

Matt Berriman

List of Publications by Year in descending order

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Version: 2024-02-01

290
papers

53,545
citations

2669

95
h-index

1589

216
g-index

352
all docs

352
docs citations

352
times ranked

51710
citing authors

#	ARTICLE	IF	CITATIONS
1	Hatching of parasitic nematode eggs: a crucial step determining infection. Trends in Parasitology, 2022, 38, 174-187.	1.5	28
2	Long-read assembly and comparative evidence-based reanalysis of <i>Cryptosporidium</i> genome sequences reveal expanded transporter repertoire and duplication of entire chromosome ends including subtelomeric regions. Genome Research, 2022, 32, 203-213.	2.4	26
3	Genomic and Phenotypic Characterization of Experimentally Selected Resistant <i>Leishmania donovani</i> Reveals a Role for Dynamin-1-Like Protein in the Mechanism of Resistance to a Novel Antileishmanial Compound. MBio, 2022, 13, e0326421.	1.8	5
4	WormBase in 2022â€”data, processes, and tools for analyzing <i>Caenorhabditis elegans</i> . Genetics, 2022, 220, .	1.2	128
5	Defining the early stages of intestinal colonisation by whipworms. Nature Communications, 2022, 13, 1725.	5.8	18
6	Geographic Origin and Vertical Transmission of <i>Leishmania infantum</i> Parasites in Hunting Hounds, United States. Emerging Infectious Diseases, 2022, 28, .	2.0	3
7	Characterising genome architectures using genome decomposition analysis. BMC Genomics, 2022, 23, .	1.2	2
8	<i>Schistosoma mansoni</i> Eggs Modulate the Timing of Granuloma Formation to Promote Transmission. Cell Host and Microbe, 2021, 29, 58-67.e5.	5.1	39
9	Tumor Necrosis Factor and <i>Schistosoma mansoni</i> egg antigen omega-1 shape distinct aspects of the early egg-induced granulomatous response. PLoS Neglected Tropical Diseases, 2021, 15, e0008814.	1.3	7
10	Individual-level variations in malaria susceptibility and acquisition of clinical protection. Wellcome Open Research, 2021, 6, 22.	0.9	6
11	Mapping immune variation and var gene switching in naive hosts infected with <i>Plasmodium falciparum</i> . ELife, 2021, 10, .	2.8	22
12	Expression profiling of <i>Echinococcus multilocularis</i> miRNAs throughout metacestode development in vitro. PLoS Neglected Tropical Diseases, 2021, 15, e0009297.	1.3	7
13	10-year longitudinal study of malaria in children: Insights into acquisition and maintenance of naturally acquired immunity. Wellcome Open Research, 2021, 6, 79.	0.9	7
14	Mapping Rora expression in resting and activated CD4+ T cells. PLoS ONE, 2021, 16, e0251233.	1.1	29
15	Whole-genome sequencing of <i>Schistosoma mansoni</i> reveals extensive diversity with limited selection despite mass drug administration. Nature Communications, 2021, 12, 4776.	5.8	28
16	The Transcriptome of <i>Schistosoma mansoni</i> Developing Eggs Reveals Key Mediators in Pathogenesis and Life Cycle Propagation. Frontiers in Tropical Diseases, 2021, 2, .	0.5	6
17	An uneven race: genome editing for parasitic worms. Nature Reviews Microbiology, 2021, 19, 621-621.	13.6	6
18	The complete genome sequence of <i>Eimeria tenella</i> (Tyzzer 1929), a common gut parasite of chickens. Wellcome Open Research, 2021, 6, 225.	0.9	14

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19	The Gene Ontology resource: enriching a GOld mine. <i>Nucleic Acids Research</i> , 2021, 49, D325-D334.	6.5	2,416
20	Daily rhythms in gene expression of the human parasite <i>Schistosoma mansoni</i> . <i>BMC Biology</i> , 2021, 19, 255.	1.7	12
21	Morphological and genomic characterisation of the <i>Schistosoma</i> hybrid infecting humans in Europe reveals admixture between <i>Schistosoma haematobium</i> and <i>Schistosoma bovis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0010062.	1.3	22
22	An Experimental Human Blood-Stage Model for Studying <i>Plasmodium malariae</i> Infection. <i>Journal of Infectious Diseases</i> , 2020, 221, 948-955.	1.9	18
23	Organoids – New Models for Host–Helminth Interactions. <i>Trends in Parasitology</i> , 2020, 36, 170-181.	1.5	43
24	Analysis of <i>Plasmodium vivax</i> schizont transcriptomes from field isolates reveals heterogeneity of expression of genes involved in host-parasite interactions. <i>Scientific Reports</i> , 2020, 10, 16667.	1.6	23
25	Development of caecaloids to study host–pathogen interactions: new insights into immunoregulatory functions of <i>Trichuris muris</i> extracellular vesicles in the caecum. <i>International Journal for Parasitology</i> , 2020, 50, 707-718.	1.3	23
26	Genomic and transcriptomic variation defines the chromosome-scale assembly of <i>Haemonchus contortus</i> , a model gastrointestinal worm. <i>Communications Biology</i> , 2020, 3, 656.	2.0	91
27	Genomic and transcriptomic evidence for descent from <i>Plasmodium</i> and loss of blood schizogony in <i>Hepatocystis</i> parasites from naturally infected red colobus monkeys. <i>PLoS Pathogens</i> , 2020, 16, e1008717.	2.1	18
28	Ecological divergence and hybridization of Neotropical <i>Leishmania</i> parasites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25159-25168.	3.3	60
29	Large-scale RNAi screening uncovers therapeutic targets in the parasite <i>Schistosoma mansoni</i> . <i>Science</i> , 2020, 369, 1649-1653.	6.0	50
30	Evaluation of whole genome amplification and bioinformatic methods for the characterization of <i>Leishmania</i> genomes at a single cell level. <i>Scientific Reports</i> , 2020, 10, 15043.	1.6	20
31	Single-cell atlas of the first intra-mammalian developmental stage of the human parasite <i>Schistosoma mansoni</i> . <i>Nature Communications</i> , 2020, 11, 6411.	5.8	51
32	Baseline Gut Microbiota Composition Is Associated With <i>Schistosoma mansoni</i> Infection Burden in Rodent Models. <i>Frontiers in Immunology</i> , 2020, 11, 593838.	2.2	21
33	Complete representation of a tapeworm genome reveals chromosomes capped by centromeres, necessitating a dual role in segregation and protection. <i>BMC Biology</i> , 2020, 18, 165.	1.7	19
34	Transcriptome of the parasitic flatworm <i>Schistosoma mansoni</i> during intra-mammalian development. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0007743.	1.3	24
35	Nearly Complete Genome Sequence of <i>Brugia malayi</i> Strain FR3. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	13
36	An integrated national scale SARS-CoV-2 genomic surveillance network. <i>Lancet Microbe</i> , The, 2020, 1, e99-e100.	3.4	232

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37	Screening of a Library of Recombinant <i>Schistosoma mansoni</i> Proteins With Sera From Murine and Human Controlled Infections Identifies Early Serological Markers. <i>Journal of Infectious Diseases</i> , 2020, , .	1.9	9
38	Refining the transcriptome of the human malaria parasite <i>Plasmodium falciparum</i> using amplification-free RNA-seq. <i>BMC Genomics</i> , 2020, 21, 395.	1.2	71
39	Sex chromosome evolution in parasitic nematodes of humans. <i>Nature Communications</i> , 2020, 11, 1964.	5.8	38
40	Genomic analysis of natural intra-specific hybrids among Ethiopian isolates of <i>Leishmania donovani</i> . <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0007143.	1.3	17
41	Large CRISPR-Cas-induced deletions in the oxamniquine resistance locus of the human parasite <i>Schistosoma mansoni</i> . <i>Wellcome Open Research</i> , 2020, 5, 178.	0.9	19
42	Large CRISPR-Cas-induced deletions in the oxamniquine resistance locus of the human parasite <i>Schistosoma mansoni</i> . <i>Wellcome Open Research</i> , 2020, 5, 178.	0.9	27
43	Population genomic evidence that human and animal infections in Africa come from the same populations of <i>Dracunculus medinensis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008623.	1.3	18
44	Extracellular non-coding RNA signatures of the metacystode stage of <i>Echinococcus multilocularis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008890.	1.3	16
45	Global genome diversity of the <i>Leishmania donovani</i> complex. <i>ELife</i> , 2020, 9, .	2.8	90
46	Transcriptome of the parasitic flatworm <i>Schistosoma mansoni</i> during intra-mammalian development. , 2020, 14, e0007743.		0
47	Transcriptome of the parasitic flatworm <i>Schistosoma mansoni</i> during intra-mammalian development. , 2020, 14, e0007743.		0
48	Transcriptome of the parasitic flatworm <i>Schistosoma mansoni</i> during intra-mammalian development. , 2020, 14, e0007743.		0
49	Transcriptome of the parasitic flatworm <i>Schistosoma mansoni</i> during intra-mammalian development. , 2020, 14, e0007743.		0
50	Title is missing!. , 2020, 16, e1008717.		0
51	Title is missing!. , 2020, 16, e1008717.		0
52	Title is missing!. , 2020, 16, e1008717.		0
53	Title is missing!. , 2020, 16, e1008717.		0
54	The Malaria Cell Atlas: Single parasite transcriptomes across the complete <i>Plasmodium</i> life cycle. <i>Science</i> , 2019, 365, .	6.0	198

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55	The global diversity of <i>Haemonchus contortus</i> is shaped by human intervention and climate. <i>Nature Communications</i> , 2019, 10, 4811.	5.8	63
56	Evaluation of DNA Extraction Methods on Individual Helminth Egg and Larval Stages for Whole-Genome Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 826.	1.1	30
57	Identification and expression profiling of microRNAs in <i>Hymenolepis</i> . <i>International Journal for Parasitology</i> , 2019, 49, 211-223.	1.3	13
58	Population genomic and evolutionary modelling analyses reveal a single major QTL for ivermectin drug resistance in the pathogenic nematode, <i>Haemonchus contortus</i> . <i>BMC Genomics</i> , 2019, 20, 218.	1.2	68
59	Repeated clinical malaria episodes are associated with modification of the immune system in children. <i>BMC Medicine</i> , 2019, 17, 60.	2.3	37
60	Genomic and Metabolomic Polymorphism among Experimentally Selected Paromomycin-Resistant <i>Leishmania donovani</i> Strains. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 64, .	1.4	16
61	Genomes of <i>Leishmania</i> parasites directly sequenced from patients with visceral leishmaniasis in the Indian subcontinent. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007900.	1.3	48
62	Comparative genomics of the major parasitic worms. <i>Nature Genetics</i> , 2019, 51, 163-174.	9.4	377
63	Exclusive dependence of IL-10R1± signalling on intestinal microbiota homeostasis and control of whipworm infection. <i>PLoS Pathogens</i> , 2019, 15, e1007265.	2.1	24
64	Progression of the canonical reference malaria parasite genome from 2002â€“2019. <i>Wellcome Open Research</i> , 2019, 4, 58.	0.9	51
65	Progression of the canonical reference malaria parasite genome from 2002â€“2019. <i>Wellcome Open Research</i> , 2019, 4, 58.	0.9	47
66	GeneDB and Wikidata. <i>Wellcome Open Research</i> , 2019, 4, 114.	0.9	2
67	Systematic screening of 96 <i>Schistosoma mansoni</i> cell-surface and secreted antigens does not identify any strongly protective vaccine candidates in a mouse model of infection. <i>Wellcome Open Research</i> , 2019, 4, 159.	0.9	30
68	Evolutionary analysis of the most polymorphic gene family in falciparum malaria. <i>Wellcome Open Research</i> , 2019, 4, 193.	0.9	64
69	Programmed genome editing of the omega-1 ribonuclease of the blood fluke, <i>Schistosoma mansoni</i> . <i>ELife</i> , 2019, 8, .	2.8	87
70	GeneDB and Wikidata. <i>Wellcome Open Research</i> , 2019, 4, 114.	0.9	0
71	Genetic Diversity of <i>Cryptosporidium hominis</i> in a Bangladeshi Community as Revealed by Whole-Genome Sequencing. <i>Journal of Infectious Diseases</i> , 2018, 218, 259-264.	1.9	47
72	Complete avian malaria parasite genomes reveal features associated with lineage-specific evolution in birds and mammals. <i>Genome Research</i> , 2018, 28, 547-560.	2.4	78

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73	A Genome Resequencing-Based Genetic Map Reveals the Recombination Landscape of an Outbred Parasitic Nematode in the Presence of Polyploidy and Polyandry. <i>Genome Biology and Evolution</i> , 2018, 10, 396-409.	1.1	58
74	Transcriptomic profiling of nematode parasites surviving vaccine exposure. <i>International Journal for Parasitology</i> , 2018, 48, 395-402.	1.3	20
75	A method for single pair mating in an obligate parasitic nematode. <i>International Journal for Parasitology</i> , 2018, 48, 159-165.	1.3	11
76	WormBase 2017: molting into a new stage. <i>Nucleic Acids Research</i> , 2018, 46, D869-D874.	6.5	172
77	Genome-wide transcriptome profiling and spatial expression analyses identify signals and switches of development in tapeworms. <i>EvoDevo</i> , 2018, 9, 21.	1.3	30
78	Pre-clinical evaluation of a <i>P. berghei</i> -based whole-sporozoite malaria vaccine candidate. <i>Npj Vaccines</i> , 2018, 3, 54.	2.9	15
79	The mRNA cap methyltransferase gene <i>TbCMT1</i> is not essential in vitro but is a virulence factor in vivo for bloodstream form <i>Trypanosoma brucei</i> . <i>PLoS ONE</i> , 2018, 13, e0201263.	1.1	2
80	Genomes of all known members of a <i>Plasmodium</i> subgenus reveal paths to virulent human malaria. <i>Nature Microbiology</i> , 2018, 3, 687-697.	5.9	129
81	Using WormBase ParaSite: An Integrated Platform for Exploring Helminth Genomic Data. <i>Methods in Molecular Biology</i> , 2018, 1757, 471-491.	0.4	48
82	Histone methylation changes are required for life cycle progression in the human parasite <i>Schistosoma mansoni</i> . <i>PLoS Pathogens</i> , 2018, 14, e1007066.	2.1	57
83	Single-cell RNA-seq reveals hidden transcriptional variation in malaria parasites. <i>ELife</i> , 2018, 7, .	2.8	171
84	Cyclin-dependent kinase 12 is a drug target for visceral leishmaniasis. <i>Nature</i> , 2018, 560, 192-197.	13.7	112
85	Flatworm-specific transcriptional regulators promote the specification of tegumental progenitors in <i>Schistosoma mansoni</i> . <i>ELife</i> , 2018, 7, .	2.8	56
86	Variant antigen repertoires in <i>Trypanosoma congolense</i> populations and experimental infections can be profiled from deep sequence data using universal protein motifs. <i>Genome Research</i> , 2018, 28, 1383-1394.	2.4	15
87	Biology and genome of a newly discovered sibling species of <i>Caenorhabditis elegans</i> . <i>Nature Communications</i> , 2018, 9, 3216.	5.8	102
88	Tissue-specific transcriptome analyses provide new insights into GPCR signalling in adult <i>Schistosoma mansoni</i> . <i>PLoS Pathogens</i> , 2018, 14, e1006718.	2.1	28
89	Eradication genomics lessons for parasite control. <i>Science</i> , 2018, 361, 130-131.	6.0	18
90	Long read assemblies of geographically dispersed <i>Plasmodium falciparum</i> isolates reveal highly structured subtelomeres. <i>Wellcome Open Research</i> , 2018, 3, 52.	0.9	114

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91	Genomic and transcriptomic comparisons of closely related malaria parasites differing in virulence and sequestration pattern. Wellcome Open Research, 2018, 3, 142.	0.9	13
92	Genomic and transcriptomic comparisons of closely related malaria parasites differing in virulence and sequestration pattern. Wellcome Open Research, 2018, 3, 142.	0.9	11
93	WormBase ParaSite â a comprehensive resource for helminth genomics. Molecular and Biochemical Parasitology, 2017, 215, 2-10.	0.5	527
94	<i>pfk13</i> -Independent Treatment Failure in Four Imported Cases of Plasmodium falciparum Malaria Treated with Artemether-Lumefantrine in the United Kingdom. Antimicrobial Agents and Chemotherapy, 2017, 61, .	1.4	91
95	Plasmodium malariae and P. ovale genomes provide insights into malaria parasite evolution. Nature, 2017, 542, 101-104.	13.7	150
96	Expansion of the Gene Ontology knowledgebase and resources. Nucleic Acids Research, 2017, 45, D331-D338.	6.5	1,838
97	Antibody-independent mechanisms regulate the establishment of chronic Plasmodium infection. Nature Microbiology, 2017, 2, 16276.	5.9	50
98	Modulation of Aneuploidy in <i>Leishmania donovani</i> during Adaptation to Different <i>In Vitro</i> and <i>In Vivo</i> Environments and Its Impact on Gene Expression. MBio, 2017, 8, .	1.8	157
99	A gene expression atlas of adult Schistosoma mansoni and their gonads. Scientific Data, 2017, 4, 170118.	2.4	52
100	Gene Expression in <i>Leishmania</i> Is Regulated Predominantly by Gene Dosage. MBio, 2017, 8, .	1.8	108
101	Utilizing the planarian voltage-gated ion channel transcriptome to resolve a role for a Ca ²⁺ channel in neuromuscular function and regeneration. Biochimica Et Biophysica Acta - Molecular Cell Research, 2017, 1864, 1036-1045.	1.9	17
102	The genome of Onchocerca volvulus, agent of river blindness. Nature Microbiology, 2017, 2, 16216.	5.9	107
103	The exported chaperone Hsp70-x supports virulence functions for Plasmodium falciparum blood stage parasites. PLoS ONE, 2017, 12, e0181656.	1.1	45
104	MiR-277/4989 regulate transcriptional landscape during juvenile to adult transition in the parasitic helminth Schistosoma mansoni. PLoS Neglected Tropical Diseases, 2017, 11, e0005559.	1.3	45
105	Genomic Characterization of Recrudescence<i> Plasmodium malariae</i> after Treatment with Artemether/Lumefantrine. Emerging Infectious Diseases, 2017, 23, 1300-1307.	2.0	36
106	An improved Plasmodium cynomolgi genome assembly reveals an unexpected methyltransferase gene expansion. Wellcome Open Research, 2017, 2, 42.	0.9	43
107	Population genomics reveals the origin and asexual evolution of human infective trypanosomes. ELife, 2016, 5, e11473.	2.8	88
108	Activation of Bicyclic Nitro-drugs by a Novel Nitroreductase (NTR2) in Leishmania. PLoS Pathogens, 2016, 12, e1005971.	2.1	73

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109	HIV-1 Integrates Widely throughout the Genome of the Human Blood Fluke <i>Schistosoma mansoni</i> . <i>PLoS Pathogens</i> , 2016, 12, e1005931.	2.1	20
110	Whole genome sequencing of <i>Plasmodium falciparum</i> from dried blood spots using selective whole genome amplification. <i>Malaria Journal</i> , 2016, 15, 597.	0.8	129
111	Dataset for a <i>Dugesia japonica</i> de novo transcriptome assembly, utilized for defining the voltage-gated like ion channel superfamily. <i>Data in Brief</i> , 2016, 9, 1044-1047.	0.5	12
112	Whole genome resequencing of the human parasite <i>Schistosoma mansoni</i> reveals population history and effects of selection. <i>Scientific Reports</i> , 2016, 6, 20954.	1.6	72
113	<i>Companion</i> : a web server for annotation and analysis of parasite genomes. <i>Nucleic Acids Research</i> , 2016, 44, W29-W34.	6.5	127
114	Stage-Specific Transcriptome and Proteome Analyses of the Filarial Parasite <i>Onchocerca volvulus</i> and Its <i>Wolbachia</i> Endosymbiont. <i>MBio</i> , 2016, 7, .	1.8	45
115	Schistosome sex matters: a deep view into gonad-specific and pairing-dependent transcriptomes reveals a complex gender interplay. <i>Scientific Reports</i> , 2016, 6, 31150.	1.6	118
116	WormBase 2016: expanding to enable helminth genomic research. <i>Nucleic Acids Research</i> , 2016, 44, D774-D780.	6.5	329
117	The genomic basis of parasitism in the <i>Strongyloides</i> clade of nematodes. <i>Nature Genetics</i> , 2016, 48, 299-307.	9.4	226
118	Nitroheterocyclic drug resistance mechanisms in <i>Trypanosoma brucei</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 625-634.	1.3	65
119	Kinetoplastid Phylogenomics Reveals the Evolutionary Innovations Associated with the Origins of Parasitism. <i>Current Biology</i> , 2016, 26, 161-172.	1.8	137
120	The nucleosome landscape of <i>Plasmodium falciparum</i> reveals chromatin architecture and dynamics of regulatory sequences. <i>Nucleic Acids Research</i> , 2016, 44, 2110-2124.	6.5	76
121	A new <i>Plasmodium vivax</i> reference sequence with improved assembly of the subtelomeres reveals an abundance of <i>pir</i> genes. <i>Wellcome Open Research</i> , 2016, 1, 4.	0.9	118
122	Evolutionary genomics of epidemic visceral leishmaniasis in the Indian subcontinent. <i>ELife</i> , 2016, 5, .	2.8	147
123	What helminth genomes have taught us about parasite evolution. <i>Parasitology</i> , 2015, 142, S85-S97.	0.7	75
124	A novel member of the let-7 microRNA family is associated with developmental transitions in filarial nematode parasites. <i>BMC Genomics</i> , 2015, 16, 331.	1.2	25
125	Genome-scale RNAi screens for high-throughput phenotyping in bloodstream-form African trypanosomes. <i>Nature Protocols</i> , 2015, 10, 106-133.	5.5	49
126	TrypanoCyc: a community-led biochemical pathways database for <i>Trypanosoma brucei</i> . <i>Nucleic Acids Research</i> , 2015, 43, D637-D644.	6.5	35

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127	Global Gene Expression Profiling through the Complete Life Cycle of <i>Trypanosoma vivax</i> . <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003975.	1.3	31
128	Genomic and Proteomic Studies on the Mode of Action of Oxaboroles against the African Trypanosome. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0004299.	1.3	34
129	The evolutionary dynamics of variant antigen genes in <i>Babesia</i> reveal a history of genomic innovation underlying host-parasite interaction. <i>Nucleic Acids Research</i> , 2014, 42, 7113-7131.	6.5	90
130	Genomic Confirmation of Hybridisation and Recent Inbreeding in a Vector-Isolated <i>Leishmania</i> Population. <i>PLoS Genetics</i> , 2014, 10, e1004092.	1.5	142
131	Optimized Whole-Genome Amplification Strategy for Extremely AT-Biased Template. <i>DNA Research</i> , 2014, 21, 661-671.	1.5	27
132	Differential PfEMP1 Expression Is Associated with Cerebral Malaria Pathology. <i>PLoS Pathogens</i> , 2014, 10, e1004537.	2.1	34
133	International Glossina Genome Initiative 2004â€“2014: A Driver for Post-Genomic Era Research on the African Continent. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3024.	1.3	5
134	Human African Trypanosomiasis Research Gets a Boost: Unraveling the Tsetse Genome. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2624.	1.3	9
135	Phosphoinositide Metabolism Links cGMP-Dependent Protein Kinase G to Essential Ca ²⁺ Signals at Key Decision Points in the Life Cycle of Malaria Parasites. <i>PLoS Biology</i> , 2014, 12, e1001806.	2.6	185
136	The genome of the sparganosis tapeworm <i>Spirometra erinaceieuropaei</i> isolated from the biopsy of a migrating brain lesion. <i>Genome Biology</i> , 2014, 15, 510.	3.8	47
137	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
138	Pyrazoleamide compounds are potent antimalarials that target Na ⁺ homeostasis in intraerythrocytic <i>Plasmodium falciparum</i> . <i>Nature Communications</i> , 2014, 5, 5521.	5.8	108
139	A comprehensive evaluation of rodent malaria parasite genomes and gene expression. <i>BMC Biology</i> , 2014, 12, 86.	1.7	251
140	Genome sequencing of chimpanzee malaria parasites reveals possible pathways of adaptation to human hosts. <i>Nature Communications</i> , 2014, 5, 4754.	5.8	124
141	A comprehensive evaluation of assembly scaffolding tools. <i>Genome Biology</i> , 2014, 15, R42.	13.9	153
142	WormBase 2014: new views of curated biology. <i>Nucleic Acids Research</i> , 2014, 42, D789-D793.	6.5	149
143	A cascade of DNA-binding proteins for sexual commitment and development in <i>Plasmodium</i> . <i>Nature</i> , 2014, 507, 253-257.	13.7	366
144	Genome Sequence of the Tsetse Fly (<i>Glossina morsitans</i>): Vector of African Trypanosomiasis. <i>Science</i> , 2014, 344, 380-386.	6.0	254

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145	Summarizing Specific Profiles in Illumina Sequencing from Whole-Genome Amplified DNA. DNA Research, 2014, 21, 243-254.	1.5	20
146	Halting harmful helminths. Science, 2014, 346, 168-169.	6.0	39
147	The genome and life-stage specific transcriptomes of <i>Globodera pallida</i> elucidate key aspects of plant parasitism by a cyst nematode. Genome Biology, 2014, 15, R43.	13.9	212
148	Genomic analysis of the causative agents of coccidiosis in domestic chickens. Genome Research, 2014, 24, 1676-1685.	2.4	176
149	Whipworm genome and dual-species transcriptome analyses provide molecular insights into an intimate host-parasite interaction. Nature Genetics, 2014, 46, 693-700.	9.4	139
150	REAPR: a universal tool for genome assembly evaluation. Genome Biology, 2013, 14, R47.	13.9	395
151	Genetic and Molecular Basis of Drug Resistance and Species-Specific Drug Action in Schistosome Parasites. Science, 2013, 342, 1385-1389.	6.0	137
152	The genome and transcriptome of <i>Haemonchus contortus</i> , a key model parasite for drug and vaccine discovery. Genome Biology, 2013, 14, R88.	13.9	293
153	Characterization and comparative analysis of the complete <i>Haemonchus contortus</i> β -tubulin gene family and implications for benzimidazole resistance in strongylid nematodes. International Journal for Parasitology, 2013, 43, 465-475.	1.3	53
154	The genomes of four tapeworm species reveal adaptations to parasitism. Nature, 2013, 496, 57-63.	13.7	603
155	Multiple populations of artemisinin-resistant <i>Plasmodium falciparum</i> in Cambodia. Nature Genetics, 2013, 45, 648-655.	9.4	424
156	Comparative Study of Transcriptome Profiles of Mechanical- and Skin-Transformed <i>Schistosoma mansoni</i> Schistosomula. PLoS Neglected Tropical Diseases, 2013, 7, e2091.	1.3	62
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