

# Makedonka Mitreva

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

195  
papers

19,133  
citations

49  
h-index

137  
g-index

223  
ext. papers

23,163  
ext. citations

8.7  
avg, IF

7.87  
L-index

#	Paper	IF	Citations
195	Horizontal gene transfer provides insights into the deep evolutionary history and biology of .. <i>Food and Waterborne Parasitology</i> , <b>2022</b> , 27, e00155	6	0
194	Characterization of a novel microfilarial antigen for diagnosis of <i>Wuchereria bancrofti</i> infections. <i>PLoS Neglected Tropical Diseases</i> , <b>2022</b> , 16, e0010407	4.8	0
193	The Differences in the Susceptibility Patterns to Triclabendazole Sulfoxide in Field Isolates of <i>Fasciola hepatica</i> Are Associated with Geographic, Seasonal, and Morphometric Variations. <i>Pathogens</i> , <b>2022</b> , 11, 625	4.5	0
192	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
191	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
190	Whipworm-Associated Intestinal Microbiome Members Consistent Across Both Human and Mouse Hosts. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2021</b> , 11, 637570	5.9	4
189	Characterization and localization of antigens for serodiagnosis of human paragonimiasis. <i>Parasitology Research</i> , <b>2021</b> , 120, 535-545	2.4	3
188	Altered ratio of dendritic cell subsets in skin-draining lymph nodes promotes Th2-driven contact hypersensitivity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	2
187	Areas of Metabolomic Exploration for Helminth Infections. <i>ACS Infectious Diseases</i> , <b>2021</b> , 7, 206-214	5.5	1
186	Isolation and characterization of a novel bacteriophage WO from <i>Allonemobius socius</i> crickets in Missouri. <i>PLoS ONE</i> , <b>2021</b> , 16, e0250051	3.7	2
185	Informs Extrasynaptic Volume Transmission in Nematodes. <i>ACS Chemical Neuroscience</i> , <b>2021</b> , 12, 3176-3188	3.8	1
184	Lung Epithelial Signaling Mediates Early Vaccine-Induced CD4 T Cell Activation and Control. <i>MBio</i> , <b>2021</b> , 12, e0146821	7.8	4
183	Phylum-Spanning Neuropeptide GPCR Identification and Prioritization: Shaping Drug Target Discovery Pipelines for Nematode Parasite Control. <i>Frontiers in Endocrinology</i> , <b>2021</b> , 12, 718363	5.7	0
182	Alteration of the fecal microbiota in Chinese patients with <i>Schistosoma japonicum</i> infection. <i>Parasite</i> , <b>2021</b> , 28, 1	3	4
181	An Integrated Approach to Identify New Anti-Filarial Leads to Treat River Blindness, a Neglected Tropical Disease. <i>Pathogens</i> , <b>2021</b> , 10,	4.5	3
180	De novo identification of toxicants that cause irreparable damage to parasitic nematode intestinal cells. <i>PLoS Neglected Tropical Diseases</i> , <b>2020</b> , 14, e0007942	4.8	3
179	Comprehensive analysis of the secreted proteome of adult <i>Necator americanus</i> hookworms. <i>PLoS Neglected Tropical Diseases</i> , <b>2020</b> , 14, e0008237	4.8	11

178	Transcriptomic analysis of hookworm <i>Ancylostoma ceylanicum</i> life cycle stages reveals changes in G-protein coupled receptor diversity associated with the onset of parasitism. <i>International Journal for Parasitology</i> , <b>2020</b> , 50, 603-610	4.3	4
177	The endosymbiont <i>Wolbachia</i> rebounds following antibiotic treatment. <i>PLoS Pathogens</i> , <b>2020</b> , 16, e1008683	6.8	7
176	Immune correlates of tuberculosis disease and risk translate across species. <i>Science Translational Medicine</i> , <b>2020</b> , 12,	17.5	24
175	Improving Characterization of Understudied Human Microbiomes Using Targeted Phylogenetics. <i>MSystems</i> , <b>2020</b> , 5,	7.6	1
174	IFN signaling and neutrophil degranulation transcriptional signatures are induced during SARS-CoV-2 infection <b>2020</b> ,		11
173	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
172	<i>Mycobacterium tuberculosis</i> HN878 Infection Induces Human-Like B-Cell Follicles in Mice. <i>Journal of Infectious Diseases</i> , <b>2020</b> , 221, 1636-1646	7	6
171	A Praziquantel Treatment Study of Immune and Transcriptome Profiles in <i>Schistosoma haematobium</i> -Infected Gabonese Schoolchildren. <i>Journal of Infectious Diseases</i> , <b>2020</b> , 222, 2103-2113	7	5
170	Comparative genomics and transcriptomics of 4 <i>Paragonimus</i> species provide insights into lung fluke parasitism and pathogenesis. <i>GigaScience</i> , <b>2020</b> , 9,	7.6	12
169	Rapid determination of nematode cell and organ susceptibility to toxic treatments. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , <b>2020</b> , 14, 167-182	4	1
168	Characterization of the Complete Mitochondrial Genomes of Two Sibling Species of Parasitic Roundworms, and. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 573395	4.5	6
167	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
166	The complete mitochondrial genome of the New Zealand parasitic roundworm (Trichostrongyloidea: Haemonchidae) field strain NZ_Teci_NP. <i>Mitochondrial DNA Part B: Resources</i> , <b>2019</b> , 4, 2869-2871	0.5	7
165	Systems analysis-based assessment of post-treatment adverse events in lymphatic filariasis. <i>PLoS Neglected Tropical Diseases</i> , <b>2019</b> , 13, e0007697	4.8	7
164	Omics-Driven Knowledge-Based Discovery of Anthelmintic Targets and Drugs <b>2019</b> , 329-358		1
163	V1 and V2 Domains of HIV Envelope Contribute to CCR5 Antagonist Resistance. <i>Journal of Virology</i> , <b>2019</b> , 93,	6.6	4
162	Omics Driven Understanding of the Intestines of Parasitic Nematodes. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 652	4.5	5
161	Identification of small molecule enzyme inhibitors as broad-spectrum anthelmintics. <i>Scientific Reports</i> , <b>2019</b> , 9, 9085	4.9	11

160	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
159	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> , <b>2019</b> , 101, 1009-1017	3.2	8
158	The mixed model for the analysis of a repeated-measurement multivariate count data. <i>Statistics in Medicine</i> , <b>2019</b> , 38, 2248-2268	2.3	8
157	De novo Assembly of the <i>Brugia malayi</i> Genome Using Long Reads from a Single MinION Flowcell. <i>Scientific Reports</i> , <b>2019</b> , 9, 19521	4.9	5
156	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
155	Conservation and global distribution of non-canonical antigens in Enterotoxigenic <i>Escherichia coli</i> . <i>PLoS Neglected Tropical Diseases</i> , <b>2019</b> , 13, e0007825	4.8	11
154	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
153	A tale of three kingdoms: members of the Phylum Nematoda independently acquired the detoxifying enzyme cyanase through horizontal gene transfer from plants and bacteria. <i>Parasitology</i> , <b>2019</b> , 146, 445-452	2.7	4
152	Tackling Hypotheticals in Helminth Genomes. <i>Trends in Parasitology</i> , <b>2018</b> , 34, 179-183	6.4	20
151	Improving eukaryotic genome annotation using single molecule mRNA sequencing. <i>BMC Genomics</i> , <b>2018</b> , 19, 172	4.5	9
150	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
149	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
148	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
147	A novel role for C-C motif chemokine receptor 2 during infection with hypervirulent <i>Mycobacterium tuberculosis</i> . <i>Mucosal Immunology</i> , <b>2018</b> , 11, 1727-1742	9.2	19
146	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
145	<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
144	A Multi-Omics Database for Parasitic Nematodes and Trematodes. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1757, 371-397	1.4	7
143	Compartmentalization of functions and predicted miRNA regulation among contiguous regions of the nematode intestine. <i>RNA Biology</i> , <b>2017</b> , 14, 1335-1352	4.8	7

142	Genome Sequence of <i>Christensenella minuta</i> DSM 22607T. <i>Genome Announcements</i> , <b>2017</b> , 5,		11
141	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
140	Direct experimental manipulation of intestinal cells in <i>Ascaris suum</i> , with minor influences on the global transcriptome. <i>International Journal for Parasitology</i> , <b>2017</b> , 47, 271-279	4.3	5
139	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
138	Insights Into <i>Onchocerca volvulus</i> Population Biology Through Multilocus Immunophenotyping. <i>Journal of Infectious Diseases</i> , <b>2017</b> , 216, 736-743	7	2
137	The Microbiome in Infectious Diseases <b>2017</b> , 68-74.e2		2
136	Monocyte dysregulation and systemic inflammation during pediatric falciparum malaria. <i>JCI Insight</i> , <b>2017</b> , 2,	9.9	36
135	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> , <b>2017</b> , 13, e1006537	6	65
134	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
133	Genome Sequences of 12 Bacterial Isolates Obtained from the Urine of Pregnant Women. <i>Genome Announcements</i> , <b>2016</b> , 4,		1
132	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
131	Characterization of parasite-specific indels and their proposed relevance for selective anthelmintic drug targeting. <i>Infection, Genetics and Evolution</i> , <b>2016</b> , 39, 201-211	4.5	6
130	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
129	Application of Taxonomic Modeling to Microbiota Data Mining for Detection of Helminth Infection in Global Populations. <i>Data</i> , <b>2016</b> , 1,	2.3	6
128	Conservation and diversification of the transcriptomes of adult <i>Paragonimus westermani</i> and <i>P. skrjabini</i> . <i>Parasites and Vectors</i> , <b>2016</b> , 9, 497	4	8
127	<i>Trichinella spiralis</i> : Adaptation and parasitism. <i>Veterinary Parasitology</i> , <b>2016</b> , 231, 8-21	2.8	11
126	The hookworm <i>Ancylostoma ceylanicum</i> intestinal transcriptome provides a platform for selecting drug and vaccine candidates. <i>Parasites and Vectors</i> , <b>2016</b> , 9, 518	4	15
125	<i>Dictyocaulus viviparus</i> genome, variome and transcriptome elucidate lungworm biology and support future intervention. <i>Scientific Reports</i> , <b>2016</b> , 6, 20316	4.9	17

124	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
123	Evolution of coreceptor utilization to escape CCR5 antagonist therapy. <i>Virology</i> , <b>2016</b> , 494, 198-214	3.6	6
122	Genome Sequences of 11 Human Vaginal Actinobacteria Strains. <i>Genome Announcements</i> , <b>2016</b> , 4,		5
121	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
120	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
119	Peptidases compartmentalized to the <i>Ascaris suum</i> intestinal lumen and apical intestinal membrane. <i>PLoS Neglected Tropical Diseases</i> , <b>2015</b> , 9, e3375	4.8	8
118	Pan-phylum Comparison of Nematode Metabolic Potential. <i>PLoS Neglected Tropical Diseases</i> , <b>2015</b> , 9, e0003788	4.8	22
117	Metabolic and metagenomic outcomes from early-life pulsed antibiotic treatment. <i>Nature Communications</i> , <b>2015</b> , 6, 7486	17.4	232
116	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
115	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
114	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
113	An Integrated Multiomics Approach to Identify Candidate Antigens for Serodiagnosis of Human Onchocerciasis. <i>Molecular and Cellular Proteomics</i> , <b>2015</b> , 14, 3224-33	7.6	9
112	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
111	Targeting Lysine Deacetylases (KDACs) in Parasites. <i>PLoS Neglected Tropical Diseases</i> , <b>2015</b> , 9, e0004026	4.8	36
110	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
109	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
108	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
107	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

106	Genome of the human hookworm <i>Necator americanus</i> . <i>Nature Genetics</i> , <b>2014</b> , 46, 261-269	36.3	139
105	Analysis of the transcriptome of adult <i>Dictyocaulus filaria</i> and comparison with <i>Dictyocaulus viviparus</i> , with a focus on molecules involved in host-parasite interactions. <i>International Journal for Parasitology</i> , <b>2014</b> , 44, 251-61	4.3	4
104	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
103	Impact of experimental hookworm infection on the human gut microbiota. <i>Journal of Infectious Diseases</i> , <b>2014</b> , 210, 1431-4	7	100
102	Proteomics elucidates key molecules involved in exsheathment in vitro in <i>Oesophagostomum dentatum</i> . <i>International Journal for Parasitology</i> , <b>2014</b> , 44, 759-64	4.3	3
101	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
100	Identification and characterization of alternative splicing in parasitic nematode transcriptomes. <i>Parasites and Vectors</i> , <b>2014</b> , 7, 151	4	4
99	Exploration of bacterial community classes in major human habitats. <i>Genome Biology</i> , <b>2014</b> , 15, R66	18.3	83
98	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
97	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
96	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
95	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
94	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
93	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
92	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
91	Gene expression analysis distinguishes tissue-specific and gender-related functions among adult <i>Ascaris suum</i> tissues. <i>Molecular Genetics and Genomics</i> , <b>2013</b> , 288, 243-60	3.1	8
90	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
89	Genomic variation landscape of the human gut microbiome. <i>Nature</i> , <b>2013</b> , 493, 45-50	50.4	571

88	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
87	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
86	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
85	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
84	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
83	Using existing drugs as leads for broad spectrum anthelmintics targeting protein kinases. <i>PLoS Pathogens</i> , <b>2013</b> , 9, e1003149	7.6	32
82	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
81	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
80	Proteomic analysis of <i>Oesophagostomum dentatum</i> (Nematoda) during larval transition, and the effects of hydrolase inhibitors on development. <i>PLoS ONE</i> , <b>2013</b> , 8, e63955	3.7	12
79	Silencing of germline-expressed genes by DNA elimination in somatic cells. <i>Developmental Cell</i> , <b>2012</b> , 23, 1072-80	10.2	79
78	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , <b>2012</b> , 486, 207-14	50.4	6938
77	A framework for human microbiome research. <i>Nature</i> , <b>2012</b> , 486, 215-21	50.4	1722
76	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> , <b>2012</b> , 19, 21	13.3	18
75	Exploring metazoan evolution through dynamic and holistic changes in protein families and domains. <i>BMC Evolutionary Biology</i> , <b>2012</b> , 12, 138	3	9
74	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
73	An analysis of the transcriptome of <i>Teladorsagia circumcincta</i> : its biological and biotechnological implications. <i>BMC Genomics</i> , <b>2012</b> , 13 Suppl 7, S10	4.5	16
72	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
71	Transcriptomic and proteomic analyses of a <i>Wolbachia</i> -free filarial parasite provide evidence of trans-kingdom horizontal gene transfer. <i>PLoS ONE</i> , <b>2012</b> , 7, e45777	3.7	20



70	Metabolic reconstruction for metagenomic data and its application to the human microbiome. <i>PLoS Computational Biology</i> , <b>2012</b> , 8, e1002358	5	730
69	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
68	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
67	Transcriptomes of Plant-Parasitic Nematodes <b>2011</b> , 119-138		4
66	RNAi effector diversity in nematodes. <i>PLoS Neglected Tropical Diseases</i> , <b>2011</b> , 5, e1176	4.8	104
65	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
64	Targeting protein-protein interactions for parasite control. <i>PLoS ONE</i> , <b>2011</b> , 6, e18381	3.7	19
63	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
62	The draft genome of the parasitic nematode <i>Trichinella spiralis</i> . <i>Nature Genetics</i> , <b>2011</b> , 43, 228-35	36.3	230
61	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , <b>2011</b> , 469, 529-33	50.4	431
60	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
59	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
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