

Arnab Pain

List of Publications by Year in descending order

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Version: 2024-02-01

205
papers

23,984
citations

17405

63
h-index

8599

146
g-index

259
all docs

259
docs citations

259
times ranked

26570
citing authors

#	ARTICLE	IF	CITATIONS
1	Metagenomics-driven rapid diagnosis of an imported fatal case of rare amoebic meningoencephalitis. <i>Journal of Travel Medicine</i> , 2022, 29, .	1.4	3
2	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
3	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
4	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
5	Variants in Bedaquiline-Candidate-Resistance Genes: Prevalence in Bedaquiline-Naive Patients, Effect on MIC, and Association with <i>Mycobacterium tuberculosis</i> Lineage. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, .	1.4	5
6	Host-directed editing of the SARS-CoV-2 genome. <i>Biochemical and Biophysical Research Communications</i> , 2021, 538, 35-39.	1.0	80
7	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
8	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
9	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
10	Quick and Easy Assembly of a One-Step qRT-PCR Kit for COVID-19 Diagnostics Using In-House Enzymes. <i>ACS Omega</i> , 2021, 6, 7374-7386.	1.6	5
11	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
12	<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
13	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
14	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
15	Insights into the ancestry evolution of the <i>Mycobacterium tuberculosis</i> complex from analysis of <i>Mycobacterium riadhense</i> . <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab070.	1.5	3
16	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
17	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
18	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

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19	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
20	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
21	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
22	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
23	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
24	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
25	Crohn's Disease Patient Infected With Multiple Co-occurring Nontuberculous <i>Mycobacteria</i> . <i>Inflammatory Bowel Diseases</i> , 2020, 26, e65-e67.	0.9	0
26	Dynamics and within-host interaction of <i>Theileria lestoquardi</i> and <i>T. ovis</i> among naive sheep in Oman. <i>Scientific Reports</i> , 2020, 10, 19802.	1.6	7
27	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
28	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
29	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
30	Novel tumour suppressor roles for GZMA and RASGRP1 in <i>Theileria annulata</i> -transformed macrophages and human B lymphoma cells. <i>Cellular Microbiology</i> , 2020, 22, e13255.	1.1	9
31	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
32	Performance of Commercially Available Rapid Serological Assays for the Detection of SARS-CoV-2 Antibodies. <i>Pathogens</i> , 2020, 9, 1067.	1.2	7
33	Early Humoral Response Correlates with Disease Severity and Outcomes in COVID-19 Patients. <i>Viruses</i> , 2020, 12, 1390.	1.5	42
34	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
35	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
36	Influx of diverse, drug resistant and transmissible <i>Plasmodium falciparum</i> into a malaria-free setting in Qatar. <i>BMC Infectious Diseases</i> , 2020, 20, 413.	1.3	5

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37	Theileria parasites subvert E2F signaling to stimulate leukocyte proliferation. Scientific Reports, 2020, 10, 3982.	1.6	10
38	Metagenomics of Imported Multidrug-Resistant Mycobacterium leprae, Saudi Arabia, 2017. Emerging Infectious Diseases, 2020, 26, 615-617.	2.0	3
39	A landscape of genomic alterations at the root of a near-untreatable tuberculosis epidemic. BMC Medicine, 2020, 18, 24.	2.3	19
40	Comparative Genomic and Transcriptomic Analyses of Mycobacterium kansasii Subtypes Provide New Insights Into Their Pathogenicity and Taxonomy. Frontiers in Cellular and Infection Microbiology, 2020, 10, 122.	1.8	10
41	Genetic tool development in marine protists: emerging model organisms for experimental cell biology. Nature Methods, 2020, 17, 481-494.	9.0	97
42	A divergent cyclin/cyclin-dependent kinase complex controls the atypical replication of a malaria parasite during gametogony and transmission. ELife, 2020, 9, .	2.8	41
43	Whole genome sequencing of amplified Plasmodium knowlesi DNA from unprocessed blood reveals genetic exchange events between Malaysian Peninsular and Borneo subpopulations. Scientific Reports, 2019, 9, 9873.	1.6	25
44	Whole genome sequencing provides additional insights into recurrent tuberculosis classified as endogenous reactivation by IS6110 DNA fingerprinting. Infection, Genetics and Evolution, 2019, 75, 103948.	1.0	13
45	Plasmodium kinesin-8X associates with mitotic spindles and is essential for oocyst development during parasite proliferation and transmission. PLoS Pathogens, 2019, 15, e1008048.	2.1	43
46	A fast and cost-effective microsampling protocol incorporating reduced animal usage for time-series transcriptomics in rodent malaria parasites. Malaria Journal, 2019, 18, 26.	0.8	8
47	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.	1.1	18
48	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. BMC Genomics, 2019, 20, 440.	1.2	25
49	Discovering, Characterizing, and Applying Acyl Homoserine Lactone-Quenching Enzymes to Mitigate Microbe-Associated Problems Under Saline Conditions. Frontiers in Microbiology, 2019, 10, 823.	1.5	13
50	First report of Klebsiella quasipneumoniae harboring blaKPC-2 in Saudi Arabia. Antimicrobial Resistance and Infection Control, 2019, 8, 203.	1.5	15
51	Understanding the antifouling mechanisms related to copper oxide and zinc oxide nanoparticles in anaerobic membrane bioreactors. Environmental Science: Nano, 2019, 6, 3467-3479.	2.2	14
52	<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
53	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.	1.0	18
54	Global mapping of protein subcellular location in apicomplexans: the parasite as we've never seen it before. Access Microbiology, 2019, 1, .	0.2	5

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55	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
56	Genome-wide analysis of multi- and extensively drug-resistant <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2018, 50, 307-316.	9.4	271
57	Mutations in <i>ppe38</i> block PE_PGRS secretion and increase virulence of <i>Mycobacterium tuberculosis</i> . <i>Nature Microbiology</i> , 2018, 3, 181-188.	5.9	112
58	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
59	Proteomic profiling of the plasma of Gambian children with cerebral malaria. <i>Malaria Journal</i> , 2018, 17, 337.	0.8	16
60	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
61	Genetic Determinants Associated With in Vivo Survival of <i>Burkholderia cenocepacia</i> in the <i>Caenorhabditis elegans</i> Model. <i>Frontiers in Microbiology</i> , 2018, 9, 1118.	1.5	15
62	Proteomic profiling of the brain of mice with experimental cerebral malaria. <i>Journal of Proteomics</i> , 2018, 180, 61-69.	1.2	5
63	Timing of host feeding drives rhythms in parasite replication. <i>PLoS Pathogens</i> , 2018, 14, e1006900.	2.1	48
64	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
65	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
66	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
67	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
68	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
69	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
70	Microfibrillar silver-coated polymeric scaffolds with tunable mechanical properties. <i>RSC Advances</i> , 2017, 7, 34331-34338.	1.7	29
71	Enteric Infections Circulating during Hajj Seasons, 2011–2013. <i>Emerging Infectious Diseases</i> , 2017, 23, .	2.0	33
72	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

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73	Rapid identification of genes controlling virulence and immunity in malaria parasites. PLoS Pathogens, 2017, 13, e1006447.	2.1	23
74	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.	1.5	18
75	Outcomes, infectiousness, and transmission dynamics of patients with extensively drug-resistant tuberculosis and home-discharged patients with programmatically incurable tuberculosis: a prospective cohort study. Lancet Respiratory Medicine, the, 2017, 5, 269-281.	5.2	106
76	Candidate Essential Genes in Burkholderia cenocepacia J2315 Identified by Genome-Wide TraDIS. Frontiers in Microbiology, 2016, 7, 1288.	1.5	51
77	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.	2.4	18
78	Diversity of extracellular proteins during the transition from the proto-apicomplexan alveolates to the apicomplexan obligate parasites. Parasitology, 2016, 143, 1-17.	0.7	56
79	Mycobacterium tuberculosis whole genome sequencing and protein structure modelling provides insights into anti-tuberculosis drug resistance. BMC Medicine, 2016, 14, 31.	2.3	102
80	Recombination in pe/ppe genes contributes to genetic variation in Mycobacterium tuberculosis lineages. BMC Genomics, 2016, 17, 151.	1.2	62
81	Genome-scale comparison of expanded gene families in Plasmodium ovale wallikeri and Plasmodium ovale curtisi with Plasmodium malariae and with other Plasmodium species. International Journal for Parasitology, 2016, 46, 685-696.	1.3	59
82	Turkish and Japanese Mycobacterium tuberculosis sublineages share a remote common ancestor. Infection, Genetics and Evolution, 2016, 45, 461-473.	1.0	8
83	Translational repression of the cpw-wpc gene family in the malaria parasite Plasmodium. Parasitology International, 2016, 65, 463-471.	0.6	18
84	Genomic and Phenotypic Analyses Reveal the Emergence of an Atypical Salmonella enterica Serovar Senftenberg Variant in China. Journal of Clinical Microbiology, 2016, 54, 2014-2022.	1.8	14
85	Identification of the genes involved in odorant reception and detection in the palm weevil Rhynchophorus ferrugineus, an important quarantine pest, by antennal transcriptome analysis. BMC Genomics, 2016, 17, 69.	1.2	102
86	Normocyte-binding protein required for human erythrocyte invasion by the zoonotic malaria parasite <i>Plasmodium knowlesi</i> . Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7231-7236.	3.3	67
87	Metabolic pathway redundancy within the apicomplexan-dinoflagellate radiation argues against an ancient chromalveolate plastid. Communicative and Integrative Biology, 2016, 9, e1116653.	0.6	26
88	Genome Sequence of a Multidrug-Resistant Strain of Stenotrophomonas maltophilia with Carbapenem Resistance, Isolated from King Abdullah Medical City, Makkah, Saudi Arabia. Genome Announcements, 2015, 3, .	0.8	2
89	Genomic expression catalogue of a global collection of BCG vaccine strains show evidence for highly diverged metabolic and cell-wall adaptations. Scientific Reports, 2015, 5, 15443.	1.6	78
90	Draft genome of the most devastating insect pest of coffee worldwide: the coffee berry borer, Hypothenemus hampei. Scientific Reports, 2015, 5, 12525.	1.6	60

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91	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
92	<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
93	Chromerid genomes reveal the evolutionary path from photosynthetic algae to obligate intracellular parasites. <i>ELife</i> , 2015, 4, e06974.	2.8	198
94	PhyTB: Phylogenetic tree visualisation and sample positioning for <i>M. tuberculosis</i> . <i>BMC Bioinformatics</i> , 2015, 16, 155.	1.2	23
95	Rapid determination of anti-tuberculosis drug resistance from whole-genome sequences. <i>Genome Medicine</i> , 2015, 7, 51.	3.6	323
96	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
97	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
98	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
99	Divergent Mitochondrial Respiratory Chains in Phototrophic Relatives of Apicomplexan Parasites. <i>Molecular Biology and Evolution</i> , 2015, 32, 1115-1131.	3.5	79
100	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
101	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. <i>FEMS Microbiology Letters</i> , 2015, 362, 1-7.	0.7	5
102	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
103	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
104	Essential Role of the ESX-5 Secretion System in Outer Membrane Permeability of Pathogenic <i>Mycobacteria</i> . <i>PLoS Genetics</i> , 2015, 11, e1005190.	1.5	154
105	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
106	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
107	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
108	Whole genome sequence analysis of <i>Mycobacterium suricattae</i> . <i>Tuberculosis</i> , 2015, 95, 682-688.	0.8	52

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109	Whole Genome Sequencing Based Characterization of Extensively Drug-Resistant Mycobacterium tuberculosis Isolates from Pakistan. PLoS ONE, 2015, 10, e0117771.	1.1	59
110	Genome-wide RIP-Chip analysis of translational repressor-bound mRNAs in the Plasmodium gametocyte. Genome Biology, 2014, 15, 493.	3.8	80
111	The evolutionary dynamics of variant antigen genes in Babesia reveal a history of genomic innovation underlying host-parasite interaction. Nucleic Acids Research, 2014, 42, 7113-7131.	6.5	90
112	Assembly of the Genome of the Disease Vector Aedes aegypti onto a Genetic Linkage Map Allows Mapping of Genes Affecting Disease Transmission. PLoS Neglected Tropical Diseases, 2014, 8, e2652.	1.3	44
113	SVAMP: sequence variation analysis, maps and phylogeny. Bioinformatics, 2014, 30, 2227-2229.	1.8	3
114	The Population Structure of Vibrio cholerae from the Chandigarh Region of Northern India. PLoS Neglected Tropical Diseases, 2014, 8, e2981.	1.3	21
115	Genome Sequences of the Oxytetracycline Production Strain Streptomyces rimosus R6-500 and Two Mutants with Chromosomal Rearrangements. Genome Announcements, 2014, 2, .	0.8	4
116	Construction of a large-scale Burkholderia cenocepacia J2315 transposon mutant library. , 2014, , .		0
117	A robust SNP barcode for typing Mycobacterium tuberculosis complex strains. Nature Communications, 2014, 5, 4812.	5.8	531
118	Identification of a Novel Conjugative Plasmid in Mycobacteria That Requires Both Type IV and Type VII Secretion. MBio, 2014, 5, e01744-14.	1.8	76
119	Unraveling Mycobacterium tuberculosis genomic diversity and evolution in Lisbon, Portugal, a highly drug resistant setting. BMC Genomics, 2014, 15, 991.	1.2	52
120	A comprehensive evaluation of rodent malaria parasite genomes and gene expression. BMC Biology, 2014, 12, 86.	1.7	251
121	Genome sequencing of chimpanzee malaria parasites reveals possible pathways of adaptation to human hosts. Nature Communications, 2014, 5, 4754.	5.8	124
122	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	13.7	1,838
123	Genome-wide Functional Analysis of Plasmodium Protein Phosphatases Reveals Key Regulators of Parasite Development and Differentiation. Cell Host and Microbe, 2014, 16, 128-140.	5.1	122
124	The genome and life-stage specific transcriptomes of Globodera pallida elucidate key aspects of plant parasitism by a cyst nematode. Genome Biology, 2014, 15, R43.	13.9	212
125	Genomic analysis of the causative agents of coccidiosis in domestic chickens. Genome Research, 2014, 24, 1676-1685.	2.4	176
126	A barcode of organellar genome polymorphisms identifies the geographic origin of Plasmodium falciparum strains. Nature Communications, 2014, 5, 4052.	5.8	130

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127	PolyTB: A genomic variation map for Mycobacterium tuberculosis. Tuberculosis, 2014, 94, 346-354.	0.8	79
128	Recombinations in Staphylococcal Cassette Chromosome mec Elements Compromise the Molecular Detection of Methicillin Resistance in Staphylococcus aureus. PLoS ONE, 2014, 9, e101419.	1.1	50
129	A Poisson hierarchical modelling approach to detecting copy number variation in sequence coverage data. BMC Genomics, 2013, 14, 128.	1.2	19
130	The rhoptry proteome of Eimeria tenella sporozoites. International Journal for Parasitology, 2013, 43, 181-188.	1.3	46
131	Light harvesting complexes of Chromera velia, photosynthetic relative of apicomplexan parasites. Biochimica Et Biophysica Acta - Bioenergetics, 2013, 1827, 723-729.	0.5	29
132	Split Photosystem Protein, Linear-Mapping Topology, and Growth of Structural Complexity in the Plastid Genome of Chromera velia. Molecular Biology and Evolution, 2013, 30, 2447-2462.	3.5	59
133	Draft Genome Sequences of Pseudomonas fluorescens BS2 and Pusillimonas noertemannii BS8, Soil Bacteria That Cooperate To Degrade the Poly- β -d -Glutamic Acid Anthrax Capsule. Genome Announcements, 2013, 1, .	0.8	6
134	Recruitment of EB1, a Master Regulator of Microtubule Dynamics, to the Surface of the Theileria annulata Schizont. PLoS Pathogens, 2013, 9, e1003346.	2.1	51
135	READSCAN: a fast and scalable pathogen discovery program with accurate genome relative abundance estimation. Bioinformatics, 2013, 29, 391-392.	1.8	51
136	Adaptation of the genetically tractable malaria pathogen <i>Plasmodium knowlesi</i> to continuous culture in human erythrocytes. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 531-536.	3.3	239
137	Comparative Genomics of the Apicomplexan Parasites Toxoplasma gondii and Neospora caninum: Coccidia Differing in Host Range and Transmission Strategy. PLoS Pathogens, 2012, 8, e1002567.	2.1	206
138	Complete Genome Sequence of Mycobacterium xenopi Type Strain RIVM700367. Journal of Bacteriology, 2012, 194, 3282-3283.	1.0	3
139	Re-evaluating the Green versus Red Signal in Eukaryotes with Secondary Plastid of Red Algal Origin. Genome Biology and Evolution, 2012, 4, 626-635.	1.1	64
140	Complete Genome Sequence of Mycobacterium vaccae Type Strain ATCC 25954. Journal of Bacteriology, 2012, 194, 6339-6340.	1.0	7
141	Complete Genome Sequence of Mycobacterium fortuitum subsp. fortuitum Type Strain DSM46621. Journal of Bacteriology, 2012, 194, 6337-6338.	1.0	7
142	Comparative Genome Analysis of Three Eukaryotic Parasites with Differing Abilities To Transform Leukocytes Reveals Key Mediators of <i>Theileria</i> -Induced Leukocyte Transformation. MBio, 2012, 3, e00204-12.	1.8	64
143	Defining the protein interaction network of human malaria parasite Plasmodium falciparum. Genomics, 2012, 99, 69-75.	1.3	28
144	Characterization and gene expression analysis of the cir multi-gene family of plasmodium chabaudi chabaudi (AS). BMC Genomics, 2012, 13, 125.	1.2	26

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145	Complete Genome Sequence of Mycobacterium phlei Type Strain RIVM601174. Journal of Bacteriology, 2012, 194, 3284-3285.	1.0	10
146	New Initiatives for Management of Red Palm Weevil Threats to Historical Arabian Date Palms[*]. Florida Entomologist, 2011, 94, 733-736.	0.2	24
147	A scalable pipeline for highly effective genetic modification of a malaria parasite. Nature Methods, 2011, 8, 1078-1082.	9.0	93
148	Targeted Disruption of py235ebp-1: Invasion of Erythrocytes by Plasmodium yoelii Using an Alternative Py235 Erythrocyte Binding Protein. PLoS Pathogens, 2011, 7, e1001288.	2.1	18
149	Transition of Plasmodium Sporozoites into Liver Stage-Like Forms Is Regulated by the RNA Binding Protein Pumilio. PLoS Pathogens, 2011, 7, e1002046.	2.1	82
150	Experimental evolution, genetic analysis and genome re-sequencing reveal the mutation conferring artemisinin resistance in an isogenic lineage of malaria parasites. BMC Genomics, 2010, 11, 499.	1.2	74
151	New insights into the blood-stage transcriptome of <i>Plasmodium falciparum</i> using RNA-seq. Molecular Microbiology, 2010, 76, 12-24.	1.2	374
152	Plant killers on the spot. Nature Reviews Microbiology, 2010, 8, 615-615.	13.6	0
153	Two Nonrecombining Sympatric Forms of the Human Malaria Parasite <i>Plasmodium ovale</i> Occur Globally. Journal of Infectious Diseases, 2010, 201, 1544-1550.	1.9	310
154	The Systematic Functional Analysis of Plasmodium Protein Kinases Identifies Essential Regulators of Mosquito Transmission. Cell Host and Microbe, 2010, 8, 377-387.	5.1	267
155	Long- and Short-Term Selective Forces on Malaria Parasite Genomes. PLoS Genetics, 2010, 6, e1001099.	1.5	30
156	SnoopCGH: software for visualizing comparative genomic hybridization data. Bioinformatics, 2009, 25, 2732-2733.	1.8	9
157	Proteomes and transcriptomes of the Apicomplexa – Where’s the message?. International Journal for Parasitology, 2009, 39, 135-143.	1.3	68
158	Plasmodium genomics: latest milestone. Nature Reviews Microbiology, 2009, 7, 180-181.	13.6	12
159	Unity in diversity: lessons from Candida. Nature Reviews Microbiology, 2009, 7, 763-763.	13.6	4
160	<i>Plasmodium falciparum var</i> gene expression is modified by host immunity. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21801-21806.	3.3	130
161	Comparative genomics of the fungal pathogens <i>Candida dubliniensis</i> and <i>Candida albicans</i>. Genome Research, 2009, 19, 2231-2244.	2.4	195
162	Expression Analysis of the Theileria parva Subtelomere-Encoded Variable Secreted Protein Gene Family. PLoS ONE, 2009, 4, e4839.	1.1	41

#	ARTICLE	IF	CITATIONS
163	Comparative genomics of the Rab protein family in Apicomplexan parasites. <i>Microbes and Infection</i> , 2008, 10, 462-470.	1.0	42
164	The genome of the simian and human malaria parasite <i>Plasmodium knowlesi</i> . <i>Nature</i> , 2008, 455, 799-803.	13.7	338
165	Genomic-scale prioritization of drug targets: the TDR Targets database. <i>Nature Reviews Drug Discovery</i> , 2008, 7, 900-907.	21.5	282
166	Genomic adaptation: a fungal perspective. <i>Nature Reviews Microbiology</i> , 2008, 6, 572-573.	13.6	6
167	Sequence data swell for nematodes. <i>Nature Reviews Microbiology</i> , 2008, 6, 800-801.	13.6	1
168	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
169	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
170	Genome variation and evolution of the malaria parasite <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2007, 39, 120-125.	9.4	184
171	Specialist fungi, versatile genomes. <i>Nature Reviews Microbiology</i> , 2007, 5, 332-333.	13.6	5
172	Variety is the spice of eukaryotic life. <i>Nature Reviews Microbiology</i> , 2007, 5, 660-661.	13.6	0
173	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
174	Advances in the genomics of ticks and tick-borne pathogens. <i>Trends in Parasitology</i> , 2007, 23, 391-396.	1.5	27
175	Hot and sexy moulds!. <i>Nature Reviews Microbiology</i> , 2006, 4, 244-245.	13.6	3
176	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
177	Comparative Apicomplexan genomics. <i>Nature Reviews Microbiology</i> , 2005, 3, 454-455.	13.6	5
178	A feast of protozoan genomes. <i>Nature Reviews Microbiology</i> , 2005, 3, 670-671.	13.6	4
179	Fungi behaving badly. <i>Nature Reviews Microbiology</i> , 2005, 3, 832-833.	13.6	0
180	The genome of the social amoeba <i>Dictyostelium discoideum</i> . <i>Nature</i> , 2005, 435, 43-57.	13.7	1,179

#	ARTICLE	IF	CITATIONS
181	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , 2005, 438, 1151-1156.	13.7	1,272
182	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
183	<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
184	A selenocysteine tRNA and SECIS element in <i>Plasmodium falciparum</i> . <i>Rna</i> , 2005, 11, 119-122.	1.6	32
185	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
186	Genome Sequence of <i>Theileria parva</i> , a Bovine Pathogen That Transforms Lymphocytes. <i>Science</i> , 2005, 309, 134-137.	6.0	309
187	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
188	Eukaryotes: not beyond compare. <i>Nature Reviews Microbiology</i> , 2004, 2, 856-857.	13.6	1
189	Strength in diversity. <i>Nature Reviews Microbiology</i> , 2004, 2, 358-359.	13.6	1
190	Genomes beyond compare. <i>Nature Reviews Microbiology</i> , 2004, 2, 616-617.	13.6	19
191	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
192	The Genetics of Resistance to Malaria. , 2004, , 479-500.		1
193	The Lipopolysaccharide and Î ² -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
194	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
195	Sequence of <i>Plasmodium falciparum</i> chromosomes 1, 3, 9 and 13. <i>Nature</i> , 2002, 419, 527-531.	13.7	156
196	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	13.7	3,881
197	Analysis of the <i>Plasmodium falciparum</i> proteome by high-accuracy mass spectrometry. <i>Nature</i> , 2002, 419, 537-542.	13.7	596
198	A non-sense mutation in Cd36 gene is associated with protection from severe malaria. <i>Lancet</i> , The, 2001, 357, 1502-1503.	6.3	101

#	ARTICLE	IF	CITATIONS
199	The normal cellular prion protein is strongly expressed by myeloid dendritic cells. <i>Blood</i> , 2001, 98, 3733-3738.	0.6	70
200	Genetics and malaria – more questions than answers. <i>Trends in Parasitology</i> , 2001, 17, 55-56.	1.5	5
201	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
202	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
203	Autoagglutination of malaria-infected red blood cells and malaria severity. <i>Lancet</i> , The, 2000, 355, 1427-1428.	6.3	57
204	<i>Plasmodium falciparum</i> -infected erythrocytes modulate the maturation of dendritic cells. <i>Nature</i> , 1999, 400, 73-77.	13.7	553
205	Spontaneous duplication of a 661-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.	1.2	38