

Matt Berriman

List of Publications by Year in descending order

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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	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	13.7	3,881
2	The Gene Ontology (GO) database and informatics resource. <i>Nucleic Acids Research</i> , 2004, 32, 258D-261.	6.5	3,462
3	The Gene Ontology resource: enriching a GOld mine. <i>Nucleic Acids Research</i> , 2021, 49, D325-D334.	6.5	2,416
4	Expansion of the Gene Ontology knowledgebase and resources. <i>Nucleic Acids Research</i> , 2017, 45, D331-D338.	6.5	1,838
5	ACT: the Artemis comparison tool. <i>Bioinformatics</i> , 2005, 21, 3422-3423.	1.8	1,536
6	The Genome of the African Trypanosome <i>Trypanosoma brucei</i> . <i>Science</i> , 2005, 309, 416-422.	6.0	1,496
7	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , 2005, 438, 1151-1156.	13.7	1,272
8	The Genome of the Kinetoplastid Parasite, <i>Leishmania major</i> . <i>Science</i> , 2005, 309, 436-442.	6.0	1,237
9	The genome of the social amoeba <i>Dictyostelium discoideum</i> . <i>Nature</i> , 2005, 435, 43-57.	13.7	1,179
10	Artemis: an integrated platform for visualization and analysis of high-throughput sequence-based experimental data. <i>Bioinformatics</i> , 2012, 28, 464-469.	1.8	1,029
11	Evolution of pathogenicity and sexual reproduction in eight <i>Candida</i> genomes. <i>Nature</i> , 2009, 459, 657-662.	13.7	963
12	The genome of the blood fluke <i>Schistosoma mansoni</i> . <i>Nature</i> , 2009, 460, 352-358.	13.7	945
13	The Gene Ontology (GO) project in 2006. <i>Nucleic Acids Research</i> , 2006, 34, D322-D326.	6.5	923
14	TriTrypDB: a functional genomic resource for the Trypanosomatidae. <i>Nucleic Acids Research</i> , 2010, 38, D457-D462.	6.5	847
15	DNAPlotter: circular and linear interactive genome visualization. <i>Bioinformatics</i> , 2009, 25, 119-120.	1.8	801
16	The genome of the protist parasite <i>Entamoeba histolytica</i> . <i>Nature</i> , 2005, 433, 865-868.	13.7	783
17	A Comprehensive Survey of the <i>Plasmodium</i> Life Cycle by Genomic, Transcriptomic, and Proteomic Analyses. <i>Science</i> , 2005, 307, 82-86.	6.0	743
18	Comparative Genomics of Trypanosomatid Parasitic Protozoa. <i>Science</i> , 2005, 309, 404-409.	6.0	713

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19	The Gene Ontology project in 2008. <i>Nucleic Acids Research</i> , 2008, 36, D440-D444.	6.5	699
20	Comparative genomic analysis of three <i>Leishmania</i> species that cause diverse human disease. <i>Nature Genetics</i> , 2007, 39, 839-847.	9.4	648
21	The genomes of four tapeworm species reveal adaptations to parasitism. <i>Nature</i> , 2013, 496, 57-63.	13.7	603
22	Artemis and ACT: viewing, annotating and comparing sequences stored in a relational database. <i>Bioinformatics</i> , 2008, 24, 2672-2676.	1.8	578
23	WormBase ParaSite â a comprehensive resource for helminth genomics. <i>Molecular and Biochemical Parasitology</i> , 2017, 215, 2-10.	0.5	527
24	Amplification-free Illumina sequencing-library preparation facilitates improved mapping and assembly of (G+C)-biased genomes. <i>Nature Methods</i> , 2009, 6, 291-295.	9.0	520
25	Analysis of <i>Plasmodium falciparum</i> diversity in natural infections by deep sequencing. <i>Nature</i> , 2012, 487, 375-379.	13.7	450
26	Multiple populations of artemisinin-resistant <i>Plasmodium falciparum</i> in Cambodia. <i>Nature Genetics</i> , 2013, 45, 648-655.	9.4	424
27	An ancestral oomycete locus contains late blight avirulence gene <i>Avr3a</i> , encoding a protein that is recognized in the host cytoplasm. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7766-7771.	3.3	414
28	ABACAS: algorithm-based automatic contiguation of assembled sequences. <i>Bioinformatics</i> , 2009, 25, 1968-1969.	1.8	406
29	High-throughput phenotyping using parallel sequencing of RNA interference targets in the African trypanosome. <i>Genome Research</i> , 2011, 21, 915-924.	2.4	404
30	A Systematically Improved High Quality Genome and Transcriptome of the Human Blood Fluke <i>Schistosoma mansoni</i> . <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1455.	1.3	400
31	REAPR: a universal tool for genome assembly evaluation. <i>Genome Biology</i> , 2013, 14, R47.	13.9	395
32	Whole genome sequencing of multiple <i>Leishmania donovani</i> clinical isolates provides insights into population structure and mechanisms of drug resistance. <i>Genome Research</i> , 2011, 21, 2143-2156.	2.4	381
33	Chromosome and gene copy number variation allow major structural change between species and strains of <i>Leishmania</i> . <i>Genome Research</i> , 2011, 21, 2129-2142.	2.4	380
34	Comparative genomics of the major parasitic worms. <i>Nature Genetics</i> , 2019, 51, 163-174.	9.4	377
35	New insights into the blood-stage transcriptome of <i>Plasmodium falciparum</i> using RNA-seq. <i>Molecular Microbiology</i> , 2010, 76, 12-24.	1.2	374
36	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

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37	Genomic Insights into the Origin of Parasitism in the Emerging Plant Pathogen <i>Bursaphelenchus xylophilus</i> . <i>PLoS Pathogens</i> , 2011, 7, e1002219.	2.1	351
38	The genome of the simian and human malaria parasite <i>Plasmodium knowlesi</i> . <i>Nature</i> , 2008, 455, 799-803.	13.7	338
39	WormBase 2016: expanding to enable helminth genomic research. <i>Nucleic Acids Research</i> , 2016, 44, D774-D780.	6.5	329
40	Genome Sequence of <i>Theileria parva</i> , a Bovine Pathogen That Transforms Lymphocytes. <i>Science</i> , 2005, 309, 134-137.	6.0	309
41	A Human-Curated Annotation of the <i>Candida albicans</i> Genome. <i>PLoS Genetics</i> , 2005, 1, e1.	1.5	293
42	The genome and transcriptome of <i>Haemonchus contortus</i> , a key model parasite for drug and vaccine discovery. <i>Genome Biology</i> , 2013, 14, R88.	13.9	293
43	RATT: Rapid Annotation Transfer Tool. <i>Nucleic Acids Research</i> , 2011, 39, e57-e57.	6.5	291
44	Genome of the Host-Cell Transforming Parasite <i>Theileria annulata</i> Compared with <i>T. parva</i> . <i>Science</i> , 2005, 309, 131-133.	6.0	285
45	Genomic-scale prioritization of drug targets: the TDR Targets database. <i>Nature Reviews Drug Discovery</i> , 2008, 7, 900-907.	21.5	282
46	High-throughput decoding of antitrypanosomal drug efficacy and resistance. <i>Nature</i> , 2012, 482, 232-236.	13.7	276
47	Improving draft assemblies by iterative mapping and assembly of short reads to eliminate gaps. <i>Genome Biology</i> , 2010, 11, R41.	13.9	264
48	Genome Sequence of the Tsetse Fly (<i>Glossina morsitans</i>): Vector of African Trypanosomiasis. <i>Science</i> , 2014, 344, 380-386.	6.0	254
49	Telomeric Expression Sites Are Highly Conserved in <i>Trypanosoma brucei</i> . <i>PLoS ONE</i> , 2008, 3, e3527.	1.1	254
50	A comprehensive evaluation of rodent malaria parasite genomes and gene expression. <i>BMC Biology</i> , 2014, 12, 86.	1.7	251
51	An integrated national scale SARS-CoV-2 genomic surveillance network. <i>Lancet Microbe</i> , The, 2020, 1, e99-e100.	3.4	232
52	The genomic basis of parasitism in the <i>Strongyloides</i> clade of nematodes. <i>Nature Genetics</i> , 2016, 48, 299-307.	9.4	226
53	GeneDB--an annotation database for pathogens. <i>Nucleic Acids Research</i> , 2012, 40, D98-D108.	6.5	217
54	Iterative Correction of Reference Nucleotides (iCORN) using second generation sequencing technology. <i>Bioinformatics</i> , 2010, 26, 1704-1707.	1.8	212

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55	The genome and life-stage specific transcriptomes of <i>Globodera pallida</i> elucidate key aspects of plant parasitism by a cyst nematode. <i>Genome Biology</i> , 2014, 15, R43.	13.9	212
56	Comparative Genomics of the Apicomplexan Parasites <i>Toxoplasma gondii</i> and <i>Neospora caninum</i> : <i>Coccidia</i> Differing in Host Range and Transmission Strategy. <i>PLoS Pathogens</i> , 2012, 8, e1002567.	2.1	206
57	GOtcha: a new method for prediction of protein function assessed by the annotation of seven genomes. <i>BMC Bioinformatics</i> , 2004, 5, 178.	1.2	205
58	GeneDB: a resource for prokaryotic and eukaryotic organisms. <i>Nucleic Acids Research</i> , 2004, 32, 339D-343.	6.5	199
59	The Malaria Cell Atlas: Single parasite transcriptomes across the complete <i>Plasmodium</i> life cycle. <i>Science</i> , 2019, 365, .	6.0	198
60	Crystal structure of <i>Trypanosoma cruzi</i> trypanothione reductase in complex with trypanothione, and the structure-based discovery of new natural product inhibitors. <i>Structure</i> , 1999, 7, 81-89.	1.6	197
61	Comparative genomics of the fungal pathogens <i>Candida dubliniensis</i> and <i>Candida albicans</i> . <i>Genome Research</i> , 2009, 19, 2231-2244.	2.4	195
62	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
63	Genome variation and evolution of the malaria parasite <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2007, 39, 120-125.	9.4	184
64	Genomic analysis of the causative agents of coccidiosis in domestic chickens. <i>Genome Research</i> , 2014, 24, 1676-1685.	2.4	176
65	WormBase 2012: more genomes, more data, new website. <i>Nucleic Acids Research</i> , 2012, 40, D735-D741.	6.5	175
66	WormBase 2017: molting into a new stage. <i>Nucleic Acids Research</i> , 2018, 46, D869-D874.	6.5	172
67	Single-cell RNA-seq reveals hidden transcriptional variation in malaria parasites. <i>ELife</i> , 2018, 7, .	2.8	171
68	Vector transmission regulates immune control of <i>Plasmodium</i> virulence. <i>Nature</i> , 2013, 498, 228-231.	13.7	168
69	A post-assembly genome-improvement toolkit (PAGIT) to obtain annotated genomes from contigs. <i>Nature Protocols</i> , 2012, 7, 1260-1284.	5.5	167
70	<i>Plasmodium falciparum</i> Variant Surface Antigen Expression Patterns during Malaria. <i>PLoS Pathogens</i> , 2005, 1, e26.	2.1	158
71	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. <i>MBio</i> , 2017, 8, .	1.8	157
72	Sequence of <i>Plasmodium falciparum</i> chromosomes 1, 3 and 13. <i>Nature</i> , 2002, 419, 527-531.	13.7	156

#	ARTICLE	IF	CITATIONS
73	A comprehensive evaluation of assembly scaffolding tools. <i>Genome Biology</i> , 2014, 15, R42.	13.9	153
74	Assembly of the <i>Candida albicans</i> genome into sixteen supercontigs aligned on the eight chromosomes. <i>Genome Biology</i> , 2007, 8, R52.	13.9	151
75	<i>Plasmodium malariae</i> and <i>P. ovale</i> genomes provide insights into malaria parasite evolution. <i>Nature</i> , 2017, 542, 101-104.	13.7	150
76	WormBase 2014: new views of curated biology. <i>Nucleic Acids Research</i> , 2014, 42, D789-D793.	6.5	149
77	Composite genome map and recombination parameters derived from three archetypal lineages of <i>Toxoplasma gondii</i> . <i>Nucleic Acids Research</i> , 2005, 33, 2980-2992.	6.5	147
78	Evolutionary genomics of epidemic visceral leishmaniasis in the Indian subcontinent. <i>ELife</i> , 2016, 5, .	2.8	147
79	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
80	Identification of Attractive Drug Targets in Neglected-Disease Pathogens Using an In Silico Approach. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e804.	1.3	141
81	Whipworm genome and dual-species transcriptome analyses provide molecular insights into an intimate host-parasite interaction. <i>Nature Genetics</i> , 2014, 46, 693-700.	9.4	139
82	RNA interference in parasitic helminths: current situation, potential pitfalls and future prospects. <i>Parasitology</i> , 2006, 134, 609-619.	0.7	138
83	Antigenic diversity is generated by distinct evolutionary mechanisms in African trypanosome species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3416-3421.	3.3	137
84	Genetic and Molecular Basis of Drug Resistance and Species-Specific Drug Action in Schistosome Parasites. <i>Science</i> , 2013, 342, 1385-1389.	6.0	137
85	Kinetoplastid Phylogenomics Reveals the Evolutionary Innovations Associated with the Origins of Parasitism. <i>Current Biology</i> , 2016, 26, 161-172.	1.8	137
86	Viewing and annotating sequence data with Artemis. <i>Briefings in Bioinformatics</i> , 2003, 4, 124-132.	3.2	136
87	<i>Plasmodium falciparum</i> var <i>...</i> gene expression is modified by host immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 21801-21806.	3.3	130
88	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
89	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
90	The Genome Sequence of <i>Trypanosoma brucei gambiense</i> , Causative Agent of Chronic Human African Trypanosomiasis. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e658.	1.3	128

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91	WormBase in 2022â€”data, processes, and tools for analyzing <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2022, 220, .	1.2	128
92	<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
93	Genome sequencing of chimpanzee malaria parasites reveals possible pathways of adaptation to human hosts. <i>Nature Communications</i> , 2014, 5, 4754.	5.8	124
94	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
95	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
96	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
97	Just one cross appears capable of dramatically altering the population biology of a eukaryotic pathogen like <i>Toxoplasma gondii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 10514-10519.	3.3	112
98	Cyclin-dependent kinase 12 is a drug target for visceral leishmaniasis. <i>Nature</i> , 2018, 560, 192-197.	13.7	112
99	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
100	Gene Expression in <i>Leishmania</i> Is Regulated Predominantly by Gene Dosage. <i>MBio</i> , 2017, 8, .	1.8	108
101	The genome of <i>Onchocerca volvulus</i> , agent of river blindness. <i>Nature Microbiology</i> , 2017, 2, 16216.	5.9	107
102	Expression of chemosensory proteins in the tsetse fly <i>Glossina morsitans morsitans</i> is related to female host-seeking behaviour. <i>Insect Molecular Biology</i> , 2012, 21, 41-48.	1.0	103
103	Biology and genome of a newly discovered sibling species of <i>Caenorhabditis elegans</i> . <i>Nature Communications</i> , 2018, 9, 3216.	5.8	102
104	Silencing of Germline-Expressed Genes by DNA Elimination in Somatic Cells. <i>Developmental Cell</i> , 2012, 23, 1072-1080.	3.1	101
105	The architecture of variant surface glycoprotein gene expression sites in <i>Trypanosoma brucei</i> . <i>Molecular and Biochemical Parasitology</i> , 2002, 122, 131-140.	0.5	98
106	A Cell-surface Phylome for African Trypanosomes. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2121.	1.3	96
107	Gene synteny and evolution of genome architecture in trypanosomatids. <i>Molecular and Biochemical Parasitology</i> , 2004, 134, 183-191.	0.5	92
108	<i>pfk13</i> -Independent Treatment Failure in Four Imported Cases of <i>Plasmodium falciparum</i> Malaria Treated with Artemether-Lumefantrine in the United Kingdom. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	91

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109	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
110	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
111	Global genome diversity of the <i>Leishmania donovani</i> complex. <i>ELife</i> , 2020, 9, .	2.8	90
112	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
113	Population genomics reveals the origin and asexual evolution of human infective trypanosomes. <i>ELife</i> , 2016, 5, e11473.	2.8	88
114	Programmed genome editing of the omega-1 ribonuclease of the blood fluke, <i>Schistosoma mansoni</i> . <i>ELife</i> , 2019, 8, .	2.8	87
115	Protein variation in blood-dwelling schistosome worms generated by differential splicing of micro-exon gene transcripts. <i>Genome Research</i> , 2010, 20, 1112-1121.	2.4	86
116	A Deep Sequencing Approach to Comparatively Analyze the Transcriptome of Lifecycle Stages of the Filarial Worm, <i>Brugia malayi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1409.	1.3	86
117	A New, Expressed Multigene Family Containing a Hot Spot for Insertion of Retroelements Is Associated with Polymorphic Subtelomeric Regions of <i>Trypanosoma brucei</i> . <i>Eukaryotic Cell</i> , 2002, 1, 137-151.	3.4	82
118	Genome-wide discovery and verification of novel structured RNAs in <i>Plasmodium falciparum</i> . <i>Genome Research</i> , 2008, 18, 281-292.	2.4	81
119	RNAseq Analysis of the Parasitic Nematode <i>Strongyloides stercoralis</i> Reveals Divergent Regulation of Canonical Dauer Pathways. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1854.	1.3	79
120	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
121	An insight into the sialome of <i>Glossina morsitans morsitans</i> . <i>BMC Genomics</i> , 2010, 11, 213.	1.2	76
122	Diversity in parasitic nematode genomes: the microRNAs of <i>Brugia pahangi</i> and <i>Haemonchus contortus</i> are largely novel. <i>BMC Genomics</i> , 2012, 13, 4.	1.2	76
123	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
124	What helminth genomes have taught us about parasite evolution. <i>Parasitology</i> , 2015, 142, S85-S97.	0.7	75
125	Activation of Bicyclic Nitro-drugs by a Novel Nitroreductase (NTR2) in <i>Leishmania</i> . <i>PLoS Pathogens</i> , 2016, 12, e1005971.	2.1	73
126	A Transcriptomic Analysis of <i>Echinococcus granulosus</i> Larval Stages: Implications for Parasite Biology and Host Adaptation. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1897.	1.3	72

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127	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
128	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
129	BamView: viewing mapped read alignment data in the context of the reference sequence. <i>Bioinformatics</i> , 2010, 26, 676-677.	1.8	70
130	Adult midgut expressed sequence tags from the tsetse fly <i>Glossina morsitans morsitans</i> and expression analysis of putative immune response genes. <i>Genome Biology</i> , 2003, 4, R63.	13.9	68
131	Using RNA-seq to determine the transcriptional landscape and the hypoxic response of the pathogenic yeast <i>Candida parapsilosis</i> . <i>BMC Genomics</i> , 2011, 12, 628.	1.2	68
132	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
133	Germline Transgenesis and Insertional Mutagenesis in <i>Schistosoma mansoni</i> Mediated by Murine Leukemia Virus. <i>PLoS Pathogens</i> , 2012, 8, e1002820.	2.1	66
134	Proteomic and Genetic Analyses Demonstrate that <i>Plasmodium berghei</i> Blood Stages Export a Large and Diverse Repertoire of Proteins. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 426-448.	2.5	65
135	Nitroheterocyclic drug resistance mechanisms in <i>Trypanosoma brucei</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 625-634.	1.3	65
136	Characterization of protein Ser/Thr phosphatases of the malaria parasite, <i>Plasmodium falciparum</i> : inhibition of the parasitic calcineurin by cyclophilin-cyclosporin complex. <i>Molecular and Biochemical Parasitology</i> , 1999, 99, 167-181.	0.5	64
137	Differential <i>var</i> gene expression in the organs of patients dying of falciparum malaria. <i>Molecular Microbiology</i> , 2007, 65, 959-967.	1.2	64
138	Evolutionary analysis of the most polymorphic gene family in falciparum malaria. <i>Wellcome Open Research</i> , 2019, 4, 193.	0.9	64
139	Efficient Depletion of Host DNA Contamination in Malaria Clinical Sequencing. <i>Journal of Clinical Microbiology</i> , 2013, 51, 745-751.	1.8	63
140	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
141	Patterns of Evolution in the Unique tRNA Gene Arrays of the Genus <i>Entamoeba</i> . <i>Molecular Biology and Evolution</i> , 2007, 25, 187-198.	3.5	62
142	Comparative Study of Transcriptome Profiles of Mechanical- and Skin-Transformed <i>Schistosoma mansoni</i> Schistosomula. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2091.	1.3	62
143	BamView: visualizing and interpretation of next-generation sequencing read alignments. <i>Briefings in Bioinformatics</i> , 2013, 14, 203-212.	3.2	60
144	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

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145	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
146	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
147	The DNA sequence of chromosome I of an African trypanosome: gene content, chromosome organisation, recombination and polymorphism. <i>Nucleic Acids Research</i> , 2003, 31, 4864-4873.	6.5	56
148	The genetic map and comparative analysis with the physical map of <i>Trypanosoma brucei</i> . <i>Nucleic Acids Research</i> , 2005, 33, 6688-6693.	6.5	56
149	Flatworm-specific transcriptional regulators promote the specification of tegumental progenitors in <i>Schistosoma mansoni</i> . <i>ELife</i> , 2018, 7, .	2.8	56
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