

Arnab Pain

List of Publications by Year in descending order

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Version: 2024-02-01

205
papers

23,984
citations

17440

63
h-index

8630

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.	27.8	3,881
2	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	27.8	1,838
3	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , 2005, 438, 1151-1156.	27.8	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.	27.8	1,250
5	The genome of the social amoeba <i>Dictyostelium discoideum</i> . <i>Nature</i> , 2005, 435, 43-57.	27.8	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.	12.6	743
7	Analysis of the <i>Plasmodium falciparum</i> proteome by high-accuracy mass spectrometry. <i>Nature</i> , 2002, 419, 537-542.	27.8	596
8	<i>Plasmodium falciparum</i> -infected erythrocytes modulate the maturation of dendritic cells. <i>Nature</i> , 1999, 400, 73-77.	27.8	553
9	A robust SNP barcode for typing <i>Mycobacterium tuberculosis</i> complex strains. <i>Nature Communications</i> , 2014, 5, 4812.	12.8	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.	2.5	374
11	The genome of the simian and human malaria parasite <i>Plasmodium knowlesi</i> . <i>Nature</i> , 2008, 455, 799-803.	27.8	338
12	Rapid determination of anti-tuberculosis drug resistance from whole-genome sequences. <i>Genome Medicine</i> , 2015, 7, 51.	8.2	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.	4.0	310
14	Genome Sequence of <i>Theileria parva</i> , a Bovine Pathogen That Transforms Lymphocytes. <i>Science</i> , 2005, 309, 134-137.	12.6	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.	12.6	285
16	Genomic-scale prioritization of drug targets: the TDR Targets database. <i>Nature Reviews Drug Discovery</i> , 2008, 7, 900-907.	46.4	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.	7.1	275
18	Genome-wide analysis of multi- and extensively drug-resistant <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2018, 50, 307-316.	21.4	271

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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.	11.0	267
20	A comprehensive evaluation of rodent malaria parasite genomes and gene expression. <i>BMC Biology</i> , 2014, 12, 86.	3.8	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.	7.1	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.	22.5	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.	2.2	226
24	Emergence of Indigenous Artemisinin-Resistant <i>Plasmodium falciparum</i> in Africa. <i>New England Journal of Medicine</i> , 2017, 376, 991-993.	27.0	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.	9.6	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.	4.7	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.	11.0	201
28	Chromerid genomes reveal the evolutionary path from photosynthetic algae to obligate intracellular parasites. <i>ELife</i> , 2015, 4, e06974.	6.0	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.	5.5	195
30	Genome variation and evolution of the malaria parasite <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2007, 39, 120-125.	21.4	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.	3.4	178
32	Genomic analysis of the causative agents of coccidiosis in domestic chickens. <i>Genome Research</i> , 2014, 24, 1676-1685.	5.5	176
33	Sequence of <i>Plasmodium falciparum</i> chromosomes 1, 3 and 13. <i>Nature</i> , 2002, 419, 527-531.	27.8	156
34	Essential Role of the ESX-5 Secretion System in Outer Membrane Permeability of Pathogenic Mycobacteria. <i>PLoS Genetics</i> , 2015, 11, e1005190.	3.5	154
35	<i>Plasmodium falciparum</i> var. 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.	7.1	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.	12.8	130

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37	Genome sequencing of chimpanzee malaria parasites reveals possible pathways of adaptation to human hosts. <i>Nature Communications</i> , 2014, 5, 4754.	12.8	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.	11.0	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.	13.3	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.	10.7	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.	5.5	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.	2.8	102
43	A non-sense mutation in Cd36 gene is associated with protection from severe malaria. <i>Lancet</i> , 2001, 357, 1502-1503.	13.7	101
44	Genetic tool development in marine protists: emerging model organisms for experimental cell biology. <i>Nature Methods</i> , 2020, 17, 481-494.	19.0	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.	3.8	96
46	A scalable pipeline for highly effective genetic modification of a malaria parasite. <i>Nature Methods</i> , 2011, 8, 1078-1082.	19.0	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.	3.1	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.	14.5	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.	7.1	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.	4.1	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.	3.3	84
52	Transition of <i>Plasmodium</i> Sporozoites into Liver Stage-Like Forms Is Regulated by the RNA Binding Protein Pumilio. <i>PLoS Pathogens</i> , 2011, 7, e1002046.	4.7	82
53	Genome-wide discovery and verification of novel structured RNAs in <i>Plasmodium falciparum</i> . <i>Genome Research</i> , 2008, 18, 281-292.	5.5	81
54	Genome-wide RIP-Chip analysis of translational repressor-bound mRNAs in the <i>Plasmodium</i> gametocyte. <i>Genome Biology</i> , 2014, 15, 493.	8.8	80

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55	Host-directed editing of the SARS-CoV-2 genome. <i>Biochemical and Biophysical Research Communications</i> , 2021, 538, 35-39.	2.1	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.	2.2	79
57	PolyTB: A genomic variation map for <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2014, 94, 346-354.	1.9	79
58	Divergent Mitochondrial Respiratory Chains in Phototrophic Relatives of Apicomplexan Parasites. <i>Molecular Biology and Evolution</i> , 2015, 32, 1115-1131.	8.9	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.	3.3	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.	4.1	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.	7.1	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.	2.8	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.	2.2	72
64	The normal cellular prion protein is strongly expressed by myeloid dendritic cells. <i>Blood</i> , 2001, 98, 3733-3738.	1.4	70
65	<i>Plasmodium</i> P-Type Cyclin CYC3 Modulates Endomitotic Growth during Oocyst Development in Mosquitoes. <i>PLoS Pathogens</i> , 2015, 11, e1005273.	4.7	70
66	Proteomes and transcriptomes of the Apicomplexa – Where’s the message?. <i>International Journal for Parasitology</i> , 2009, 39, 135-143.	3.1	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.	7.1	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.	2.5	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.	2.5	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.	4.1	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.	2.8	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.	3.3	60

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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.	8.9	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.	3.1	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.	2.5	59
76	Autoagglutination of malaria-infected red blood cells and malaria severity. <i>Lancet</i> , The, 2000, 355, 1427-1428.	13.7	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.	1.5	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.	2.1	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.	2.8	52
80	Whole genome sequence analysis of <i>Mycobacterium suricattae</i> . <i>Tuberculosis</i> , 2015, 95, 682-688.	1.9	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.	4.7	51
82	READSCAN: a fast and scalable pathogen discovery program with accurate genome relative abundance estimation. <i>Bioinformatics</i> , 2013, 29, 391-392.	4.1	51
83	Candidate Essential Genes in <i>Burkholderia cenocepacia</i> J2315 Identified by Genome-Wide TraDIS. <i>Frontiers in Microbiology</i> , 2016, 7, 1288.	3.5	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.	2.5	50
85	Timing of host feeding drives rhythms in parasite replication. <i>PLoS Pathogens</i> , 2018, 14, e1006900.	4.7	48
86	The rhoptry proteome of <i>Eimeria tenella</i> sporozoites. <i>International Journal for Parasitology</i> , 2013, 43, 181-188.	3.1	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.	5.6	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.	3.0	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.	4.7	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.	3.3	43

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91	Comparative genomics of the Rab protein family in Apicomplexan parasites. <i>Microbes and Infection</i> , 2008, 10, 462-470.	1.9	42
92	Early Humoral Response Correlates with Disease Severity and Outcomes in COVID-19 Patients. <i>Viruses</i> , 2020, 12, 1390.	3.3	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.	3.3	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.	12.8	41
95	Expression Analysis of the <i>Theileria parva</i> Subtelomere-Encoded Variable Secreted Protein Gene Family. <i>PLoS ONE</i> , 2009, 4, e4839.	2.5	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, .	6.0	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.	3.9	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.	12.8	40
99	Spontaneous duplication of a 661â€bp 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.	2.5	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.	2.8	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.	4.0	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.	4.7	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.	2.3	35
104	Enteric Infections Circulating during Hajj Seasons, 2011â€“2013. <i>Emerging Infectious Diseases</i> , 2017, 23, .	4.3	33
105	A selenocysteine tRNA and SECIS element in <i>Plasmodium falciparum</i> . <i>Rna</i> , 2005, 11, 119-122.	3.5	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.	2.2	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.	3.9	30
108	Long- and Short-Term Selective Forces on Malaria Parasite Genomes. <i>PLoS Genetics</i> , 2010, 6, e1001099.	3.5	30

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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.	1.0	29
110	Microfibrinous silver-coated polymeric scaffolds with tunable mechanical properties. <i>RSC Advances</i> , 2017, 7, 34331-34338.	3.6	29
111	Defining the protein interaction network of human malaria parasite <i>Plasmodium falciparum</i> . <i>Genomics</i> , 2012, 99, 69-75.	2.9	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.	2.5	28
113	Advances in the genomics of ticks and tick-borne pathogens. <i>Trends in Parasitology</i> , 2007, 23, 391-396.	3.3	27
114	Proteogenomic Investigation of Strain Variation in Clinical <i>Mycobacterium tuberculosis</i> Isolates. <i>Journal of Proteome Research</i> , 2017, 16, 3841-3851.	3.7	27
115	Characterization and gene expression analysis of the <i>cir</i> multi-gene family of <i>plasmodium chabaudi</i> <i>chabaudi</i> (AS). <i>BMC Genomics</i> , 2012, 13, 125.	2.8	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.	1.4	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.	2.8	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.	3.3	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.	2.8	25
120	New Initiatives for Management of Red Palm Weevil Threats to Historical Arabian Date Palms. <i>Florida Entomologist</i> , 2011, 94, 733-736.	0.5	24
121	PhyTB: Phylogenetic tree visualisation and sample positioning for <i>M. tuberculosis</i> . <i>BMC Bioinformatics</i> , 2015, 16, 155.	2.6	23
122	Rapid identification of genes controlling virulence and immunity in malaria parasites. <i>PLoS Pathogens</i> , 2017, 13, e1006447.	4.7	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.	3.0	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.	3.8	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.	3.1	20
126	Genomes beyond compare. <i>Nature Reviews Microbiology</i> , 2004, 2, 616-617.	28.6	19

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127	A Poisson hierarchical modelling approach to detecting copy number variation in sequence coverage data. BMC Genomics, 2013, 14, 128.	2.8	19
128	The draft genome of Mycobacterium aurum, a potential model organism for investigating drugs against Mycobacterium tuberculosis and Mycobacterium leprae. International Journal of Mycobacteriology, 2015, 4, 207-216.	0.6	19
129	A landscape of genomic alterations at the root of a near-untreatable tuberculosis epidemic. BMC Medicine, 2020, 18, 24.	5.5	19
130	Targeted Disruption of py235ebp-1: Invasion of Erythrocytes by Plasmodium yoelii Using an Alternative Py235 Erythrocyte Binding Protein. PLoS Pathogens, 2011, 7, e1001288.	4.7	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. Journal of Agricultural and Food Chemistry, 2016, 64, 3101-3110.	5.2	18
132	Translational repression of the cpw-wpc gene family in the malaria parasite Plasmodium. Parasitology International, 2016, 65, 463-471.	1.3	18
133	Analysis of nuclear and organellar genomes of Plasmodium knowlesi in humans reveals ancient population structure and recent recombination among host-specific subpopulations. PLoS Genetics, 2017, 13, e1007008.	3.5	18
134	Integrated transcriptomic and proteomic analysis of pathogenic mycobacteria and their esx-1 mutants reveal secretion-dependent regulation of ESX-1 substrates and WhiB6 as a transcriptional regulator. PLoS ONE, 2019, 14, e0211003.	2.5	18
135	Clonal expansion across the seas as seen through CPLP-TB database: A joint effort in cataloguing Mycobacterium tuberculosis genetic diversity in Portuguese-speaking countries. Infection, Genetics and Evolution, 2019, 72, 44-58.	2.3	18
136	miR-126-5p by direct targeting of JNK-interacting protein-2 (JIP-2) plays a key role in Theileria-infected macrophage virulence. PLoS Pathogens, 2018, 14, e1006942.	4.7	18
137	Short sequence motif dynamics in the SARS-CoV-2 genome suggest a role for cytosine deamination in CpG reduction. Journal of Molecular Cell Biology, 2021, 13, 225-227.	3.3	17
138	Antennal transcriptome sequencing and identification of candidate chemoreceptor proteins from an invasive pest, the American palm weevil, Rhynchophorus palmarum. Scientific Reports, 2021, 11, 8334.	3.3	17
139	Protein phosphatase 1 regulates atypical mitotic and meiotic division in Plasmodium sexual stages. Communications Biology, 2021, 4, 760.	4.4	17
140	Proteomic profiling of the plasma of Gambian children with cerebral malaria. Malaria Journal, 2018, 17, 337.	2.3	16
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