

# Arnab Pain

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3235966/publications.pdf>

Version: 2024-02-01

205  
papers

23,984  
citations

17429

63  
h-index

8618

146  
g-index

259  
all docs

259  
docs citations

259  
times ranked

26570  
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	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	13.7	1,838
3	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , 2005, 438, 1151-1156.	13.7	1,272
4	Sequencing of <i>Aspergillus nidulans</i> and comparative analysis with <i>A. fumigatus</i> and <i>A. oryzae</i> . <i>Nature</i> , 2005, 438, 1105-1115.	13.7	1,250
5	The genome of the social amoeba <i>Dictyostelium discoideum</i> . <i>Nature</i> , 2005, 435, 43-57.	13.7	1,179
6	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
7	Analysis of the <i>Plasmodium falciparum</i> proteome by high-accuracy mass spectrometry. <i>Nature</i> , 2002, 419, 537-542.	13.7	596
8	<i>Plasmodium falciparum</i> -infected erythrocytes modulate the maturation of dendritic cells. <i>Nature</i> , 1999, 400, 73-77.	13.7	553
9	A robust SNP barcode for typing <i>Mycobacterium tuberculosis</i> complex strains. <i>Nature Communications</i> , 2014, 5, 4812.	5.8	531
10	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
11	The genome of the simian and human malaria parasite <i>Plasmodium knowlesi</i> . <i>Nature</i> , 2008, 455, 799-803.	13.7	338
12	Rapid determination of anti-tuberculosis drug resistance from whole-genome sequences. <i>Genome Medicine</i> , 2015, 7, 51.	3.6	323
13	Two Nonrecombining Sympatric Forms of the Human Malaria Parasite <i>Plasmodium ovale</i> Occur Globally. <i>Journal of Infectious Diseases</i> , 2010, 201, 1544-1550.	1.9	310
14	Genome Sequence of <i>Theileria parva</i> , a Bovine Pathogen That Transforms Lymphocytes. <i>Science</i> , 2005, 309, 134-137.	6.0	309
15	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
16	Genomic-scale prioritization of drug targets: the TDR Targets database. <i>Nature Reviews Drug Discovery</i> , 2008, 7, 900-907.	21.5	282
17	Platelet-mediated clumping of <i>Plasmodium falciparum</i> -infected erythrocytes is a common adhesive phenotype and is associated with severe malaria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 1805-1810.	3.3	275
18	Genome-wide analysis of multi- and extensively drug-resistant <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2018, 50, 307-316.	9.4	271

#	ARTICLE	IF	CITATIONS
19	The Systematic Functional Analysis of Plasmodium Protein Kinases Identifies Essential Regulators of Mosquito Transmission. <i>Cell Host and Microbe</i> , 2010, 8, 377-387.	5.1	267
20	A comprehensive evaluation of rodent malaria parasite genomes and gene expression. <i>BMC Biology</i> , 2014, 12, 86.	1.7	251
21	Adaptation of the genetically tractable malaria pathogen <i>Plasmodium knowlesi</i> to continuous culture in human erythrocytes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 531-536.	3.3	239
22	Rapid single-molecule detection of COVID-19 and MERS antigens via nanobody-functionalized organic electrochemical transistors. <i>Nature Biomedical Engineering</i> , 2021, 5, 666-677.	11.6	235
23	iSCAN: An RT-LAMP-coupled CRISPR-Cas12 module for rapid, sensitive detection of SARS-CoV-2. <i>Virus Research</i> , 2020, 288, 198129.	1.1	226
24	Emergence of Indigenous Artemisinin-Resistant <i>Plasmodium falciparum</i> in Africa. <i>New England Journal of Medicine</i> , 2017, 376, 991-993.	13.9	219
25	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
26	Comparative Genomics of the Apicomplexan Parasites <i>Toxoplasma gondii</i> and <i>Neospora caninum</i> : Coccidia Differing in Host Range and Transmission Strategy. <i>PLoS Pathogens</i> , 2012, 8, e1002567.	2.1	206
27	A Comprehensive Subcellular Atlas of the <i>Toxoplasma</i> Proteome via hyperLOPIT Provides Spatial Context for Protein Functions. <i>Cell Host and Microbe</i> , 2020, 28, 752-766.e9.	5.1	201
28	Chromerid genomes reveal the evolutionary path from photosynthetic algae to obligate intracellular parasites. <i>ELife</i> , 2015, 4, e06974.	2.8	198
29	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
30	Genome variation and evolution of the malaria parasite <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2007, 39, 120-125.	9.4	184
31	The Lipopolysaccharide and Î²-1,3-Glucan Binding Protein Gene Is Upregulated in White Spot Virus-Infected Shrimp ( <i>Penaeus stylirostris</i> ). <i>Journal of Virology</i> , 2002, 76, 7140-7149.	1.5	178
32	Genomic analysis of the causative agents of coccidiosis in domestic chickens. <i>Genome Research</i> , 2014, 24, 1676-1685.	2.4	176
33	Sequence of <i>Plasmodium falciparum</i> chromosomes 1, 3 and 9 and 13. <i>Nature</i> , 2002, 419, 527-531.	13.7	156
34	Essential Role of the ESX-5 Secretion System in Outer Membrane Permeability of Pathogenic Mycobacteria. <i>PLoS Genetics</i> , 2015, 11, e1005190.	1.5	154
35	<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
36	A barcode of organellar genome polymorphisms identifies the geographic origin of <i>Plasmodium falciparum</i> strains. <i>Nature Communications</i> , 2014, 5, 4052.	5.8	130

#	ARTICLE	IF	CITATIONS
37	Genome sequencing of chimpanzee malaria parasites reveals possible pathways of adaptation to human hosts. <i>Nature Communications</i> , 2014, 5, 4754.	5.8	124
38	Genome-wide Functional Analysis of Plasmodium Protein Phosphatases Reveals Key Regulators of Parasite Development and Differentiation. <i>Cell Host and Microbe</i> , 2014, 16, 128-140.	5.1	122
39	Mutations in ppe38 block PE_PGRS secretion and increase virulence of <i>Mycobacterium tuberculosis</i> . <i>Nature Microbiology</i> , 2018, 3, 181-188.	5.9	112
40	Outcomes, infectiousness, and transmission dynamics of patients with extensively drug-resistant tuberculosis and home-discharged patients with programmatically incurable tuberculosis: a prospective cohort study. <i>Lancet Respiratory Medicine</i> , 2017, 5, 269-281.	5.2	106
41	<i>Mycobacterium tuberculosis</i> whole genome sequencing and protein structure modelling provides insights into anti-tuberculosis drug resistance. <i>BMC Medicine</i> , 2016, 14, 31.	2.3	102
42	Identification of the genes involved in odorant reception and detection in the palm weevil <i>Rhynchophorus ferrugineus</i> , an important quarantine pest, by antennal transcriptome analysis. <i>BMC Genomics</i> , 2016, 17, 69.	1.2	102
43	A non-sense mutation in Cd36 gene is associated with protection from severe malaria. <i>Lancet</i> , 2001, 357, 1502-1503.	6.3	101
44	Genetic tool development in marine protists: emerging model organisms for experimental cell biology. <i>Nature Methods</i> , 2020, 17, 481-494.	9.0	97
45	Population genomics reveals that an anthropophilic population of <i>Aedes aegypti</i> mosquitoes in West Africa recently gave rise to American and Asian populations of this major disease vector. <i>BMC Biology</i> , 2017, 15, 16.	1.7	96
46	A scalable pipeline for highly effective genetic modification of a malaria parasite. <i>Nature Methods</i> , 2011, 8, 1078-1082.	9.0	93
47	Alteration of host cell phenotype by <i>Theileria annulata</i> and <i>Theileria parva</i> : mining for manipulators in the parasite genomes. <i>International Journal for Parasitology</i> , 2006, 36, 9-21.	1.3	91
48	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
49	Endosymbiosis undone by stepwise elimination of the plastid in a parasitic dinoflagellate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5767-5772.	3.3	88
50	A promoter polymorphism in the gene encoding interleukin-12 p40 (IL12B) is associated with mortality from cerebral malaria and with reduced nitric oxide production. <i>Genes and Immunity</i> , 2002, 3, 414-418.	2.2	87
51	SARS-CoV-2 S1 and N-based serological assays reveal rapid seroconversion and induction of specific antibody response in COVID-19 patients. <i>Scientific Reports</i> , 2020, 10, 16561.	1.6	84
52	Transition of Plasmodium Sporozoites into Liver Stage-Like Forms Is Regulated by the RNA Binding Protein Pumilio. <i>PLoS Pathogens</i> , 2011, 7, e1002046.	2.1	82
53	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
54	Genome-wide RIP-Chip analysis of translational repressor-bound mRNAs in the Plasmodium gametocyte. <i>Genome Biology</i> , 2014, 15, 493.	3.8	80

#	ARTICLE	IF	CITATIONS
55	Host-directed editing of the SARS-CoV-2 genome. <i>Biochemical and Biophysical Research Communications</i> , 2021, 538, 35-39.	1.0	80
56	Functional Characterization of the <i>Plasmodium falciparum</i> and <i>P. berghei</i> Homologues of Macrophage Migration Inhibitory Factor. <i>Infection and Immunity</i> , 2007, 75, 1116-1128.	1.0	79
57	PolyTB: A genomic variation map for <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2014, 94, 346-354.	0.8	79
58	Divergent Mitochondrial Respiratory Chains in Phototrophic Relatives of Apicomplexan Parasites. <i>Molecular Biology and Evolution</i> , 2015, 32, 1115-1131.	3.5	79
59	Genomic expression catalogue of a global collection of BCG vaccine strains show evidence for highly diverged metabolic and cell-wall adaptations. <i>Scientific Reports</i> , 2015, 5, 15443.	1.6	78
60	Identification of a Novel Conjugative Plasmid in <i>Mycobacteria</i> That Requires Both Type IV and Type VII Secretion. <i>MBio</i> , 2014, 5, e01744-14.	1.8	76
61	Population genomic structure and adaptation in the zoonotic malaria parasite <i>Plasmodium knowlesi</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13027-13032.	3.3	75
62	Experimental evolution, genetic analysis and genome re-sequencing reveal the mutation conferring artemisinin resistance in an isogenic lineage of malaria parasites. <i>BMC Genomics</i> , 2010, 11, 499.	1.2	74
63	Genome-Wide Transposon Mutagenesis Indicates that <i>Mycobacterium marinum</i> Customizes Its Virulence Mechanisms for Survival and Replication in Different Hosts. <i>Infection and Immunity</i> , 2015, 83, 1778-1788.	1.0	72
64	The normal cellular prion protein is strongly expressed by myeloid dendritic cells. <i>Blood</i> , 2001, 98, 3733-3738.	0.6	70
65	<i>Plasmodium</i> P-Type Cyclin CYC3 Modulates Endomitotic Growth during Oocyst Development in Mosquitoes. <i>PLoS Pathogens</i> , 2015, 11, e1005273.	2.1	70
66	Proteomes and transcriptomes of the Apicomplexa – Where’s the message?. <i>International Journal for Parasitology</i> , 2009, 39, 135-143.	1.3	68
67	Normocyte-binding protein required for human erythrocyte invasion by the zoonotic malaria parasite <i>Plasmodium knowlesi</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 7231-7236.	3.3	67
68	Differential <i>var</i> gene expression in the organs of patients dying of <i>falciparum</i> malaria. <i>Molecular Microbiology</i> , 2007, 65, 959-967.	1.2	64
69	Re-evaluating the Green versus Red Signal in Eukaryotes with Secondary Plastid of Red Algal Origin. <i>Genome Biology and Evolution</i> , 2012, 4, 626-635.	1.1	64
70	Comparative Genome Analysis of Three Eukaryotic Parasites with Differing Abilities To Transform Leukocytes Reveals Key Mediators of <i>Theileria</i> -Induced Leukocyte Transformation. <i>MBio</i> , 2012, 3, e00204-12.	1.8	64
71	Recombination in <i>pe/ppe</i> genes contributes to genetic variation in <i>Mycobacterium tuberculosis</i> lineages. <i>BMC Genomics</i> , 2016, 17, 151.	1.2	62
72	Draft genome of the most devastating insect pest of coffee worldwide: the coffee berry borer, <i>Hypothenemus hampei</i> . <i>Scientific Reports</i> , 2015, 5, 12525.	1.6	60

#	ARTICLE	IF	CITATIONS
73	Split Photosystem Protein, Linear-Mapping Topology, and Growth of Structural Complexity in the Plastid Genome of <i>Chromera velia</i> . <i>Molecular Biology and Evolution</i> , 2013, 30, 2447-2462.	3.5	59
74	Genome-scale comparison of expanded gene families in <i>Plasmodium ovale wallikeri</i> and <i>Plasmodium ovale curtisi</i> with <i>Plasmodium malariae</i> and with other <i>Plasmodium</i> species. <i>International Journal for Parasitology</i> , 2016, 46, 685-696.	1.3	59
75	Whole Genome Sequencing Based Characterization of Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> Isolates from Pakistan. <i>PLoS ONE</i> , 2015, 10, e0117771.	1.1	59
76	Autoagglutination of malaria-infected red blood cells and malaria severity. <i>Lancet</i> , The, 2000, 355, 1427-1428.	6.3	57
77	Diversity of extracellular proteins during the transition from the <i>~proto-apicomplexan~</i> alveolates to the apicomplexan obligate parasites. <i>Parasitology</i> , 2016, 143, 1-17.	0.7	56
78	Insight into the genome of <i>Aspergillus fumigatus</i> : analysis of a 922kb region encompassing the nitrate assimilation gene cluster. <i>Fungal Genetics and Biology</i> , 2004, 41, 443-453.	0.9	55
79	Unraveling <i>Mycobacterium tuberculosis</i> genomic diversity and evolution in Lisbon, Portugal, a highly drug resistant setting. <i>BMC Genomics</i> , 2014, 15, 991.	1.2	52
80	Whole genome sequence analysis of <i>Mycobacterium suricattae</i> . <i>Tuberculosis</i> , 2015, 95, 682-688.	0.8	52
81	Recruitment of EB1, a Master Regulator of Microtubule Dynamics, to the Surface of the <i>Theileria annulata</i> Schizont. <i>PLoS Pathogens</i> , 2013, 9, e1003346.	2.1	51
82	READSCAN: a fast and scalable pathogen discovery program with accurate genome relative abundance estimation. <i>Bioinformatics</i> , 2013, 29, 391-392.	1.8	51
83	Candidate Essential Genes in <i>Burkholderia cenocepacia</i> J2315 Identified by Genome-Wide TraDIS. <i>Frontiers in Microbiology</i> , 2016, 7, 1288.	1.5	51
84	Recombinations in Staphylococcal Cassette Chromosome mec Elements Compromise the Molecular Detection of Methicillin Resistance in <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , 2014, 9, e101419.	1.1	50
85	Timing of host feeding drives rhythms in parasite replication. <i>PLoS Pathogens</i> , 2018, 14, e1006900.	2.1	48
86	The rhoptry proteome of <i>Eimeria tenella</i> sporozoites. <i>International Journal for Parasitology</i> , 2013, 43, 181-188.	1.3	46
87	Highly diverged novel subunit composition of apicomplexan F-type ATP synthase identified from <i>Toxoplasma gondii</i> . <i>PLoS Biology</i> , 2018, 16, e2006128.	2.6	45
88	Assembly of the Genome of the Disease Vector <i>Aedes aegypti</i> onto a Genetic Linkage Map Allows Mapping of Genes Affecting Disease Transmission. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2652.	1.3	44
89	<i>Plasmodium</i> kinesin-8X associates with mitotic spindles and is essential for oocyst development during parasite proliferation and transmission. <i>PLoS Pathogens</i> , 2019, 15, e1008048.	2.1	43
90	A genetic barcode of SARS-CoV-2 for monitoring global distribution of different clades during the COVID-19 pandemic. <i>International Journal of Infectious Diseases</i> , 2020, 100, 216-223.	1.5	43

#	ARTICLE	IF	CITATIONS
91	Comparative genomics of the Rab protein family in Apicomplexan parasites. <i>Microbes and Infection</i> , 2008, 10, 462-470.	1.0	42
92	Early Humoral Response Correlates with Disease Severity and Outcomes in COVID-19 Patients. <i>Viruses</i> , 2020, 12, 1390.	1.5	42
93	Genome-wide mutagenesis and multi-drug resistance in American trypanosomes induced by the front-line drug benznidazole. <i>Scientific Reports</i> , 2017, 7, 14407.	1.6	41
94	Malaria parasites regulate intra-erythrocytic development duration via serpentine receptor 10 to coordinate with host rhythms. <i>Nature Communications</i> , 2020, 11, 2763.	5.8	41
95	Expression Analysis of the <i>Theileria parva</i> Subtelomere-Encoded Variable Secreted Protein Gene Family. <i>PLoS ONE</i> , 2009, 4, e4839.	1.1	41
96	A divergent cyclin/cyclin-dependent kinase complex controls the atypical replication of a malaria parasite during gametogony and transmission. <i>ELife</i> , 2020, 9, .	2.8	41
97	Functional Pangenome Analysis Shows Key Features of E Protein Are Preserved in SARS and SARS-CoV-2. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 405.	1.8	40
98	SARS-CoV-2 genomes from Saudi Arabia implicate nucleocapsid mutations in host response and increased viral load. <i>Nature Communications</i> , 2022, 13, 601.	5.8	40
99	Spontaneous duplication of a 661â€ƒbp element within a two-component sensor regulator gene causes phenotypic switching in colonies of <i>Pseudomonas tolaasii</i> , cause of brown blotch disease of mushrooms. <i>Molecular Microbiology</i> , 1997, 25, 211-218.	1.2	38
100	Genes involved in sex pheromone biosynthesis of <i>Ephestia cautella</i> , an important food storage pest, are determined by transcriptome sequencing. <i>BMC Genomics</i> , 2015, 16, 532.	1.2	38
101	<i>Plasmodium falciparum</i> Antigenic Variation: Relationships between In Vivo Selection, Acquired Antibody Response, and Disease Severity. <i>Journal of Infectious Diseases</i> , 2005, 192, 1119-1126.	1.9	37
102	Exome and Transcriptome Sequencing of <i>Aedes aegypti</i> Identifies a Locus That Confers Resistance to <i>Brugia malayi</i> and Alters the Immune Response. <i>PLoS Pathogens</i> , 2015, 11, e1004765.	2.1	37
103	Progenitor strain introduction of <i>Mycobacterium bovis</i> at the wildlife-livestock interface can lead to clonal expansion of the disease in a single ecosystem. <i>Infection, Genetics and Evolution</i> , 2017, 51, 235-238.	1.0	35
104	Enteric Infections Circulating during Hajj Seasons, 2011â€ƒ2013. <i>Emerging Infectious Diseases</i> , 2017, 23, .	2.0	33
105	A selenocysteine tRNA and SECIS element in <i>Plasmodium falciparum</i> . <i>Rna</i> , 2005, 11, 119-122.	1.6	32
106	Analysis of the Role of <i>recA</i> in Phenotypic Switching of <i>Pseudomonas tolaasii</i> . <i>Journal of Bacteriology</i> , 2000, 182, 6532-6535.	1.0	30
107	Pheromone receptor of the globally invasive quarantine pest of the palm tree, the red palm weevil ( <i>Rhynchophorus ferrugineus</i> ). <i>Molecular Ecology</i> , 2021, 30, 2025-2039.	2.0	30
108	Long- and Short-Term Selective Forces on Malaria Parasite Genomes. <i>PLoS Genetics</i> , 2010, 6, e1001099.	1.5	30

#	ARTICLE	IF	CITATIONS
109	Light harvesting complexes of <i>Chromera velia</i> , photosynthetic relative of apicomplexan parasites. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2013, 1827, 723-729.	0.5	29
110	Microfibrinous silver-coated polymeric scaffolds with tunable mechanical properties. <i>RSC Advances</i> , 2017, 7, 34331-34338.	1.7	29
111	Defining the protein interaction network of human malaria parasite <i>Plasmodium falciparum</i> . <i>Genomics</i> , 2012, 99, 69-75.	1.3	28
112	Comprehensive Evaluation of <i>Toxoplasma gondii</i> VEG and <i>Neospora caninum</i> LIV Genomes with Tachyzoite Stage Transcriptome and Proteome Defines Novel Transcript Features. <i>PLoS ONE</i> , 2015, 10, e0124473.	1.1	28
113	Advances in the genomics of ticks and tick-borne pathogens. <i>Trends in Parasitology</i> , 2007, 23, 391-396.	1.5	27
114	Proteogenomic Investigation of Strain Variation in Clinical <i>Mycobacterium tuberculosis</i> Isolates. <i>Journal of Proteome Research</i> , 2017, 16, 3841-3851.	1.8	27
115	Characterization and gene expression analysis of the <i>cir</i> multi-gene family of <i>plasmodium chabaudi chabaudi</i> (AS). <i>BMC Genomics</i> , 2012, 13, 125.	1.2	26
116	Metabolic pathway redundancy within the apicomplexan-dinoflagellate radiation argues against an ancient chromalveolate plastid. <i>Communicative and Integrative Biology</i> , 2016, 9, e1116653.	0.6	26
117	A multiple genome analysis of <i>Mycobacterium tuberculosis</i> reveals specific novel genes and mutations associated with pyrazinamide resistance. <i>BMC Genomics</i> , 2017, 18, 769.	1.2	26
118	Whole genome sequencing of amplified <i>Plasmodium knowlesi</i> DNA from unprocessed blood reveals genetic exchange events between Malaysian Peninsular and Borneo subpopulations. <i>Scientific Reports</i> , 2019, 9, 9873.	1.6	25
119	Global transcriptome profiling and functional analysis reveal that tissue-specific constitutive overexpression of cytochrome P450s confers tolerance to imidacloprid in palm weevils in date palm fields. <i>BMC Genomics</i> , 2019, 20, 440.	1.2	25
120	New Initiatives for Management of Red Palm Weevil Threats to Historical Arabian Date Palms. <i>Florida Entomologist</i> , 2011, 94, 733-736.	0.2	24
121	PhyTB: Phylogenetic tree visualisation and sample positioning for <i>M. tuberculosis</i> . <i>BMC Bioinformatics</i> , 2015, 16, 155.	1.2	23
122	Rapid identification of genes controlling virulence and immunity in malaria parasites. <i>PLoS Pathogens</i> , 2017, 13, e1006447.	2.1	23
123	The Population Structure of <i>Vibrio cholerae</i> from the Chandigarh Region of Northern India. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2981.	1.3	21
124	The genome of the zoonotic malaria parasite <i>Plasmodium simium</i> reveals adaptations to host switching. <i>BMC Biology</i> , 2021, 19, 219.	1.7	21
125	A reference genome and methylome for the <i>Plasmodium knowlesi</i> A1-H.1 line. <i>International Journal for Parasitology</i> , 2018, 48, 191-196.	1.3	20
126	Genomes beyond compare. <i>Nature Reviews Microbiology</i> , 2004, 2, 616-617.	13.6	19



#	ARTICLE	IF	CITATIONS
127	A Poisson hierarchical modelling approach to detecting copy number variation in sequence coverage data. <i>BMC Genomics</i> , 2013, 14, 128.	1.2	19
128	The draft genome of <i>Mycobacterium aurum</i> , a potential model organism for investigating drugs against <i>Mycobacterium tuberculosis</i> and <i>Mycobacterium leprae</i> . <i>International Journal of Mycobacteriology</i> , 2015, 4, 207-216.	0.3	19
129	A landscape of genomic alterations at the root of a near-untreatable tuberculosis epidemic. <i>BMC Medicine</i> , 2020, 18, 24.	2.3	19
130	Targeted Disruption of <i>py235ebp-1</i> : Invasion of Erythrocytes by <i>Plasmodium yoelii</i> Using an Alternative <i>Py235</i> Erythrocyte Binding Protein. <i>PLoS Pathogens</i> , 2011, 7, e1001288.	2.1	18
131	Proteomic Investigation of <i>Rhizoctonia solani</i> AG 4 Identifies Secretome and Mycelial Proteins with Roles in Plant Cell Wall Degradation and Virulence. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 3101-3110.	2.4	18
132	Translational repression of the <i>cpw-wpc</i> gene family in the malaria parasite <i>Plasmodium</i> . <i>Parasitology International</i> , 2016, 65, 463-471.	0.6	18
133	Analysis of nuclear and organellar genomes of <i>Plasmodium knowlesi</i> in humans reveals ancient population structure and recent recombination among host-specific subpopulations. <i>PLoS Genetics</i> , 2017, 13, e1007008.	1.5	18
134	Integrated transcriptomic and proteomic analysis of pathogenic mycobacteria and their <i>esx-1</i> mutants reveal secretion-dependent regulation of <i>ESX-1</i> substrates and <i>WhiB6</i> as a transcriptional regulator. <i>PLoS ONE</i> , 2019, 14, e0211003.	1.1	18
135	Clonal expansion across the seas as seen through CPLP-TB database: A joint effort in cataloguing <i>Mycobacterium tuberculosis</i> genetic diversity in Portuguese-speaking countries. <i>Infection, Genetics and Evolution</i> , 2019, 72, 44-58.	1.0	18
136	miR-126-5p by direct targeting of JNK-interacting protein-2 (JIP-2) plays a key role in <i>Theileria</i> -infected macrophage virulence. <i>PLoS Pathogens</i> , 2018, 14, e1006942.	2.1	18
137	Short sequence motif dynamics in the SARS-CoV-2 genome suggest a role for cytosine deamination in CpG reduction. <i>Journal of Molecular Cell Biology</i> , 2021, 13, 225-227.	1.5	17
138	Antennal transcriptome sequencing and identification of candidate chemoreceptor proteins from an invasive pest, the American palm weevil, <i>Rhynchophorus palmarum</i> . <i>Scientific Reports</i> , 2021, 11, 8334.	1.6	17
139	Protein phosphatase 1 regulates atypical mitotic and meiotic division in <i>Plasmodium</i> sexual stages. <i>Communications Biology</i> , 2021, 4, 760.	2.0	17
140	Proteomic profiling of the plasma of Gambian children with cerebral malaria. <i>Malaria Journal</i> , 2018, 17, 337.	0.8	16
141	Simultaneous detection and mutation surveillance of SARS-CoV-2 and multiple respiratory viruses by rapid field-deployable sequencing. <i>Med</i> , 2021, 2, 689-700.e4.	2.2	16
142	Accelerating Early Antituberculosis Drug Discovery by Creating Mycobacterial Indicator Strains That Predict Mode of Action. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	15
143	Genetic Determinants Associated With <i>in Vivo</i> Survival of <i>Burkholderia cenocepacia</i> in the <i>Caenorhabditis elegans</i> Model. <i>Frontiers in Microbiology</i> , 2018, 9, 1118.	1.5	15
144	First report of <i>Klebsiella quasipneumoniae</i> harboring <i>blaKPC-2</i> in Saudi Arabia. <i>Antimicrobial Resistance and Infection Control</i> , 2019, 8, 203.	1.5	15

#	ARTICLE	IF	CITATIONS
145	Genomic and Phenotypic Analyses Reveal the Emergence of an Atypical <i>Salmonella enterica</i> Serovar Senftenberg Variant in China. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2014-2022.	1.8	14
146	Understanding the antifouling mechanisms related to copper oxide and zinc oxide nanoparticles in anaerobic membrane bioreactors. <i>Environmental Science: Nano</i> , 2019, 6, 3467-3479.	2.2	14
147	Emergence of multidrug-resistant <i>Mycobacterium tuberculosis</i> of the Beijing lineage in Portugal and Guinea-Bissau: a snapshot of moving clones by whole-genome sequencing. <i>Emerging Microbes and Infections</i> , 2020, 9, 1342-1353.	3.0	14
148	Pangenome Analysis of the Soilborne Fungal Phytopathogen <i>Rhizoctonia solani</i> and Development of a Comprehensive Web Resource: RsolaniDB. <i>Frontiers in Microbiology</i> , 2022, 13, 839524.	1.5	14
149	Multidrug-Resistant <i>Mycobacterium tuberculosis</i> of the Latin American Mediterranean Lineage, Wrongly Identified as <i>Mycobacterium pinnipedii</i> (Spoligotype International Type 863 [SIT863]), Causing Active Tuberculosis in South Brazil. <i>Journal of Clinical Microbiology</i> , 2015, 53, 3805-3811.	1.8	13
150	Whole genome sequencing provides additional insights into recurrent tuberculosis classified as endogenous reactivation by IS6110 DNA fingerprinting. <i>Infection, Genetics and Evolution</i> , 2019, 75, 103948.	1.0	13
151	Discovering, Characterizing, and Applying Acyl Homoserine Lactone-Quenching Enzymes to Mitigate Microbe-Associated Problems Under Saline Conditions. <i>Frontiers in Microbiology</i> , 2019, 10, 823.	1.5	13
152	Plasmodium genomics: latest milestone. <i>Nature Reviews Microbiology</i> , 2009, 7, 180-181.	13.6	12
153	Complete Genome Sequence of <i>Mycobacterium phlei</i> Type Strain RIVM601174. <i>Journal of Bacteriology</i> , 2012, 194, 3284-3285.	1.0	10
154	<i>Theileria</i> parasites subvert E2F signaling to stimulate leukocyte proliferation. <i>Scientific Reports</i> , 2020, 10, 3982.	1.6	10
155	Comparative Genomic and Transcriptomic Analyses of <i>Mycobacterium kansasii</i> Subtypes Provide New Insights Into Their Pathogenicity and Taxonomy. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 122.	1.8	10
156	A Robust, Safe, and Scalable Magnetic Nanoparticle Workflow for RNA Extraction of Pathogens from Clinical and Wastewater Samples. <i>Global Challenges</i> , 2021, 5, 2000068.	1.8	10
157	<i>Plasmodium vinckei</i> genomes provide insights into the pan-genome and evolution of rodent malaria parasites. <i>BMC Biology</i> , 2021, 19, 69.	1.7	10
158	SnoopCGH: software for visualizing comparative genomic hybridization data. <i>Bioinformatics</i> , 2009, 25, 2732-2733.	1.8	9
159	Novel tumour suppressor roles for <i>GZMA</i> and <i>RASGRP1</i> in <i>Theileria annulata</i> -transformed macrophages and human B lymphoma cells. <i>Cellular Microbiology</i> , 2020, 22, e13255.	1.1	9
160	Meningococcal carriage among Hajj pilgrims, risk factors for carriage and records of vaccination: a study of pilgrims to Mecca. <i>Tropical Medicine and International Health</i> , 2021, 26, 453-461.	1.0	9
161	Turkish and Japanese <i>Mycobacterium tuberculosis</i> sublineages share a remote common ancestor. <i>Infection, Genetics and Evolution</i> , 2016, 45, 461-473.	1.0	8
162	A fast and cost-effective microsampling protocol incorporating reduced animal usage for time-series transcriptomics in rodent malaria parasites. <i>Malaria Journal</i> , 2019, 18, 26.	0.8	8

#	ARTICLE	IF	CITATIONS
163	Complete Genome Sequence of Mycobacterium vaccae Type Strain ATCC 25954. Journal of Bacteriology, 2012, 194, 6339-6340.	1.0	7
164	Complete Genome Sequence of Mycobacterium fortuitum subsp. fortuitum Type Strain DSM46621. Journal of Bacteriology, 2012, 194, 6337-6338.	1.0	7
165	<i>Theileria</i> hijacks JNK2 into a complex with the macroschizont GPI (GlycosylPhosphatidylinositol)-anchored surface protein p104. Cellular Microbiology, 2019, 21, e12973.	1.1	7
166	Dynamics and within-host interaction of <i>Theileria lestoquardi</i> and <i>T. ovis</i> among naive sheep in Oman. Scientific Reports, 2020, 10, 19802.	1.6	7
167	Performance of Commercially Available Rapid Serological Assays for the Detection of SARS-CoV-2 Antibodies. Pathogens, 2020, 9, 1067.	1.2	7
168	Genomic adaptation: a fungal perspective. Nature Reviews Microbiology, 2008, 6, 572-573.	13.6	6
169	Draft Genome Sequences of <i>Pseudomonas fluorescens</i> BS2 and <i>Pseudomonas noertemannii</i> BS8, Soil Bacteria That Cooperate To Degrade the Poly- $\gamma$ -D-Glutamic Acid Anthrax Capsule. Genome Announcements, 2013, 1, .	0.8	6
170	Genetics and malaria – more questions than answers. Trends in Parasitology, 2001, 17, 55-56.	1.5	5
171	Comparative Apicomplexan genomics. Nature Reviews Microbiology, 2005, 3, 454-455.	13.6	5
172	Specialist fungi, versatile genomes. Nature Reviews Microbiology, 2007, 5, 332-333.	13.6	5
173	A proportion of mutations fixed in the genomes of in vitro selected isogenic drug-resistant <i>Mycobacterium tuberculosis</i> mutants can be detected as minority variants in the parent culture. FEMS Microbiology Letters, 2015, 362, 1-7.	0.7	5
174	Influx of diverse, drug resistant and transmissible <i>Plasmodium falciparum</i> into a malaria-free setting in Qatar. BMC Infectious Diseases, 2020, 20, 413.	1.3	5
175	Quick and Easy Assembly of a One-Step qRT-PCR Kit for COVID-19 Diagnostics Using In-House Enzymes. ACS Omega, 2021, 6, 7374-7386.	1.6	5
176	Proteomic profiling of the brain of mice with experimental cerebral malaria. Journal of Proteomics, 2018, 180, 61-69.	1.2	5
177	Global mapping of protein subcellular location in apicomplexans: the parasite as we've never seen it before. Access Microbiology, 2019, 1, .	0.2	5
178	Variants in Bedaquiline-Candidate-Resistance Genes: Prevalence in Bedaquiline-Naive Patients, Effect on MIC, and Association with <i>Mycobacterium tuberculosis</i> Lineage. Antimicrobial Agents and Chemotherapy, 2022, 66, .	1.4	5
179	A feast of protozoan genomes. Nature Reviews Microbiology, 2005, 3, 670-671.	13.6	4
180	Unity in diversity: lessons from <i>Candida</i> . Nature Reviews Microbiology, 2009, 7, 763-763.	13.6	4

#	ARTICLE	IF	CITATIONS
181	Genome Sequences of the Oxytetracycline Production Strain <i>Streptomyces rimosus</i> R6-500 and Two Mutants with Chromosomal Rearrangements. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
182	Development of the Myzozoan Aquatic Parasite <i>Perkinsus marinus</i> as A Versatile Experimental Genetic Model Organism. <i>Protist</i> , 2021, 172, 125830.	0.6	4
183	Hot and sexy moulds!. <i>Nature Reviews Microbiology</i> , 2006, 4, 244-245.	13.6	3
184	Complete Genome Sequence of <i>Mycobacterium xenopi</i> Type Strain RIVM700367. <i>Journal of Bacteriology</i> , 2012, 194, 3282-3283.	1.0	3
185	SVAMP: sequence variation analysis, maps and phylogeny. <i>Bioinformatics</i> , 2014, 30, 2227-2229.	1.8	3
186	Identification of gene fusion events in <i>Mycobacterium tuberculosis</i> that encode chimeric proteins. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa033.	1.5	3
187	Metagenomics of Imported Multidrug-Resistant <i>Mycobacterium leprae</i> , Saudi Arabia, 2017. <i>Emerging Infectious Diseases</i> , 2020, 26, 615-617.	2.0	3
188	Insights into the ancestry evolution of the <i>Mycobacterium tuberculosis</i> complex from analysis of <i>Mycobacterium riyadhense</i> . <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab070.	1.5	3
189	Whole-genome sequencing as a tool for studying the microevolution of drug-resistant serial <i>Mycobacterium tuberculosis</i> isolates. <i>Tuberculosis</i> , 2021, 131, 102137.	0.8	3
190	Metagenomics-driven rapid diagnosis of an imported fatal case of rare amoebic meningoencephalitis. <i>Journal of Travel Medicine</i> , 2022, 29, .	1.4	3
191	Genome Sequence of a Multidrug-Resistant Strain of <i>Stenotrophomonas maltophilia</i> with Carbapenem Resistance, Isolated from King Abdullah Medical City, Makkah, Saudi Arabia. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
192	MRE11 Is Crucial for Malaria Parasite Transmission and Its Absence Affects Expression of Interconnected Networks of Key Genes Essential for Life. <i>Cells</i> , 2020, 9, 2590.	1.8	2
193	Global research alliance in infectious disease: a collaborative effort to combat infectious diseases through dissemination of portable sequencing. <i>BMC Research Notes</i> , 2022, 15, 44.	0.6	2
194	Eukaryotes: not beyond compare. <i>Nature Reviews Microbiology</i> , 2004, 2, 856-857.	13.6	1
195	Strength in diversity. <i>Nature Reviews Microbiology</i> , 2004, 2, 358-359.	13.6	1
196	Sequence data swell for nematodes. <i>Nature Reviews Microbiology</i> , 2008, 6, 800-801.	13.6	1
197	Whole genome sequencing-based characterization of extensively drug resistant (XDR) strains of <i>Mycobacterium tuberculosis</i> from Pakistan. <i>International Journal of Mycobacteriology</i> , 2015, 4, 11-12.	0.3	1
198	The Genetics of Resistance to Malaria. , 2004, , 479-500.		1

#	ARTICLE	IF	CITATIONS
199	Fungi behaving badly. <i>Nature Reviews Microbiology</i> , 2005, 3, 832-833.	13.6	0
200	Variety is the spice of eukaryotic life. <i>Nature Reviews Microbiology</i> , 2007, 5, 660-661.	13.6	0
201	Plant killers on the spot. <i>Nature Reviews Microbiology</i> , 2010, 8, 615-615.	13.6	0
202	Construction of a large-scale <i>Burkholderia cenocepacia</i> J2315 transposon mutant library. , 2014, , .		0
203	Genomic diversity of drug-resistant <i>Mycobacterium tuberculosis</i> isolates in Lisbon Portugal: Towards tuberculosis genomic epidemiology. <i>International Journal of Mycobacteriology</i> , 2015, 4, 27-28.	0.3	0
204	Crohn's Disease Patient Infected With Multiple Co-occurring Nontuberculous Mycobacteria. <i>Inflammatory Bowel Diseases</i> , 2020, 26, e65-e67.	0.9	0
205	Cover Image: Novel tumour suppressor roles for GZMA and RASGRP1 in <i>Theileria annulata</i> -transformed macrophages and human B lymphoma cells ( <i>Cellular Microbiology</i> 12/2020). <i>Cellular Microbiology</i> , 2020, 22, e13285.	1.1	0