List of Publications by Year in descending order

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	31976	7518
25,341	53	151
citations	h-index	g-index
223	223	32614
docs citations	times ranked	citing authors
	25,341 citations 223 docs citations	25,341 53 citations h-index 223 223 docs citations 223 times ranked

#	Article	IF	CITATIONS
1	Structure, function and diversity of the healthy human microbiome. Nature, 2012, 486, 207-214.	27.8	9,614
2	A framework for human microbiome research. Nature, 2012, 486, 215-221.	27.8	2,249
3	Metabolic Reconstruction for Metagenomic Data and Its Application to the Human Microbiome. PLoS Computational Biology, 2012, 8, e1002358.	3.2	939
4	Genomic variation landscape of the human gut microbiome. Nature, 2013, 493, 45-50.	27.8	783
5	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	27.8	657
6	A Catalog of Reference Genomes from the Human Microbiome. Science, 2010, 328, 994-999.	12.6	621
7	A Systematic Analysis of Biosynthetic Gene Clusters in the Human Microbiome Reveals a Common Family of Antibiotics. Cell, 2014, 158, 1402-1414.	28.9	573
8	Draft Genome of the Filarial Nematode Parasite <i>Brugia malayi</i> . Science, 2007, 317, 1756-1760.	12.6	571
9	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	27.8	541
10	Alpha-gliadin genes from the A, B, and D genomes of wheat contain different sets of celiac disease epitopes. BMC Genomics, 2006, 7, 1.	2.8	445
11	Metabolic and metagenomic outcomes from early-life pulsed antibiotic treatment. Nature Communications, 2015, 6, 7486.	12.8	317
12	The Pristionchus pacificus genome provides a unique perspective on nematode lifestyle and parasitism. Nature Genetics, 2008, 40, 1193-1198.	21.4	310
13	The draft genome of the parasitic nematode Trichinella spiralis. Nature Genetics, 2011, 43, 228-235.	21.4	285
14	A transcriptomic analysis of the phylum Nematoda. Nature Genetics, 2004, 36, 1259-1267.	21.4	239
15	Microbiome Signatures Associated With Steatohepatitis and Moderate to Severe Fibrosis in Children With Nonalcoholic Fatty Liver Disease. Gastroenterology, 2019, 157, 1109-1122.	1.3	184
16	Widespread Colonization of the Lung by <i>Tropheryma whipplei</i> in HIV Infection. American Journal of Respiratory and Critical Care Medicine, 2013, 187, 1110-1117.	5.6	175
17	Genome of the human hookworm Necator americanus. Nature Genetics, 2014, 46, 261-269.	21.4	166
18	Sepsis From the Gut: The Enteric Habitat of Bacteria That Cause Late-Onset Neonatal Bloodstream Infections. Clinical Infectious Diseases, 2014, 58, 1211-1218.	5.8	160

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19	Deep small RNA sequencing from the nematode <i>Ascaris</i> reveals conservation, functional diversification, and novel developmental profiles. Genome Research, 2011, 21, 1462-1477.	5.5	158
20	Responses to acute infection with SARS-CoV-2 in the lungs of rhesus macaques, baboons and marmosets. Nature Microbiology, 2021, 6, 73-86.	13.3	156
21	Impact of Experimental Hookworm Infection on the Human Gut Microbiota. Journal of Infectious Diseases, 2014, 210, 1431-1434.	4.0	153
22	Comparative genomics of nematodes. Trends in Genetics, 2005, 21, 573-581.	6.7	141
23	Dynamic Changes in the Subgingival Microbiome and Their Potential for Diagnosis and Prognosis of Periodontitis. MBio, 2015, 6, e01926-14.	4.1	139
24	Analysis and functional classification of transcripts from the nematode Meloidogyne incognita. Genome Biology, 2003, 4, R26.	9.6	133
25	RNAi Effector Diversity in Nematodes. PLoS Neglected Tropical Diseases, 2011, 5, e1176.	3.0	119
26	Exploration of bacterial community classes in major human habitats. Genome Biology, 2014, 15, R66.	9.6	109
27	Endosymbiont DNA in Endobacteria-Free Filarial Nematodes Indicates Ancient Horizontal Genetic Transfer. PLoS ONE, 2010, 5, e11029.	2.5	105
28	Differential human gut microbiome assemblages during soil-transmitted helminth infections in Indonesia and Liberia. Microbiome, 2018, 6, 33.	11.1	102
29	Silencing of Germline-Expressed Genes by DNA Elimination in Somatic Cells. Developmental Cell, 2012, 23, 1072-1080.	7.0	101
30	Genomes of Fasciola hepatica from the Americas Reveal Colonization with Neorickettsia Endobacteria Related to the Agents of Potomac Horse and Human Sennetsu Fevers. PLoS Genetics, 2017, 13, e1006537.	3.5	100
31	The Prevalence of Species and Strains in the Human Microbiome: A Resource for Experimental Efforts. PLoS ONE, 2014, 9, e97279.	2.5	93
32	Mycobacterium tuberculosis carrying a rifampicin drug resistance mutation reprograms macrophage metabolism through cell wall lipid changes. Nature Microbiology, 2018, 3, 1099-1108.	13.3	90
33	Secreted Proteomes of Different Developmental Stages of the Gastrointestinal Nematode Nippostrongylus brasiliensis. Molecular and Cellular Proteomics, 2014, 13, 2736-2751.	3.8	88
34	Comparative Genomics of Gene Expression in the Parasitic and Free-Living Nematodes Strongyloides stercoralis and Caenorhabditis elegans. Genome Research, 2004, 14, 209-220.	5.5	87
35	Helminth-induced arginase-1 exacerbates lung inflammation and disease severity in tuberculosis. Journal of Clinical Investigation, 2015, 125, 4699-4713.	8.2	87
36	Helminth Genomics: The Implications for Human Health. PLoS Neglected Tropical Diseases, 2009, 3, e538.	3.0	86

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37	Experimental hookworm infection and escalating gluten challenges are associated with increased microbial richness in celiac subjects. Scientific Reports, 2015, 5, 13797.	3.3	86
38	Life Cycle Stage-resolved Proteomic Analysis of the Excretome/Secretome from Strongyloides ratti—Identification of Stage-specific Proteases. Molecular and Cellular Proteomics, 2011, 10, M111.010157.	3.8	78
39	Nematode.net: a tool for navigating sequences from parasitic and free-living nematodes. Nucleic Acids Research, 2004, 32, 423D-426.	14.5	76
40	IFN signaling and neutrophil degranulation transcriptional signatures are induced during SARS-CoV-2 infection. Communications Biology, 2021, 4, 290.	4.4	74
41	Novel venom gene discovery in the platypus. Genome Biology, 2010, 11, R95.	9.6	72
42	A Symbiont-Independent Endo-1,4-β-Xylanase from the Plant-Parasitic Nematode Meloidogyne incognita. Molecular Plant-Microbe Interactions, 2006, 19, 521-529.	2.6	71
43	Discovery of Anthelmintic Drug Targets and Drugs Using Chokepoints in Nematode Metabolic Pathways. PLoS Pathogens, 2013, 9, e1003505.	4.7	69
44	Genomic introgression mapping of field-derived multiple-anthelmintic resistance in Teladorsagia circumcincta. PLoS Genetics, 2017, 13, e1006857.	3.5	67
45	Massively Parallel Sequencing and Analysis of the Necator americanus Transcriptome. PLoS Neglected Tropical Diseases, 2010, 4, e684.	3.0	66
46	Mining the secretome of the root-knot nematode Meloidogyne chitwoodi for candidate parasitism genes. Molecular Plant Pathology, 2007, 9, 071031023555002-???.	4.2	62
47	A practical, bioinformatic workflow system for large data sets generated by next-generation sequencing. Nucleic Acids Research, 2010, 38, e171-e171.	14.5	62
48	400â€^000 nematode ESTs on the Net. Trends in Parasitology, 2003, 19, 283-286.	3.3	61
49	Codon usage patterns in Nematoda: analysis based on over 25 million codons in thirty-two species. Genome Biology, 2006, 7, R75.	9.6	60
50	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
51	Helminth.net: expansions to Nematode.net and an introduction to Trematode.net. Nucleic Acids Research, 2015, 43, D698-D706.	14.5	58
52	The Dynamic Genome and Transcriptome of the Human Fungal Pathogen Blastomyces and Close Relative Emmonsia. PLoS Genetics, 2015, 11, e1005493.	3.5	57
53	Gene discovery in the adenophorean nematode Trichinella spiralis: an analysis of transcription from three life cycle stages. Molecular and Biochemical Parasitology, 2004, 137, 277-291.	1.1	56
54	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

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55	Role of Horizontal Gene Transfer in the Evolution of Plant Parasitism Among Nematodes. Methods in Molecular Biology, 2009, 532, 517-535.	0.9	54
56	Monocyte dysregulation and systemic inflammation during pediatric falciparum malaria. JCI Insight, 2017, 2, .	5.0	54
57	Exploring the transcriptome of the burrowing nematode Radopholus similis. Molecular Genetics and Genomics, 2008, 280, 1-17.	2.1	53
58	The effect of dietary resistant starch type 2 on the microbiota and markers of gut inflammation in rural Malawi children. Microbiome, 2015, 3, 37.	11.1	53
59	Genomic diversity in Onchocerca volvulus and its Wolbachia endosymbiont. Nature Microbiology, 2017, 2, 16207.	13.3	53
60	Immune correlates of tuberculosis disease and risk translate across species. Science Translational Medicine, 2020, 12, .	12.4	52
61	mRNA sequences for Haemonchus contortus intestinal cathepsin B-like cysteine proteases display an extreme in abundance and diversity compared with other adult mammalian parasitic nematodes. Molecular and Biochemical Parasitology, 2004, 137, 297-305.	1.1	51
62	Expressed sequence tags of the peanut pod nematode Ditylenchus africanus: The first transcriptome analysis of an Anguinid nematode. Molecular and Biochemical Parasitology, 2009, 167, 32-40.	1.1	50
63	Genome-Wide Tissue-Specific Gene Expression, Co-expression and Regulation of Co-expressed Genes in Adult Nematode Ascaris suum. PLoS Neglected Tropical Diseases, 2014, 8, e2678.	3.0	50
64	Characterizing Ancylostoma caninum transcriptome and exploring nematode parasitic adaptation. BMC Genomics, 2010, 11, 307.	2.8	48
65	Optimizing Read Mapping to Reference Genomes to Determine Composition and Species Prevalence in Microbial Communities. PLoS ONE, 2012, 7, e36427.	2.5	48
66	Investigating hookworm genomes by comparative analysis of two Ancylostoma species. BMC Genomics, 2005, 6, 58.	2.8	47
67	Targeting Lysine Deacetylases (KDACs) in Parasites. PLoS Neglected Tropical Diseases, 2015, 9, e0004026.	3.0	47
68	Detection of putative secreted proteins in the plant-parasitic nematode Heterodera schachtii. Parasitology Research, 2006, 98, 414-424.	1.6	46
69	Transcriptome Analysis of Female and Male Xiphophorus maculatus Jp 163 A. PLoS ONE, 2011, 6, e18379.	2.5	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. Parasitology, 2013, 140, 499-508.	1.5	45
71	Mining Novel Effector Proteins from the Esophageal Gland Cells of <i>Meloidogyne incognita</i> . Molecular Plant-Microbe Interactions, 2014, 27, 965-974.	2.6	45
72	Biology and genome of Trichinella spiralis. WormBook, 2006, , 1-21.	5.3	45

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73	Dynamic changes in human-gut microbiome in relation to a placebo-controlled anthelminthic trial in Indonesia. PLoS Neglected Tropical Diseases, 2018, 12, e0006620.	3.0	44
74	Parasitic nematodes—From genomes to control. Veterinary Parasitology, 2007, 148, 31-42.	1.8	43
75	Sequence mining and transcript profiling to explore cyst nematode parasitism. BMC Genomics, 2009, 10, 58.	2.8	43
76	A novel role for C–C motif chemokine receptor 2 during infection with hypervirulent Mycobacterium tuberculosis. Mucosal Immunology, 2018, 11, 1727-1742.	6.0	43
77	Intestinal Transcriptomes of Nematodes: Comparison of the Parasites Ascaris suum and Haemonchus contortus with the Free-living Caenorhabditis elegans. PLoS Neglected Tropical Diseases, 2008, 2, e269.	3.0	42
78	Profiling of gender-regulated gene transcripts in the filarial nematode Brugia malayi by cDNA oligonucleotide array analysis. Molecular and Biochemical Parasitology, 2005, 143, 49-57.	1.1	41
79	Divergent evolution of arrested development in the dauer stage of Caenorhabditis elegans and the infective stage of Heterodera glycines. Genome Biology, 2007, 8, R211.	9.6	40
80	Nematode.net update 2011: addition of data sets and tools featuring next-generation sequencing data. Nucleic Acids Research, 2012, 40, D720-D728.	14.5	40
81	An expressed sequence tag analysis of the life-cycle of the parasitic nematode Strongyloides ratti. Molecular and Biochemical Parasitology, 2005, 142, 32-46.	1.1	39
82	Analysis of the Trichuris suis excretory/secretory proteins as a function of life cycle stage and their immunomodulatory properties. Scientific Reports, 2018, 8, 15921.	3.3	37
83	The canine hookworm genome: Analysis and classification of Ancylostoma caninum survey sequences. Molecular and Biochemical Parasitology, 2008, 157, 187-192.	1.1	36
84	Transcription profiling reveals stage- and function-dependent expression patterns in the filarial nematode Brugia malayi. BMC Genomics, 2012, 13, 184.	2.8	36
85	Using Existing Drugs as Leads for Broad Spectrum Anthelmintics Targeting Protein Kinases. PLoS Pathogens, 2013, 9, e1003149.	4.7	36
86	Transcriptomes and pathways associated with infectivity, survival and immunogenicity in Brugia malayi L3. BMC Genomics, 2009, 10, 267.	2.8	35
87	Transcripts analysis of the entomopathogenic nematode Steinernema carpocapsae induced in vitro with insect haemolymph. Molecular and Biochemical Parasitology, 2010, 169, 79-86.	1.1	35
88	Precise Dissection of an Escherichia coli O157:H7 Outbreak by Single Nucleotide Polymorphism Analysis. Journal of Clinical Microbiology, 2013, 51, 3950-3954.	3.9	35
89	Inter and intra-specific diversity of parasites that cause lymphatic filariasis. Infection, Genetics and Evolution, 2013, 14, 137-146.	2.3	34
90	Nematode.net update 2008: improvements enabling more efficient data mining and comparative nematode genomics. Nucleic Acids Research, 2009, 37, D571-D578.	14.5	33

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91	Coverage theories for metagenomic DNA sequencing based on a generalization of Stevens' theorem. Journal of Mathematical Biology, 2013, 67, 1141-1161.	1.9	33
92	Genome-Wide Analysis Reveals Novel Genes Essential for Heme Homeostasis in Caenorhabditis elegans. PLoS Genetics, 2010, 6, e1001044.	3.5	32
93	A vertebrate case study of the quality of assemblies derived from next-generation sequences. Genome Biology, 2011, 12, R31.	9.6	32
94	Targeting Protein-Protein Interactions for Parasite Control. PLoS ONE, 2011, 6, e18381.	2.5	31
95	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
96	Transcriptome analyses reveal protein and domain families that delineate stage-related development in the economically important parasitic nematodes, Ostertagia ostertagi and Cooperia oncophora. BMC Genomics, 2013, 14, 118.	2.8	31
97	Gene diversity and genetic variation in lung flukes (genusParagonimus). Transactions of the Royal Society of Tropical Medicine and Hygiene, 2016, 110, 6-12.	1.8	31
98	Tackling Hypotheticals in Helminth Genomes. Trends in Parasitology, 2018, 34, 179-183.	3.3	29
99	Stageâ€specific excretory–secretory small heat shock proteins from the parasitic nematode <i>Strongyloidesâ€fratti</i> – putative links to host's intestinal mucosal defense system. FEBS Journal, 2011, 278, 3319-3336.	4.7	28
100	Adaptive Radiation of the Flukes of the Family Fasciolidae Inferred from Genome-Wide Comparisons of Key Species. Molecular Biology and Evolution, 2020, 37, 84-99.	8.9	28
101	Downregulation of the Syk Signaling Pathway in Intestinal Dendritic Cells Is Sufficient To Induce Dendritic Cells That Inhibit Colitis. Journal of Immunology, 2016, 197, 2948-2957.	0.8	27
102	Conservation and global distribution of non-canonical antigens in Enterotoxigenic Escherichia coli. PLoS Neglected Tropical Diseases, 2019, 13, e0007825.	3.0	27
103	NemaPath: online exploration of KEGG-based metabolic pathways for nematodes. BMC Genomics, 2008, 9, 525.	2.8	26
104	Gender-Associated Genes in Filarial Nematodes Are Important for Reproduction and Potential Intervention Targets. PLoS Neglected Tropical Diseases, 2011, 5, e947.	3.0	26
105	Pan-phylum Comparison of Nematode Metabolic Potential. PLoS Neglected Tropical Diseases, 2015, 9, e0003788.	3.0	26
106	Skin Ecology during Sebaceous Drought—How SkinÂMicrobes Respond to Isotretinoin. Journal of Investigative Dermatology, 2019, 139, 732-735.	0.7	26
107	Stunting Is Preceded by Intestinal Mucosal Damage and Microbiome Changes and Is Associated with Systemic Inflammation in a Cohort of Peruvian Infants. American Journal of Tropical Medicine and Hygiene, 2019, 101, 1009-1017.	1.4	26
108	Identification of small molecule enzyme inhibitors as broad-spectrum anthelmintics. Scientific Reports, 2019, 9, 9085.	3.3	25

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109	Comprehensive analysis of the secreted proteome of adult Necator americanusÂhookworms. PLoS Neglected Tropical Diseases, 2020, 14, e0008237.	3.0	25
110	The bandit, a New DNA Transposon from a Hookworm—Possible Horizontal Genetic Transfer between Host and Parasite. PLoS Neglected Tropical Diseases, 2007, 1, e35.	3.0	24
111	Systematic analysis of insertions and deletions specific to nematode proteins and their proposed functional and evolutionary relevance. BMC Evolutionary Biology, 2009, 9, 23.	3.2	24
112	Systems Biology Studies of Adult Paragonimus Lung Flukes Facilitate the Identification of Immunodominant Parasite Antigens. PLoS Neglected Tropical Diseases, 2014, 8, e3242.	3.0	24
113	Variant in a common odorant-binding protein gene is associated with bitter sensitivity in people. Behavioural Brain Research, 2017, 329, 200-204.	2.2	24
114	The Effect of Gut Microbiome Composition on Human Immune Responses: An Exploration of Interference by Helminth Infections. Frontiers in Genetics, 2019, 10, 1028.	2.3	24
115	In-Depth Proteomic and Glycomic Analysis of the Adult-StageCooperia oncophoraExcretome/Secretome. Journal of Proteome Research, 2013, 12, 3900-3911.	3.7	23
116	Functional and Phylogenetic Characterization of Proteins Detected in Various Nematode Intestinal Compartments*. Molecular and Cellular Proteomics, 2015, 14, 812-827.	3.8	23
117	Dictyocaulus viviparus genome, variome and transcriptome elucidate lungworm biology and support future intervention. Scientific Reports, 2016, 6, 20316.	3.3	23
118	Effects of Doxycycline on gene expression in Wolbachia and Brugia malayi adult female worms in vivo. Journal of Biomedical Science, 2012, 19, 21.	7.0	22
119	Expressed sequence tags from life cycle stages of Trichinella spiralis: Application to biology and parasite control. Veterinary Parasitology, 2005, 132, 13-17.	1.8	21
120	A nuclear single-nucleotide polymorphism (SNP) potentially useful for the separation of Rhodnius prolixus from members of the Rhodnius robustus cryptic species complex (Hemiptera: Reduviidae). Infection, Genetics and Evolution, 2013, 14, 426-433.	2.3	21
121	Cracking the nodule worm code advances knowledge of parasite biology and biotechnology to tackle major diseases of livestock. Biotechnology Advances, 2015, 33, 980-991.	11.7	21
122	Transcriptomic and Proteomic Analyses of a Wolbachia-Free Filarial Parasite Provide Evidence of Trans-Kingdom Horizontal Gene Transfer. PLoS ONE, 2012, 7, e45777.	2.5	20
123	Pan-Nematoda Transcriptomic Elucidation of Essential Intestinal Functions and Therapeutic Targets With Broad Potential. EBioMedicine, 2015, 2, 1079-1089.	6.1	20
124	The genome of a blood fluke associated with human cancer. Nature Genetics, 2012, 44, 116-118.	21.4	19
125	The hookworm Ancylostoma ceylanicum intestinal transcriptome provides a platform for selecting drug and vaccine candidates. Parasites and Vectors, 2016, 9, 518.	2.5	19
126	Genome Sequence of Christensenella minuta DSM 22607 ^T . Genome Announcements, 2017, 5,	0.8	19

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127	Strategies for Undertaking Expressed Sequence Tag (EST) Projects. Methods in Molecular Biology, 2009, 533, 13-32.	0.9	19
128	An analysis of the transcriptome of Teladorsagia circumcincta: its biological and biotechnological implications. BMC Genomics, 2012, 13, S10.	2.8	18
129	TIMPs of parasitic helminths – a large-scale analysis of high-throughput sequence datasets. Parasites and Vectors, 2013, 6, 156.	2.5	18
130	Small Molecule Inhibitors of Metabolic Enzymes Repurposed as a New Class of Anthelmintics. ACS Infectious Diseases, 2018, 4, 1130-1145.	3.8	18
131	Comparative genomics and transcriptomics of 4 Paragonimus species provide insights into lung fluke parasitism and pathogenesis. GigaScience, 2020, 9, .	6.4	18
132	Improving eukaryotic genome annotation using single molecule mRNA sequencing. BMC Genomics, 2018, 19, 172.	2.8	17
133	HelmCoP: An Online Resource for Helminth Functional Genomics and Drug and Vaccine Targets Prioritization. PLoS ONE, 2011, 6, e21832.	2.5	17
134	Identification of Hookworm DAF-16/FOXO Response Elements and Direct Gene Targets. PLoS ONE, 2010, 5, e12289.	2.5	16
135	Alteration of the fecal microbiota in Chinese patients with <i>Schistosoma japonicum</i> infection. Parasite, 2021, 28, 1.	2.0	16
136	An Integrated Approach to Identify New Anti-Filarial Leads to Treat River Blindness, a Neglected Tropical Disease. Pathogens, 2021, 10, 71.	2.8	16
137	Proteomic Analysis of Oesophagostomum dentatum (Nematoda) during Larval Transition, and the Effects of Hydrolase Inhibitors on Development. PLoS ONE, 2013, 8, e63955.	2.5	16
138	mBLAST: Keeping up with the Sequencing Explosion for (Meta) Genome Analysis. Journal of Data Mining in Genomics & Proteomics, 2013, 04, .	0.5	16
139	Identification and analysis of genes expressed in the adult filarial parasitic nematode Dirofilaria immitis. International Journal for Parasitology, 2006, 36, 829-839.	3.1	15
140	The mixed model for the analysis of a repeatedâ€measurement multivariate count data. Statistics in Medicine, 2019, 38, 2248-2268.	1.6	15
141	Mycobacterium tuberculosis HN878 Infection Induces Human-Like B-Cell Follicles in Mice. Journal of Infectious Diseases, 2020, 221, 1636-1646.	4.0	15
142	The endosymbiont WolbachiaÂrebounds following antibiotic treatment. PLoS Pathogens, 2020, 16, e1008623.	4.7	15
143	Peptidases Compartmentalized to the Ascaris suum Intestinal Lumen and Apical Intestinal Membrane. PLoS Neglected Tropical Diseases, 2015, 9, e3375.	3.0	14
144	Trichinella spiralis : Adaptation and parasitism. Veterinary Parasitology, 2016, 231, 8-21.	1.8	14

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145	Omics Driven Understanding of the Intestines of Parasitic Nematodes. Frontiers in Genetics, 2019, 10, 652.	2.3	13
146	Systems analysis-based assessment of post-treatment adverse events in lymphatic filariasis. PLoS Neglected Tropical Diseases, 2019, 13, e0007697.	3.0	13
147	Characterization of the Complete Mitochondrial Genomes of Two Sibling Species of Parasitic Roundworms, Haemonchus contortus and Teladorsagia circumcincta. Frontiers in Genetics, 2020, 11, 573395.	2.3	13
148	Whipworm-Associated Intestinal Microbiome Members Consistent Across Both Human and Mouse Hosts. Frontiers in Cellular and Infection Microbiology, 2021, 11, 637570.	3.9	13
149	<i>Ascaris suum</i> Informs Extrasynaptic Volume Transmission in Nematodes. ACS Chemical Neuroscience, 2021, 12, 3176-3188.	3.5	13
150	An Integrated Multiomics Approach to Identify Candidate Antigens for Serodiagnosis of Human Onchocerciasis*. Molecular and Cellular Proteomics, 2015, 14, 3224-3233.	3.8	12
151	A Praziquantel Treatment Study of Immune and Transcriptome Profiles in <i>Schistosoma haematobium</i> -Infected Gabonese Schoolchildren. Journal of Infectious Diseases, 2020, 222, 2103-2113.	4.0	12
152	Nematode gene sequences: update for december 2005. Journal of Nematology, 2005, 37, 417-21.	0.9	12
153	Molecular determinants archetypical to the phylum Nematoda. BMC Genomics, 2009, 10, 114.	2.8	11
154	The transcriptomes of the cattle parasitic nematode Ostertagia ostartagi. Veterinary Parasitology, 2009, 162, 89-99.	1.8	11
155	Large-Scale Sequencing and Analytical Processing of ESTs. Methods in Molecular Biology, 2009, 533, 153-187.	0.9	11
156	Compartmentalization of functions and predicted miRNA regulation among contiguous regions of the nematode intestine. RNA Biology, 2017, 14, 1335-1352.	3.1	11
157	The complete mitochondrial genome of the New Zealand parasitic roundworm Teladorsagia circumcincta (Trichostrongyloidea: Haemonchidae) field strain NZ_Teci_NP. Mitochondrial DNA Part B: Resources, 2019, 4, 2869-2871.	0.4	11
158	Areas of Metabolomic Exploration for Helminth Infections. ACS Infectious Diseases, 2021, 7, 206-214.	3.8	11
159	Lung Epithelial Signaling Mediates Early Vaccine-Induced CD4 ⁺ T Cell Activation and <i>Mycobacterium tuberculosis</i> Control. MBio, 2021, 12, e0146821.	4.1	11
160	Phylum-Spanning Neuropeptide GPCR Identification and Prioritization: Shaping Drug Target Discovery Pipelines for Nematode Parasite Control. Frontiers in Endocrinology, 2021, 12, 718363.	3.5	11
161	Advances in the sequencing of the genome of the adenophorean nematode Trichinella spiralis. Parasitology, 2008, 135, 869-880.	1.5	10
162	Identification and characterization of alternative splicing in parasitic nematode transcriptomes. Parasites and Vectors, 2014, 7, 151.	2.5	10

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163	Conservation and diversification of the transcriptomes of adult Paragonimus westermani and P. skrjabini. Parasites and Vectors, 2016, 9, 497.	2.5	10
164	A Multi-Omics Database for Parasitic Nematodes and Trematodes. Methods in Molecular Biology, 2018, 1757, 371-397.	0.9	10
165	De novo identification of toxicants that cause irreparable damage to parasitic nematode intestinal cells. PLoS Neglected Tropical Diseases, 2020, 14, e0007942.	3.0	10
166	Exploring metazoan evolution through dynamic and holistic changes in protein families and domains. BMC Evolutionary Biology, 2012, 12, 138.	3.2	9
167	Gene expression analysis distinguishes tissue-specific and gender-related functions among adult Ascaris suum tissues. Molecular Genetics and Genomics, 2013, 288, 243-260.	2.1	9
168	De novo Assembly of the Brugia malayi Genome Using Long Reads from a Single MinION Flowcell. Scientific Reports, 2019, 9, 19521.	3.3	9
169	A tale of three kingdoms: members of the Phylum Nematoda independently acquired the detoxifying enzyme cyanase through horizontal gene transfer from plants and bacteria. Parasitology, 2019, 146, 445-452.	1.5	9
170	Transcriptomic analysis of hookworm Ancylostoma ceylanicum life cycle stages reveals changes in G-protein coupled receptor diversity associated with the onset of parasitism. International Journal for Parasitology, 2020, 50, 603-610.	3.1	9
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