

Matt Berriman

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.

313
papers

40,200
citations

90
h-index

198
g-index

352
ext. papers

48,780
ext. citations

12.4
avg, IF

7.59
L-index

#	Paper	IF	Citations
313	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.. <i>MBio</i> , 2022 , e0326421	7.8	0
312	WormBase in 2022-data, processes, and tools for analyzing <i>Caenorhabditis elegans</i> .. <i>Genetics</i> , 2022 ,	4	4
311	Defining the early stages of intestinal colonisation by whipworms.. <i>Nature Communications</i> , 2022 , 13, 1725	17.4	1
310	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	4.8	0
309	Long-read assembly and comparative evidence-based reanalysis of genome sequences reveals expanded transporter repertoire and duplication of entire chromosome ends including subtelomeric regions. <i>Genome Research</i> , 2021 ,	9.7	3
308	Daily rhythms in gene expression of the human parasite <i>Schistosoma mansoni</i> . <i>BMC Biology</i> , 2021 , 19, 255	7.3	2
307	The Gene Ontology resource: enriching a GOld mine. <i>Nucleic Acids Research</i> , 2021 , 49, D325-D334	20.1	494
306	Mapping immune variation and gene switching in naive hosts infected with. <i>ELife</i> , 2021 , 10,	8.9	3
305	Expression profiling of <i>Echinococcus multilocularis</i> miRNAs throughout metacestode development in vitro. <i>PLoS Neglected Tropical Diseases</i> , 2021 , 15, e0009297	4.8	3
304	10-year longitudinal study of malaria in children: Insights into acquisition and maintenance of naturally acquired immunity.. <i>Wellcome Open Research</i> , 2021 , 6, 79	4.8	3
303	Mapping Rora expression in resting and activated CD4+ T cells. <i>PLoS ONE</i> , 2021 , 16, e0251233	3.7	8
302	<i>Schistosoma mansoni</i> Eggs Modulate the Timing of Granuloma Formation to Promote Transmission. <i>Cell Host and Microbe</i> , 2021 , 29, 58-67.e5	23.4	16
301	Tumor Necrosis Factor and <i>Schistosoma mansoni</i> egg antigen omega-1 shape distinct aspects of the early egg-induced granulomatous response. <i>PLoS Neglected Tropical Diseases</i> , 2021 , 15, e0008814	4.8	4
300	Individual-level variations in malaria susceptibility and acquisition of clinical protection.. <i>Wellcome Open Research</i> , 2021 , 6, 22	4.8	1
299	Whole-genome sequencing of <i>Schistosoma mansoni</i> reveals extensive diversity with limited selection despite mass drug administration. <i>Nature Communications</i> , 2021 , 12, 4776	17.4	12
298	The Transcriptome of <i>Schistosoma mansoni</i> Developing Eggs Reveals Key Mediators in Pathogenesis and Life Cycle Propagation. <i>Frontiers in Tropical Diseases</i> , 2021 , 2,		1
297	An uneven race: genome editing for parasitic worms. <i>Nature Reviews Microbiology</i> , 2021 , 19, 621	22.2	3

296	Hatching of parasitic nematode eggs: a crucial step determining infection. <i>Trends in Parasitology</i> , 2021 ,	6.4	5
295	The complete genome sequence of (Tyzzer 1929), a common gut parasite of chickens. <i>Wellcome Open Research</i> , 2021 , 6, 225	4.8	2
294	An Experimental Human Blood-Stage Model for Studying Plasmodium malariae Infection. <i>Journal of Infectious Diseases</i> , 2020 , 221, 948-955	7	12
293	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	7.3	10
292	Transcriptome of the parasitic flatworm Schistosoma mansoni during intra-mammalian development. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0007743	4.8	9
291	Nearly Complete Genome Sequence of Brugia malayi Strain FR3. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	7
290	An integrated national scale SARS-CoV-2 genomic surveillance network. <i>Lancet Microbe</i> , 2020 , 1, e99-e100	22.2	127
289	Screening of a library of recombinant Schistosoma mansoni proteins with sera from murine and human controlled infections identifies early serological markers. <i>Journal of Infectious Diseases</i> , 2020 ,	7	5
288	Refining the transcriptome of the human malaria parasite Plasmodium falciparum using amplification-free RNA-seq. <i>BMC Genomics</i> , 2020 , 21, 395	4.5	19
287	Sex chromosome evolution in parasitic nematodes of humans. <i>Nature Communications</i> , 2020 , 11, 1964	17.4	20
286	Large CRISPR-Cas-induced deletions in the oxamniquine resistance locus of the human parasite Schistosoma mansoni. <i>Wellcome Open Research</i> , 2020 , 5, 178	4.8	13
285	Population genomic evidence that human and animal infections in Africa come from the same populations of Dracunculus medinensis. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0008623	4.8	4
284	Extracellular non-coding RNA signatures of the metacystode stage of Echinococcus multilocularis. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0008890	4.8	3
283	Global genome diversity of the complex. <i>ELife</i> , 2020 , 9,	8.9	37
282	Organoids - New Models for Host-Helminth Interactions. <i>Trends in Parasitology</i> , 2020 , 36, 170-181	6.4	27
281	Analysis of Plasmodium vivax schizont transcriptomes from field isolates reveals heterogeneity of expression of genes involved in host-parasite interactions. <i>Scientific Reports</i> , 2020 , 10, 16667	4.9	6
280	Development of caecaloids to study host-pathogen interactions: new insights into immunoregulatory functions of Trichuris muris extracellular vesicles in the caecum. <i>International Journal for Parasitology</i> , 2020 , 50, 707-718	4.3	11
279	Genomic and transcriptomic variation defines the chromosome-scale assembly of Haemonchus contortus, a model gastrointestinal worm. <i>Communications Biology</i> , 2020 , 3, 656	6.7	26

278	Genomic and transcriptomic evidence for descent from Plasmodium and loss of blood schizogony in Hepatocystis parasites from naturally infected red colobus monkeys. <i>PLoS Pathogens</i> , 2020 , 16, e1008717	7.6	11
277	Ecological divergence and hybridization of Neotropical parasites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 25159-25168	11.5	22
276	Large-scale RNAi screening uncovers therapeutic targets in the parasite. <i>Science</i> , 2020 , 369, 1649-1653	33.3	20
275	Evaluation of whole genome amplification and bioinformatic methods for the characterization of Leishmania genomes at a single cell level. <i>Scientific Reports</i> , 2020 , 10, 15043	4.9	7
274	Single-cell atlas of the first intra-mammalian developmental stage of the human parasite Schistosoma mansoni. <i>Nature Communications</i> , 2020 , 11, 6411	17.4	14
273	Baseline Gut Microbiota Composition Is Associated With Infection Burden in Rodent Models. <i>Frontiers in Immunology</i> , 2020 , 11, 593838	8.4	5
272	Genomic analysis of natural intra-specific hybrids among Ethiopian isolates of Leishmania donovani. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0007143	4.8	10
271	Large CRISPR-Cas-induced deletions in the oxamniquine resistance locus of the human parasite. <i>Wellcome Open Research</i> , 2020 , 5, 178	4.8	12
270	Transcriptome of the parasitic flatworm Schistosoma mansoni during intra-mammalian development 2020 , 14, e0007743		
269	Transcriptome of the parasitic flatworm Schistosoma mansoni during intra-mammalian development 2020 , 14, e0007743		
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263	Genomic and transcriptomic evidence for descent from Plasmodium and loss of blood schizogony in Hepatocystis parasites from naturally infected red colobus monkeys 2020 , 16, e1008717		
262	Evaluation of DNA Extraction Methods on Individual Helminth Egg and Larval Stages for Whole-Genome Sequencing. <i>Frontiers in Genetics</i> , 2019 , 10, 826	4.5	11
261	Identification and expression profiling of microRNAs in Hymenolepis. <i>International Journal for Parasitology</i> , 2019 , 49, 211-223	4.3	10

260	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	4.5	35
259	Repeated clinical malaria episodes are associated with modification of the immune system in children. <i>BMC Medicine</i> , 2019 , 17, 60	11.4	20
258	The Malaria Cell Atlas: Single parasite transcriptomes across the complete life cycle. <i>Science</i> , 2019 , 365,	33.3	90
257	The global diversity of <i>Haemonchus contortus</i> is shaped by human intervention and climate. <i>Nature Communications</i> , 2019 , 10, 4811	17.4	26
256	Progression of the canonical reference malaria parasite genome from 2002-2019. <i>Wellcome Open Research</i> , 2019 , 4, 58	4.8	26
255	Progression of the canonical reference malaria parasite genome from 2002-2019. <i>Wellcome Open Research</i> , 2019 , 4, 58	4.8	24
254	GeneDB and Wikidata. <i>Wellcome Open Research</i> , 2019 , 4, 114	4.8	1
253	Systematic screening of 96 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	4.8	8
252	Evolutionary analysis of the most polymorphic gene family in malaria. <i>Wellcome Open Research</i> , 2019 , 4, 193	4.8	29
251	Programmed genome editing of the omega-1 ribonuclease of the blood fluke. <i>ELife</i> , 2019 , 8,	8.9	51
250	GeneDB and Wikidata. <i>Wellcome Open Research</i> , 2019 , 4, 114	4.8	
249	Genomic and Metabolomic Polymorphism among Experimentally Selected Paromomycin-Resistant <i>Leishmania donovani</i> Strains. <i>Antimicrobial Agents and Chemotherapy</i> , 2019 , 64,	5.9	8
248	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	4.8	23
247	Comparative genomics of the major parasitic worms. <i>Nature Genetics</i> , 2019 , 51, 163-174	36.3	201
246	Exclusive dependence of IL-10R signalling on intestinal microbiota homeostasis and control of whipworm infection. <i>PLoS Pathogens</i> , 2019 , 15, e1007265	7.6	15
245	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	7	30
244	Complete avian malaria parasite genomes reveal features associated with lineage-specific evolution in birds and mammals. <i>Genome Research</i> , 2018 , 28, 547-560	9.7	53
243	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	3.9	38

242	Transcriptomic profiling of nematode parasites surviving vaccine exposure. <i>International Journal for Parasitology</i> , 2018 , 48, 395-402	4.3	14
241	A method for single pair mating in an obligate parasitic nematode. <i>International Journal for Parasitology</i> , 2018 , 48, 159-165	4.3	9
240	WormBase 2017: molting into a new stage. <i>Nucleic Acids Research</i> , 2018 , 46, D869-D874	20.1	138
239	Single-cell RNA-seq reveals hidden transcriptional variation in malaria parasites. <i>ELife</i> , 2018 , 7,	8.9	94
238	Cyclin-dependent kinase 12 is a drug target for visceral leishmaniasis. <i>Nature</i> , 2018 , 560, 192-197	50.4	73
237	Flatworm-specific transcriptional regulators promote the specification of tegumental progenitors in. <i>ELife</i> , 2018 , 7,	8.9	36
236	Variant antigen repertoires in populations and experimental infections can be profiled from deep sequence data using universal protein motifs. <i>Genome Research</i> , 2018 , 28, 1383-1394	9.7	8
235	Biology and genome of a newly discovered sibling species of <i>Caenorhabditis elegans</i> . <i>Nature Communications</i> , 2018 , 9, 3216	17.4	44
234	Tissue-specific transcriptome analyses provide new insights into GPCR signalling in adult <i>Schistosoma mansoni</i> . <i>PLoS Pathogens</i> , 2018 , 14, e1006718	7.6	17
233	Eradication genomics-lessons for parasite control. <i>Science</i> , 2018 , 361, 130-131	33.3	9
232	Long read assemblies of geographically dispersed isolates reveal highly structured subtelomeres. <i>Wellcome Open Research</i> , 2018 , 3, 52	4.8	54
231	Genomic and transcriptomic comparisons of closely related malaria parasites differing in virulence and sequestration pattern. <i>Wellcome Open Research</i> , 2018 , 3, 142	4.8	10
230	Genomic and transcriptomic comparisons of closely related malaria parasites differing in virulence and sequestration pattern. <i>Wellcome Open Research</i> , 2018 , 3, 142	4.8	7
229	Genome-wide transcriptome profiling and spatial expression analyses identify signals and switches of development in tapeworms. <i>EvoDevo</i> , 2018 , 9, 21	3.2	17
228	Pre-clinical evaluation of a -based whole-sporozoite malaria vaccine candidate. <i>Npj Vaccines</i> , 2018 , 3, 54	9.5	8
227	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	3.7	2
226	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	26.6	85
225	Using WormBase ParaSite: An Integrated Platform for Exploring Helminth Genomic Data. <i>Methods in Molecular Biology</i> , 2018 , 1757, 471-491	1.4	22

224	Histone methylation changes are required for life cycle progression in the human parasite <i>Schistosoma mansoni</i> . <i>PLoS Pathogens</i> , 2018 , 14, e1007066	7.6	29
223	WormBase ParaSite - a comprehensive resource for helminth genomics. <i>Molecular and Biochemical Parasitology</i> , 2017 , 215, 2-10	1.9	264
222	-Independent Treatment Failure in Four Imported Cases of Plasmodium falciparum Malaria Treated with Artemether-Lumefantrine in the United Kingdom. <i>Antimicrobial Agents and Chemotherapy</i> , 2017 , 61,	5.9	71
221	Plasmodium malariae and P. ovale genomes provide insights into malaria parasite evolution. <i>Nature</i> , 2017 , 542, 101-104	50.4	99
220	Expansion of the Gene Ontology knowledgebase and resources. <i>Nucleic Acids Research</i> , 2017 , 45, D331-D338	12.8	1258
219	Antibody-independent mechanisms regulate the establishment of chronic Plasmodium infection. <i>Nature Microbiology</i> , 2017 , 2, 16276	26.6	35
218	Modulation of Aneuploidy in during Adaptation to Different and Environments and Its Impact on Gene Expression. <i>MBio</i> , 2017 , 8,	7.8	95
217	The exported chaperone Hsp70-x supports virulence functions for Plasmodium falciparum blood stage parasites. <i>PLoS ONE</i> , 2017 , 12, e0181656	3.7	34
216	MiR-277/4989 regulate transcriptional landscape during juvenile to adult transition in the parasitic helminth <i>Schistosoma mansoni</i> . <i>PLoS Neglected Tropical Diseases</i> , 2017 , 11, e0005559	4.8	21
215	Genomic Characterization of Recrudescence Plasmodium malariae after Treatment with Artemether/Lumefantrine. <i>Emerging Infectious Diseases</i> , 2017 , 23, 1300-1307	10.2	24
214	A gene expression atlas of adult <i>Schistosoma mansoni</i> and their gonads. <i>Scientific Data</i> , 2017 , 4, 1701188.2	4.8	27
213	Gene Expression in Is Regulated Predominantly by Gene Dosage. <i>MBio</i> , 2017 , 8,	7.8	72
212	Utilizing the planarian voltage-gated ion channel transcriptome to resolve a role for a Ca channel in neuromuscular function and regeneration. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2017 , 1864, 1036-1045	4.9	12
211	An improved genome assembly reveals an unexpected methyltransferase gene expansion. <i>Wellcome Open Research</i> , 2017 , 2, 42	4.8	29
210	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,	7.8	37
209	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	4.9	74
208	WormBase 2016: expanding to enable helminth genomic research. <i>Nucleic Acids Research</i> , 2016 , 44, D774-D800	4.8	217
207	The genomic basis of parasitism in the Strongyloides clade of nematodes. <i>Nature Genetics</i> , 2016 , 48, 299-307	36.3	150

206	Nitroheterocyclic drug resistance mechanisms in <i>Trypanosoma brucei</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2016 , 71, 625-34	5.1	49
205	Kinetoplastid Phylogenomics Reveals the Evolutionary Innovations Associated with the Origins of Parasitism. <i>Current Biology</i> , 2016 , 26, 161-172	6.3	98
204	The nucleosome landscape of <i>Plasmodium falciparum</i> reveals chromatin architecture and dynamics of regulatory sequences. <i>Nucleic Acids Research</i> , 2016 , 44, 2110-24	20.1	56
203	The genome of <i>Onchocerca volvulus</i> , agent of river blindness. <i>Nature Microbiology</i> , 2016 , 2, 16216	26.6	69
202	A new reference sequence with improved assembly of the subtelomeres reveals an abundance of genes. <i>Wellcome Open Research</i> , 2016 , 1, 4	4.8	69
201	Evolutionary genomics of epidemic visceral leishmaniasis in the Indian subcontinent. <i>ELife</i> , 2016 , 5,	8.9	107
200	Population genomics reveals the origin and asexual evolution of human infective trypanosomes. <i>ELife</i> , 2016 , 5, e11473	8.9	62
199	Activation of Bicyclic Nitro-drugs by a Novel Nitroreductase (NTR2) in <i>Leishmania</i> . <i>PLoS Pathogens</i> , 2016 , 12, e1005971	7.6	53
198	HIV-1 Integrates Widely throughout the Genome of the Human Blood Fluke <i>Schistosoma mansoni</i> . <i>PLoS Pathogens</i> , 2016 , 12, e1005931	7.6	14
197	Whole genome sequencing of <i>Plasmodium falciparum</i> from dried blood spots using selective whole genome amplification. <i>Malaria Journal</i> , 2016 , 15, 597	3.6	74
196	Dataset for a de novo transcriptome assembly, utilized for defining the voltage-gated like ion channel superfamily. <i>Data in Brief</i> , 2016 , 9, 1044-1047	1.2	9
195	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	4.9	43
194	Companion: a web server for annotation and analysis of parasite genomes. <i>Nucleic Acids Research</i> , 2016 , 44, W29-34	20.1	68
193	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	4.5	20
192	Genome-scale RNAi screens for high-throughput phenotyping in bloodstream-form African trypanosomes. <i>Nature Protocols</i> , 2015 , 10, 106-33	18.8	39
191	TrypanoCyc: a community-led biochemical pathways database for <i>Trypanosoma brucei</i> . <i>Nucleic Acids Research</i> , 2015 , 43, D637-44	20.1	28
190	What helminth genomes have taught us about parasite evolution. <i>Parasitology</i> , 2015 , 142 Suppl 1, S85-97.	61	
189	Global Gene Expression Profiling through the Complete Life Cycle of <i>Trypanosoma vivax</i> . <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0003975	4.8	24

188	Genomic and Proteomic Studies on the Mode of Action of Oxaboroles against the African Trypanosome. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0004299	4.8	26
187	A cascade of DNA-binding proteins for sexual commitment and development in Plasmodium. <i>Nature</i> , 2014 , 507, 253-257	50.4	269
186	Genome sequence of the tsetse fly (<i>Glossina morsitans</i>): vector of African trypanosomiasis. <i>Science</i> , 2014 , 344, 380-6	33.3	192
185	Summarizing specific profiles in Illumina sequencing from whole-genome amplified DNA. <i>DNA Research</i> , 2014 , 21, 243-54	4.5	11
184	Medicine. Halting harmful helminths. <i>Science</i> , 2014 , 346, 168-9	33.3	30
183	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	18.3	155
182	Genomic analysis of the causative agents of coccidiosis in domestic chickens. <i>Genome Research</i> , 2014 , 24, 1676-85	9.7	121
181	Whipworm genome and dual-species transcriptome analyses provide molecular insights into an intimate host-parasite interaction. <i>Nature Genetics</i> , 2014 , 46, 693-700	36.3	101
180	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, 7113-31	20.1	66
179	Genomic confirmation of hybridisation and recent inbreeding in a vector-isolated <i>Leishmania</i> population. <i>PLoS Genetics</i> , 2014 , 10, e1004092	6	108
178	Optimized whole-genome amplification strategy for extremely AT-biased template. <i>DNA Research</i> , 2014 , 21, 661-71	4.5	23
177	Differential PfEMP1 expression is associated with cerebral malaria pathology. <i>PLoS Pathogens</i> , 2014 , 10, e1004537	7.6	26
176	International glossina genome initiative 2004-2014: a driver for post-genomic era research on the African continent. <i>PLoS Neglected Tropical Diseases</i> , 2014 , 8, e3024	4.8	5
175	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	9.7	136
174	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	18.3	33
173	Secreted proteomes of different developmental stages of the gastrointestinal nematode <i>Nippostrongylus brasiliensis</i> . <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2736-51	7.6	63
172	Pyrazoleamide compounds are potent antimalarials that target Na ⁺ homeostasis in intraerythrocytic <i>Plasmodium falciparum</i> . <i>Nature Communications</i> , 2014 , 5, 5521	17.4	85
171	A comprehensive evaluation of rodent malaria parasite genomes and gene expression. <i>BMC Biology</i> , 2014 , 12, 86	7.3	174

170	Genome sequencing of chimpanzee malaria parasites reveals possible pathways of adaptation to human hosts. <i>Nature Communications</i> , 2014 , 5, 4754	17.4	107
169	A comprehensive evaluation of assembly scaffolding tools. <i>Genome Biology</i> , 2014 , 15, R42	18.3	118
168	WormBase 2014: new views of curated biology. <i>Nucleic Acids Research</i> , 2014 , 42, D789-93	20.1	126
167	REAPR: a universal tool for genome assembly evaluation. <i>Genome Biology</i> , 2013 , 14, R47	18.3	304
166	Genetic and molecular basis of drug resistance and species-specific drug action in schistosome parasites. <i>Science</i> , 2013 , 342, 1385-9	33.3	104
165	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	18.3	225
164	Characterization and comparative analysis of the complete <i>Haemonchus contortus</i> β -tubulin gene family and implications for benzimidazole resistance in strongylid nematodes. <i>International Journal for Parasitology</i> , 2013 , 43, 465-75	4.3	37
163	The genomes of four tapeworm species reveal adaptations to parasitism. <i>Nature</i> , 2013 , 496, 57-63	50.4	483
162	SchistoDB: an updated genome resource for the three key schistosomes of humans. <i>Nucleic Acids Research</i> , 2013 , 41, D728-31	20.1	41
161	Multiple populations of artemisinin-resistant <i>Plasmodium falciparum</i> in Cambodia. <i>Nature Genetics</i> , 2013 , 45, 648-55	36.3	350
160	Comparative study of transcriptome profiles of mechanical- and skin-transformed <i>Schistosoma mansoni</i> schistosomula. <i>PLoS Neglected Tropical Diseases</i> , 2013 , 7, e2091	4.8	50
159	Vector transmission regulates immune control of <i>Plasmodium</i> virulence. <i>Nature</i> , 2013 , 498, 228-31	50.4	113
158	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, 426-48	7.6	52
157	BamView: visualizing and interpretation of next-generation sequencing read alignments. <i>Briefings in Bioinformatics</i> , 2013 , 14, 203-12	13.4	50
156	A cell-surface phylome for African trypanosomes. <i>PLoS Neglected Tropical Diseases</i> , 2013 , 7, e2121	4.8	72
155	Genes involved in host-parasite interactions can be revealed by their correlated expression. <i>Nucleic Acids Research</i> , 2013 , 41, 1508-18	20.1	20
154	Genome-wide profiling of chromosome interactions in <i>Plasmodium falciparum</i> characterizes nuclear architecture and reconfigurations associated with antigenic variation. <i>Molecular Microbiology</i> , 2013 , 90, 519-37	4.1	37
153	Efficient depletion of host DNA contamination in malaria clinical sequencing. <i>Journal of Clinical Microbiology</i> , 2013 , 51, 745-51	9.7	57

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28	Extensive genomic and transcriptomic variation defines the chromosome-scale assembly of <i>Haemonchus contortus</i> , a model gastrointestinal worm		2
27	Evaluation of whole genome amplification and bioinformatic methods for the characterization of <i>Leishmania</i> genomes at a single cell level		1

26	Complete avian malaria parasite genomes reveal features associated with lineage specific evolution in birds and mammals	4
25	Genomes of all known members of a Plasmodium subgenus reveal paths to virulent human malaria	4
24	Single-cell transcriptomics of malaria parasites	2
23	Transcriptomic profiling of nematode parasites surviving after vaccine exposure	2
22	Large-scale RNAi screening uncovers new therapeutic targets in the human parasite Schistosoma mansoni	6
21	Complete representation of a tapeworm genome reveals chromosomes capped by centromeres, necessitating a dual role in segregation and protection	2
20	Development of caecaloids to study host-pathogen interactions: new insights into immunoregulatory functions of Trichuris muris extracellular vesicles in the caecum	1
19	Defining the early stages of intestinal colonisation by whipworms	3
18	Population genomic and evolutionary modelling analyses reveal a single major QTL for ivermectin drug resistance in the pathogenic nematode, Haemonchus contortus	4
17	Meta-analysis of RNA-seq studies reveals genes responsible for life stage-dominant functions in Schistosoma mansoni	6
16	A web portal for gene expression across all life stages of Schistosoma mansoni	8
15	Programmed genome editing of the omega-1 ribonuclease 1 of the blood fluke, Schistosoma mansoni	2
14	Morphological and genomic characterisation of the hybrid schistosome infecting humans in Europe reveals a complex admixture between Schistosoma haematobium and Schistosoma bovis parasites	2
13	The global diversity of the major parasitic nematode Haemonchus contortus shaped by human intervention and climate	3
12	Genomic analysis of natural intra-specific hybrids among Ethiopian isolates of Leishmania donovani	2
11	The Malaria Cell Atlas: a comprehensive reference of single parasite transcriptomes across the complete Plasmodium life cycle	6
10	Genomes of Leishmania parasites directly sequenced from patients with visceral leishmaniasis in the Indian subcontinent	5
9	Single-cell atlas of the first intra-mammalian developmental stage of the human parasite Schistosoma mansoni	7

8	Transcriptome of the parasitic flatworm <i>Schistosoma mansoni</i> during intra-mammalian development	4
7	Population genomic evidence that human and animal infections in Africa come from the same populations of <i>Dracunculus medinensis</i>	1
6	Refining the transcriptome of the human malaria parasite <i>Plasmodium falciparum</i> using amplification-free RNA-seq	2
5	Whole genome sequencing of <i>Plasmodium falciparum</i> from dried blood spots using selective whole genome amplification	1
4	Daily rhythms in the transcriptomes of the human parasite <i>Schistosoma mansoni</i>	1
3	Long-read assembly and comparative evidence-based reanalysis of <i>Cryptosporidium</i> genome sequences reveal new biological insights	2
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