

# Matt Berriman

## List of Publications by Citations

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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	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , <b>2002</b> , 419, 498-511	50.4	3336
312	The Gene Ontology (GO) database and informatics resource. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D258-61	20.1	2536
311	The genome of the African trypanosome <i>Trypanosoma brucei</i> . <i>Science</i> , <b>2005</b> , 309, 416-22	33.3	1323
310	ACT: the Artemis Comparison Tool. <i>Bioinformatics</i> , <b>2005</b> , 21, 3422-3	7.2	1269
309	Expansion of the Gene Ontology knowledgebase and resources. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D331-D338	12.3	1258
308	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , <b>2005</b> , 438, 1151-6	50.4	1114
307	The genome of the kinetoplastid parasite, <i>Leishmania major</i> . <i>Science</i> , <b>2005</b> , 309, 436-42	33.3	1101
306	The genome of the social amoeba <i>Dictyostelium discoideum</i> . <i>Nature</i> , <b>2005</b> , 435, 43-57	50.4	1042
305	The genome of the blood fluke <i>Schistosoma mansoni</i> . <i>Nature</i> , <b>2009</b> , 460, 352-8	50.4	822
304	The Gene Ontology (GO) project in 2006. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D322-6	20.1	794
303	Evolution of pathogenicity and sexual reproduction in eight <i>Candida</i> genomes. <i>Nature</i> , <b>2009</b> , 459, 657-62	50.4	764
302	The genome of the protist parasite <i>Entamoeba histolytica</i> . <i>Nature</i> , <b>2005</b> , 433, 865-8	50.4	701
301	Artemis: an integrated platform for visualization and analysis of high-throughput sequence-based experimental data. <i>Bioinformatics</i> , <b>2012</b> , 28, 464-9	7.2	665
300	A comprehensive survey of the <i>Plasmodium</i> life cycle by genomic, transcriptomic, and proteomic analyses. <i>Science</i> , <b>2005</b> , 307, 82-6	33.3	662
299	TriTrypDB: a functional genomic resource for the Trypanosomatidae. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D457-62	20.1	625
298	Comparative genomics of trypanosomatid parasitic protozoa. <i>Science</i> , <b>2005</b> , 309, 404-9	33.3	614
297	DNAPlotter: circular and linear interactive genome visualization. <i>Bioinformatics</i> , <b>2009</b> , 25, 119-20	7.2	601

296	Comparative genomic analysis of three Leishmania species that cause diverse human disease. <i>Nature Genetics</i> , <b>2007</b> , 39, 839-47	36.3	569
295	The Gene Ontology project in 2008. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D440-4	20.1	564
294	The Gene Ontology resource: enriching a GOld mine. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D325-D334	20.1	494
293	The genomes of four tapeworm species reveal adaptations to parasitism. <i>Nature</i> , <b>2013</b> , 496, 57-63	50.4	483
292	Artemis and ACT: viewing, annotating and comparing sequences stored in a relational database. <i>Bioinformatics</i> , <b>2008</b> , 24, 2672-6	7.2	462
291	Amplification-free Illumina sequencing-library preparation facilitates improved mapping and assembly of (G+C)-biased genomes. <i>Nature Methods</i> , <b>2009</b> , 6, 291-5	21.6	431
290	An ancestral oomycete locus contains late blight avirulence gene Avr3a, 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> , <b>2005</b> , 102, 7766-71	11.5	362
289	Multiple populations of artemisinin-resistant Plasmodium falciparum in Cambodia. <i>Nature Genetics</i> , <b>2013</b> , 45, 648-55	36.3	350
288	Analysis of Plasmodium falciparum diversity in natural infections by deep sequencing. <i>Nature</i> , <b>2012</b> , 487, 375-9	50.4	345
287	High-throughput phenotyping using parallel sequencing of RNA interference targets in the African trypanosome. <i>Genome Research</i> , <b>2011</b> , 21, 915-24	9.7	332
286	ABACAS: algorithm-based automatic contiguation of assembled sequences. <i>Bioinformatics</i> , <b>2009</b> , 25, 1968-9	7.2	323
285	Whole genome sequencing of multiple Leishmania donovani clinical isolates provides insights into population structure and mechanisms of drug resistance. <i>Genome Research</i> , <b>2011</b> , 21, 2143-56	9.7	319
284	A systematically improved high quality genome and transcriptome of the human blood fluke Schistosoma mansoni. <i>PLoS Neglected Tropical Diseases</i> , <b>2012</b> , 6, e1455	4.8	306
283	REAPR: a universal tool for genome assembly evaluation. <i>Genome Biology</i> , <b>2013</b> , 14, R47	18.3	304
282	Chromosome and gene copy number variation allow major structural change between species and strains of Leishmania. <i>Genome Research</i> , <b>2011</b> , 21, 2129-42	9.7	299
281	The genome of the simian and human malaria parasite Plasmodium knowlesi. <i>Nature</i> , <b>2008</b> , 455, 799-803	50.4	289
280	New insights into the blood-stage transcriptome of Plasmodium falciparum using RNA-Seq. <i>Molecular Microbiology</i> , <b>2010</b> , 76, 12-24	4.1	283
279	Genomic insights into the origin of parasitism in the emerging plant pathogen Bursaphelenchus xylophilus. <i>PLoS Pathogens</i> , <b>2011</b> , 7, e1002219	7.6	279

278	A cascade of DNA-binding proteins for sexual commitment and development in Plasmodium. <i>Nature</i> , <b>2014</b> , 507, 253-257	50.4	269
277	WormBase ParaSite - a comprehensive resource for helminth genomics. <i>Molecular and Biochemical Parasitology</i> , <b>2017</b> , 215, 2-10	1.9	264
276	Genome sequence of Theileria parva, a bovine pathogen that transforms lymphocytes. <i>Science</i> , <b>2005</b> , 309, 134-7	33.3	259
275	A human-curated annotation of the Candida albicans genome. <i>PLoS Genetics</i> , <b>2005</b> , 1, 36-57	6	249
274	Genomic-scale prioritization of drug targets: the TDR Targets database. <i>Nature Reviews Drug Discovery</i> , <b>2008</b> , 7, 900-7	64.1	244
273	Improving draft assemblies by iterative mapping and assembly of short reads to eliminate gaps. <i>Genome Biology</i> , <b>2010</b> , 11, R41	18.3	236
272	Genome of the host-cell transforming parasite Theileria annulata compared with T. parva. <i>Science</i> , <b>2005</b> , 309, 131-3	33.3	235
271	High-throughput decoding of antitrypanosomal drug efficacy and resistance. <i>Nature</i> , <b>2012</b> , 482, 232-6	50.4	229
270	The genome and transcriptome of Haemonchus contortus, a key model parasite for drug and vaccine discovery. <i>Genome Biology</i> , <b>2013</b> , 14, R88	18.3	225
269	RATT: Rapid Annotation Transfer Tool. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, e57	20.1	224
268	WormBase 2016: expanding to enable helminth genomic research. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D774-80	4.8	217
267	Telomeric expression sites are highly conserved in Trypanosoma brucei. <i>PLoS ONE</i> , <b>2008</b> , 3, e3527	3.7	208
266	Comparative genomics of the major parasitic worms. <i>Nature Genetics</i> , <b>2019</b> , 51, 163-174	36.3	201
265	Genome sequence of the tsetse fly (Glossina morsitans): vector of African trypanosomiasis. <i>Science</i> , <b>2014</b> , 344, 380-6	33.3	192
264	GeneDB: a resource for prokaryotic and eukaryotic organisms. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D339-43	20.1	190
263	GeneDB--an annotation database for pathogens. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D98-108	20.1	186
262	Iterative Correction of Reference Nucleotides (iCORN) using second generation sequencing technology. <i>Bioinformatics</i> , <b>2010</b> , 26, 1704-7	7.2	184
261	Crystal structure of Trypanosoma cruzi trypanothione reductase in complex with trypanothione, and the structure-based discovery of new natural product inhibitors. <i>Structure</i> , <b>1999</b> , 7, 81-9	5.2	181

260	A comprehensive evaluation of rodent malaria parasite genomes and gene expression. <i>BMC Biology</i> , <b>2014</b> , 12, 86	7.3	174
259	GOTcha: a new method for prediction of protein function assessed by the annotation of seven genomes. <i>BMC Bioinformatics</i> , <b>2004</b> , 5, 178	3.6	168
258	Comparative genomics of the fungal pathogens <i>Candida dubliniensis</i> and <i>Candida albicans</i> . <i>Genome Research</i> , <b>2009</b> , 19, 2231-44	9.7	165
257	WormBase 2012: more genomes, more data, new website. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D735-41	20.1	159
256	Genome variation and evolution of the malaria parasite <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , <b>2007</b> , 39, 120-5	36.3	159
255	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> , <b>2014</b> , 15, R43	18.3	155
254	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> , <b>2012</b> , 8, e1002567	7.6	154
253	The genomic basis of parasitism in the Strongyloides clade of nematodes. <i>Nature Genetics</i> , <b>2016</b> , 48, 299-307	36.3	150
252	A post-assembly genome-improvement toolkit (PAGIT) to obtain annotated genomes from contigs. <i>Nature Protocols</i> , <b>2012</b> , 7, 1260-84	18.8	144
251	WormBase 2017: molting into a new stage. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D869-D874	20.1	138
250	Phosphoinositide metabolism links cGMP-dependent protein kinase G to essential Ca <sup>2+</sup> signals at key decision points in the life cycle of malaria parasites. <i>PLoS Biology</i> , <b>2014</b> , 12, e1001806	9.7	136
249	Composite genome map and recombination parameters derived from three archetypal lineages of <i>Toxoplasma gondii</i> . <i>Nucleic Acids Research</i> , <b>2005</b> , 33, 2980-92	20.1	133
248	<i>Plasmodium falciparum</i> variant surface antigen expression patterns during malaria. <i>PLoS Pathogens</i> , <b>2005</b> , 1, e26	7.6	132
247	Assembly of the <i>Candida albicans</i> genome into sixteen supercontigs aligned on the eight chromosomes. <i>Genome Biology</i> , <b>2007</b> , 8, R52	18.3	128
246	An integrated national scale SARS-CoV-2 genomic surveillance network. <i>Lancet Microbe</i> , <b>2020</b> , 1, e99-e100	22.2	127
245	Sequence of <i>Plasmodium falciparum</i> chromosomes 1, 3-9 and 13. <i>Nature</i> , <b>2002</b> , 419, 527-31	50.4	127
244	WormBase 2014: new views of curated biology. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D789-93	20.1	126
243	Identification of attractive drug targets in neglected-disease pathogens using an in silico approach. <i>PLoS Neglected Tropical Diseases</i> , <b>2010</b> , 4, e804	4.8	123

242	RNA interference in parasitic helminths: current situation, potential pitfalls and future prospects. <i>Parasitology</i> , <b>2007</b> , 134, 609-19	2.7	122
241	Genomic analysis of the causative agents of coccidiosis in domestic chickens. <i>Genome Research</i> , <b>2014</b> , 24, 1676-85	9.7	121
240	Viewing and annotating sequence data with Artemis. <i>Briefings in Bioinformatics</i> , <b>2003</b> , 4, 124-32	13.4	121
239	A comprehensive evaluation of assembly scaffolding tools. <i>Genome Biology</i> , <b>2014</b> , 15, R42	18.3	118
238	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> , <b>2012</b> , 109, 3416-21	11.5	114
237	Vector transmission regulates immune control of Plasmodium virulence. <i>Nature</i> , <b>2013</b> , 498, 228-31	50.4	113
236	Plasmodium falciparum var gene expression is modified by host immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 21801-6	11.5	111
235	Genomic confirmation of hybridisation and recent inbreeding in a vector-isolated Leishmania population. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004092	6	108
234	Genome sequencing of chimpanzee malaria parasites reveals possible pathways of adaptation to human hosts. <i>Nature Communications</i> , <b>2014</b> , 5, 4754	17.4	107
233	The genome sequence of Trypanosoma brucei gambiense, causative agent of chronic human african trypanosomiasis. <i>PLoS Neglected Tropical Diseases</i> , <b>2010</b> , 4, e658	4.8	107
232	Evolutionary genomics of epidemic visceral leishmaniasis in the Indian subcontinent. <i>ELife</i> , <b>2016</b> , 5,	8.9	107
231	Genetic and molecular basis of drug resistance and species-specific drug action in schistosome parasites. <i>Science</i> , <b>2013</b> , 342, 1385-9	33.3	104
230	Just one cross appears capable of dramatically altering the population biology of a eukaryotic pathogen like Toxoplasma gondii. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 10514-10519	11.5	102
229	Whipworm genome and dual-species transcriptome analyses provide molecular insights into an intimate host-parasite interaction. <i>Nature Genetics</i> , <b>2014</b> , 46, 693-700	36.3	101
228	Plasmodium malariae and P. ovale genomes provide insights into malaria parasite evolution. <i>Nature</i> , <b>2017</b> , 542, 101-104	50.4	99
227	Kinetoplastid Phylogenomics Reveals the Evolutionary Innovations Associated with the Origins of Parasitism. <i>Current Biology</i> , <b>2016</b> , 26, 161-172	6.3	98
226	Modulation of Aneuploidy in during Adaptation to Different and Environments and Its Impact on Gene Expression. <i>MBio</i> , <b>2017</b> , 8,	7.8	95
225	Single-cell RNA-seq reveals hidden transcriptional variation in malaria parasites. <i>ELife</i> , <b>2018</b> , 7,	8.9	94

224	The Malaria Cell Atlas: Single parasite transcriptomes across the complete life cycle. <i>Science</i> , <b>2019</b> , 365,	33.3	90
223	The architecture of variant surface glycoprotein gene expression sites in <i>Trypanosoma brucei</i> . <i>Molecular and Biochemical Parasitology</i> , <b>2002</b> , 122, 131-40	1.9	88
222	Pyrazoleamide compounds are potent antimalarials that target Na <sup>+</sup> homeostasis in intraerythrocytic <i>Plasmodium falciparum</i> . <i>Nature Communications</i> , <b>2014</b> , 5, 5521	17.4	85
221	Genomes of all known members of a <i>Plasmodium</i> subgenus reveal paths to virulent human malaria. <i>Nature Microbiology</i> , <b>2018</b> , 3, 687-697	26.6	85
220	Gene synteny and evolution of genome architecture in trypanosomatids. <i>Molecular and Biochemical Parasitology</i> , <b>2004</b> , 134, 183-91	1.9	83
219	Silencing of germline-expressed genes by DNA elimination in somatic cells. <i>Developmental Cell</i> , <b>2012</b> , 23, 1072-80	10.2	79
218	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> , <b>2012</b> , 21, 41-8	3.4	76
217	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> , <b>2002</b> , 1, 137-51		75
216	Schistosome sex matters: a deep view into gonad-specific and pairing-dependent transcriptomes reveals a complex gender interplay. <i>Scientific Reports</i> , <b>2016</b> , 6, 31150	4.9	74
215	Protein variation in blood-dwelling schistosome worms generated by differential splicing of micro-exon gene transcripts. <i>Genome Research</i> , <b>2010</b> , 20, 1112-21	9.7	74
214	Whole genome sequencing of <i>Plasmodium falciparum</i> from dried blood spots using selective whole genome amplification. <i>Malaria Journal</i> , <b>2016</b> , 15, 597	3.6	74
213	Cyclin-dependent kinase 12 is a drug target for visceral leishmaniasis. <i>Nature</i> , <b>2018</b> , 560, 192-197	50.4	73
212	Gene Expression in Is Regulated Predominantly by Gene Dosage. <i>MBio</i> , <b>2017</b> , 8,	7.8	72
211	A cell-surface phylome for African trypanosomes. <i>PLoS Neglected Tropical Diseases</i> , <b>2013</b> , 7, e2121	4.8	72
210	Genome-wide discovery and verification of novel structured RNAs in <i>Plasmodium falciparum</i> . <i>Genome Research</i> , <b>2008</b> , 18, 281-92	9.7	72
209	-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> , <b>2017</b> , 61,	5.9	71
208	The genome of <i>Onchocerca volvulus</i> , agent of river blindness. <i>Nature Microbiology</i> , <b>2016</b> , 2, 16216	26.6	69
207	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> , <b>2011</b> , 5, e1409	4.8	69

206	An insight into the sialome of <i>Glossina morsitans morsitans</i> . <i>BMC Genomics</i> , <b>2010</b> , 11, 213	4.5	69
205	A new reference sequence with improved assembly of the subtelomeres reveals an abundance of genes. <i>Wellcome Open Research</i> , <b>2016</b> , 1, 4	4.8	69
204	Companion: a web server for annotation and analysis of parasite genomes. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, W29-34	20.1	68
203	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> , <b>2014</b> , 42, 7113-31	20.1	66
202	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
201	RNAseq analysis of the parasitic nematode <i>Strongyloides stercoralis</i> reveals divergent regulation of canonical dauer pathways. <i>PLoS Neglected Tropical Diseases</i> , <b>2012</b> , 6, e1854	4.8	63
200	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> , <b>2003</b> , 4, R63	18.3	62
199	Population genomics reveals the origin and asexual evolution of human infective trypanosomes. <i>ELife</i> , <b>2016</b> , 5, e11473	8.9	62
198	What helminth genomes have taught us about parasite evolution. <i>Parasitology</i> , <b>2015</b> , 142 Suppl 1, S85-97.	7	61
197	Using RNA-seq to determine the transcriptional landscape and the hypoxic response of the pathogenic yeast <i>Candida parapsilosis</i> . <i>BMC Genomics</i> , <b>2011</b> , 12, 628	4.5	59
196	BamView: viewing mapped read alignment data in the context of the reference sequence. <i>Bioinformatics</i> , <b>2010</b> , 26, 676-7	7.2	58
195	Efficient depletion of host DNA contamination in malaria clinical sequencing. <i>Journal of Clinical Microbiology</i> , <b>2013</b> , 51, 745-51	9.7	57
194	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> , <b>1999</b> , 99, 167-81	1.9	57
193	The nucleosome landscape of <i>Plasmodium falciparum</i> reveals chromatin architecture and dynamics of regulatory sequences. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 2110-24	20.1	56
192	Diversity in parasitic nematode genomes: the microRNAs of <i>Brugia pahangi</i> and <i>Haemonchus contortus</i> are largely novel. <i>BMC Genomics</i> , <b>2012</b> , 13, 4	4.5	55
191	Differential var gene expression in the organs of patients dying of falciparum malaria. <i>Molecular Microbiology</i> , <b>2007</b> , 65, 959-67	4.1	54
190	Long read assemblies of geographically dispersed isolates reveal highly structured subtelomeres. <i>Wellcome Open Research</i> , <b>2018</b> , 3, 52	4.8	54
189	Complete avian malaria parasite genomes reveal features associated with lineage-specific evolution in birds and mammals. <i>Genome Research</i> , <b>2018</b> , 28, 547-560	9.7	53



188	Germline transgenesis and insertional mutagenesis in <i>Schistosoma mansoni</i> mediated by murine leukemia virus. <i>PLoS Pathogens</i> , <b>2012</b> , 8, e1002820	7.6	53
187	The genetic map and comparative analysis with the physical map of <i>Trypanosoma brucei</i> . <i>Nucleic Acids Research</i> , <b>2005</b> , 33, 6688-93	20.1	53
186	Activation of Bicyclic Nitro-drugs by a Novel Nitroreductase (NTR2) in <i>Leishmania</i> . <i>PLoS Pathogens</i> , <b>2016</b> , 12, e1005971	7.6	53
185	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> , <b>2013</b> , 12, 426-48	7.6	52
184	A transcriptomic analysis of <i>Echinococcus granulosus</i> larval stages: implications for parasite biology and host adaptation. <i>PLoS Neglected Tropical Diseases</i> , <b>2012</b> , 6, e1897	4.8	51
183	Øming in on schistosomes: prospects and limitations for post-genomics. <i>Trends in Parasitology</i> , <b>2007</b> , 23, 14-20	6.4	51
182	Programmed genome editing of the omega-1 ribonuclease of the blood fluke. <i>ELife</i> , <b>2019</b> , 8,	8.9	51
181	Comparative study of transcriptome profiles of mechanical- and skin-transformed <i>Schistosoma mansoni</i> schistosomula. <i>PLoS Neglected Tropical Diseases</i> , <b>2013</b> , 7, e2091	4.8	50
180	BamView: visualizing and interpretation of next-generation sequencing read alignments. <i>Briefings in Bioinformatics</i> , <b>2013</b> , 14, 203-12	13.4	50
179	Nitroheterocyclic drug resistance mechanisms in <i>Trypanosoma brucei</i> . <i>Journal of Antimicrobial Chemotherapy</i> , <b>2016</b> , 71, 625-34	5.1	49
178	Common inheritance of chromosome Ia associated with clonal expansion of <i>Toxoplasma gondii</i> . <i>Genome Research</i> , <b>2006</b> , 16, 1119-25	9.7	49
177	Genome-wide SNP and microsatellite variation illuminate population-level epidemiology in the <i>Leishmania donovani</i> species complex. <i>Infection, Genetics and Evolution</i> , <b>2012</b> , 12, 149-59	4.5	47
176	The DNA sequence of chromosome I of an African trypanosome: gene content, chromosome organisation, recombination and polymorphism. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 4864-73	20.1	47
175	What the genome sequence is revealing about trypanosome antigenic variation. <i>Biochemical Society Transactions</i> , <b>2005</b> , 33, 986-9	5.1	45
174	Biology and genome of a newly discovered sibling species of <i>Caenorhabditis elegans</i> . <i>Nature Communications</i> , <b>2018</b> , 9, 3216	17.4	44
173	Whole genome resequencing of the human parasite <i>Schistosoma mansoni</i> reveals population history and effects of selection. <i>Scientific Reports</i> , <b>2016</b> , 6, 20954	4.9	43
172	Sequencing and analysis of chromosome 1 of <i>Eimeria tenella</i> reveals a unique segmental organization. <i>Genome Research</i> , <b>2007</b> , 17, 311-9	9.7	42
171	SchistoDB: an updated genome resource for the three key schistosomes of humans. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D728-31	20.1	41

170	Detailed characterization of a cyclophilin from the human malaria parasite <i>Plasmodium falciparum</i> . <i>Biochemical Journal</i> , <b>1998</b> , 334 ( Pt 2), 437-45	3.8	41
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69	Meta-analysis of RNA-seq studies reveals genes responsible for life stage-dominant functions in <i>Schistosoma mansoni</i>		6
68	The Malaria Cell Atlas: a comprehensive reference of single parasite transcriptomes across the complete <i>Plasmodium</i> life cycle		6
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56	Genomes of all known members of a <i>Plasmodium</i> subgenus reveal paths to virulent human malaria		4
55	Population genomic and evolutionary modelling analyses reveal a single major QTL for ivermectin drug resistance in the pathogenic nematode, <i>Haemonchus contortus</i>		4
54	Transcriptome of the parasitic flatworm <i>Schistosoma mansoni</i> during intra-mammalian development		4
53	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> , <b>2021</b> , 15, e0008814	4.8	4
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48	Defining the early stages of intestinal colonisation by whipworms		3
47	The global diversity of the major parasitic nematode <i>Haemonchus contortus</i> shaped by human intervention and climate		3
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39	Genomic landscape of drug response reveals novel mediators of anthelmintic resistance		2
38	Daily rhythms in gene expression of the human parasite <i>Schistosoma mansoni</i> . <i>BMC Biology</i> , <b>2021</b> , 19, 255	7.3	2
37	Extensive genomic and transcriptomic variation defines the chromosome-scale assembly of <i>Haemonchus contortus</i> , a model gastrointestinal worm		2
36	Single-cell transcriptomics of malaria parasites		2
35	Transcriptomic profiling of nematode parasites surviving after vaccine exposure		2
34	Complete representation of a tapeworm genome reveals chromosomes capped by centromeres, necessitating a dual role in segregation and protection		2
33	Programmed genome editing of the omega-1 ribonuclease 1 of the blood fluke, <i>Schistosoma mansoni</i>		2
32	Morphological and genomic characterisation of the hybrid schistosome infecting humans in Europe reveals a complex admixture between <i>Schistosoma haematobium</i> and <i>Schistosoma bovis</i> parasites		2
31	Genomic analysis of natural intra-specific hybrids among Ethiopian isolates of <i>Leishmania donovani</i>		2
30	Refining the transcriptome of the human malaria parasite <i>Plasmodium falciparum</i> using amplification-free RNA-seq		2
29	Long-read assembly and comparative evidence-based reanalysis of <i>Cryptosporidium</i> genome sequences reveal new biological insights		2
28	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> , <b>2018</b> , 13, e0201263	3.7	2
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22	A library of cell-surface and secreted proteins from <i>Schistosoma mansoni</i> identifies early serological markers of infection		1
21	Global genome diversity of the <i>Leishmania donovani</i> complex		1
20	Evaluation of whole genome amplification and bioinformatic methods for the characterization of <i>Leishmania</i> genomes at a single cell level		1
19	Development of caecaloids to study host-pathogen interactions: new insights into immunoregulatory functions of <i>Trichuris muris</i> extracellular vesicles in the caecum		1
18	Population genomic evidence that human and animal infections in Africa come from the same populations of <i>Dracunculus medinensis</i>		1
17	Whole genome sequencing of <i>Plasmodium falciparum</i> from dried blood spots using selective whole genome amplification		1
16	Daily rhythms in the transcriptomes of the human parasite <i>Schistosoma mansoni</i>		1
15	Individual-level variations in malaria susceptibility and acquisition of clinical protection. <i>Wellcome Open Research</i> , <b>2021</b> , 6, 22	4.8	1
14	The Transcriptome of <i>Schistosoma mansoni</i> Developing Eggs Reveals Key Mediators in Pathogenesis and Life Cycle Propagation. <i>Frontiers in Tropical Diseases</i> , <b>2021</b> , 2,		1
13	Individual-level variations in malaria susceptibility and acquisition of clinical protection. <i>Wellcome Open Research</i> , <b>2021</b> , 6, 22	4.8	1
12	Defining the early stages of intestinal colonisation by whipworms. <i>Nature Communications</i> , <b>2022</b> , 13, 1725	17.4	1
11	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> , <b>2022</b> , e0326421	7.8	0
10	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> , <b>2021</b> , 15, e0010062	4.8	0
9	GeneDB and Wikidata. <i>Wellcome Open Research</i> , <b>2019</b> , 4, 114	4.8	

- 8 Transcriptome of the parasitic flatworm *Schistosoma mansoni* during intra-mammalian development **2020**, 14, e0007743
- 7 Transcriptome of the parasitic flatworm *Schistosoma mansoni* during intra-mammalian development **2020**, 14, e0007743
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- 4 Genomic and transcriptomic evidence for descent from *Plasmodium* and loss of blood schizogony in *Hepaticystis* parasites from naturally infected red colobus monkeys **2020**, 16, e1008717
- 3 Genomic and transcriptomic evidence for descent from *Plasmodium* and loss of blood schizogony in *Hepaticystis* parasites from naturally infected red colobus monkeys **2020**, 16, e1008717
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