ESTs. <i>Methods in Molecular Biology</i> , <b>2009</b> , 533, 153-87.4		11
58	IFN signaling and neutrophil degranulation transcriptional signatures are induced during SARS-CoV-2 infection <b>2020</b> ,		11
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