

Arnab Pain

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

202
papers

18,564
citations

57
h-index

135
g-index

259
ext. papers

22,107
ext. citations

11.4
avg, IF

5.76
L-index

#	Paper	IF	Citations
202	SARS-CoV-2 genomes from Saudi Arabia implicate nucleocapsid mutations in host response and increased viral load.. <i>Nature Communications</i> , 2022 , 13, 601	17.4	4
201	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	2.3	0
200	Pangenome Analysis of the Soilborne Fungal Phytopathogen and Development of a Comprehensive Web Resource: RsolaniDB.. <i>Frontiers in Microbiology</i> , 2022 , 13, 839524	5.7	1
199	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	2.6	0
198	Short sequence motif dynamics in the SARS-CoV-2 genome suggest a role for cytosine deamination in CpG reduction 2021 ,		2
197	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	3.9	2
196	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	5.7	10
195	<i>Plasmodium vinckei</i> genomes provide insights into the pan-genome and evolution of rodent malaria parasites. <i>BMC Biology</i> , 2021 , 19, 69	7.3	1
194	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 ^{4.9}	4.9	4
193	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	19	78
192	Insights into the ancestry evolution of the complex from analysis of. <i>NAR Genomics and Bioinformatics</i> , 2021 , 3, lqab070	3.7	1
191	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	31.7	7
190	Protein phosphatase 1 regulates atypical mitotic and meiotic division in <i>Plasmodium</i> sexual stages. <i>Communications Biology</i> , 2021 , 4, 760	6.7	4
189	Host-directed editing of the SARS-CoV-2 genome. <i>Biochemical and Biophysical Research Communications</i> , 2021 , 538, 35-39	3.4	34
188	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	2.3	1
187	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	6.3	9
186	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	4.3	6

185	Development of the Myzozoan Aquatic Parasite <i>Perkinsus marinus</i> as A Versatile Experimental Genetic Model Organism. <i>Protist</i> , 2021 , 172, 125830	2.5	0
184	The genome of the zoonotic malaria parasite <i>Plasmodium simium</i> reveals adaptations to host switching. <i>BMC Biology</i> , 2021 , 19, 219	7.3	6
183	Early Humoral Response Correlates with Disease Severity and Outcomes in COVID-19 Patients. <i>Viruses</i> , 2020 , 12,	6.2	21
182	Malaria parasites regulate intra-erythrocytic development duration via serpentine receptor 10 to coordinate with host rhythms. <i>Nature Communications</i> , 2020 , 11, 2763	17.4	23
181	Emergence of multidrug-resistant 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	18.9	8
180	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	4	5
179	<i>Theileria</i> parasites subvert E2F signaling to stimulate leukocyte proliferation. <i>Scientific Reports</i> , 2020 , 10, 3982	4.9	5
178	Metagenomics of Imported Multidrug-Resistant <i>Mycobacterium leprae</i> , Saudi Arabia, 2017. <i>Emerging Infectious Diseases</i> , 2020 , 26, 615-617	10.2	3
177	A landscape of genomic alterations at the root of a near-untreatable tuberculosis epidemic. <i>BMC Medicine</i> , 2020 , 18, 24	11.4	10
176	Comparative Genomic and Transcriptomic Analyses of Subtypes Provide New Insights Into Their Pathogenicity and Taxonomy. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020 , 10, 122	5.9	7
175	Genetic tool development in marine protists: emerging model organisms for experimental cell biology. <i>Nature Methods</i> , 2020 , 17, 481-494	21.6	39
174	A divergent cyclin/cyclin-dependent kinase complex controls the atypical replication of a malaria parasite during gametogony and transmission. <i>ELife</i> , 2020 , 9,	8.9	17
173	Identification of gene fusion events in that encode chimeric proteins. <i>NAR Genomics and Bioinformatics</i> , 2020 , 2, lqaa033	3.7	1
172	iSCAN: An RT-LAMP-coupled CRISPR-Cas12 module for rapid, sensitive detection of SARS-CoV-2. <i>Virus Research</i> , 2020 , 288, 198129	6.4	102
171	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	23.4	61
170	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	4.9	51
169	Crohn's Disease Patient Infected With Multiple Co-occurring Nontuberculous <i>Mycobacteria</i> . <i>Inflammatory Bowel Diseases</i> , 2020 , 26, e65-e67	4.5	
168	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	4.9	2

167	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	5.9	25
166	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	3.9	5
165	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	10.5	33
164	Performance of Commercially Available Rapid Serological Assays for the Detection of SARS-CoV-2 Antibodies. <i>Pathogens</i> , 2020 , 9,	4.5	3
163	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	3.6	5
162	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. <i>PLoS ONE</i> , 2019 , 14, e0211003	3.7	9
161	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	4.5	14
160	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	5.7	9
159	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	4.9	13
158	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	4.5	7
157	<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	7.6	13
156	Molecular pathogenesis of malaria 2019 , 193-206		
155	Global mapping of protein subcellular location in apicomplexans: the parasite as we've never seen it before. <i>Access Microbiology</i> , 2019 , 1,	1	3
154	First report of harboring in Saudi Arabia. <i>Antimicrobial Resistance and Infection Control</i> , 2019 , 8, 203	6.2	7
153	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	7.1	4
152	<i>Theileria</i> hijacks JNK2 into a complex with the macroschizont GPI (GlycosylPhosphatidylinositol)-anchored surface protein p104. <i>Cellular Microbiology</i> , 2019 , 21, e12973	3.9	5
151	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	4.5	14
150	Accelerating Early Antituberculosis Drug Discovery by Creating Mycobacterial Indicator Strains That Predict Mode of Action. <i>Antimicrobial Agents and Chemotherapy</i> , 2018 , 62,	5.9	14

149	Genome-wide analysis of multi- and extensively drug-resistant Mycobacterium tuberculosis. <i>Nature Genetics</i> , 2018 , 50, 307-316	36.3	160
148	Mutations in ppe38 block PE_PGRS secretion and increase virulence of Mycobacterium tuberculosis. <i>Nature Microbiology</i> , 2018 , 3, 181-188	26.6	74
147	A reference genome and methylome for the Plasmodium knowlesi A1-H.1 line. <i>International Journal for Parasitology</i> , 2018 , 48, 191-196	4.3	12
146	Highly diverged novel subunit composition of apicomplexan F-type ATP synthase identified from Toxoplasma gondii. <i>PLoS Biology</i> , 2018 , 16, e2006128	9.7	28
145	Genetic Determinants Associated With Survival of in the Model. <i>Frontiers in Microbiology</i> , 2018 , 9, 1118	5.7	8
144	Timing of host feeding drives rhythms in parasite replication. <i>PLoS Pathogens</i> , 2018 , 14, e1006900	7.6	35
143	miR-126-5p by direct targeting of JNK-interacting protein-2 (JIP-2) plays a key role in Theileria-infected macrophage virulence. <i>PLoS Pathogens</i> , 2018 , 14, e1006942	7.6	9
142	Proteomic profiling of the brain of mice with experimental cerebral malaria. <i>Journal of Proteomics</i> , 2018 , 180, 61-69	3.9	3
141	Proteomic profiling of the plasma of Gambian children with cerebral malaria. <i>Malaria Journal</i> , 2018 , 17, 337	3.6	10
140	Emergence of Indigenous Artemisinin-Resistant Plasmodium falciparum in Africa. <i>New England Journal of Medicine</i> , 2017 , 376, 991-3	59.2	178
139	Population genomics reveals that an anthropophilic population of Aedes aegypti mosquitoes in West Africa recently gave rise to American and Asian populations of this major disease vector. <i>BMC Biology</i> , 2017 , 15, 16	7.3	62
138	Progenitor strain introduction of Mycobacterium bovis 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	4.5	24
137	Genome-wide mutagenesis and multi-drug resistance in American trypanosomes induced by the front-line drug benzimidazole. <i>Scientific Reports</i> , 2017 , 7, 14407	4.9	31
136	Rapid identification of genes controlling virulence and immunity in malaria parasites. <i>PLoS Pathogens</i> , 2017 , 13, e1006447	7.6	14
135	Analysis of nuclear and organellar genomes of Plasmodium knowlesi in humans reveals ancient population structure and recent recombination among host-specific subpopulations. <i>PLoS Genetics</i> , 2017 , 13, e1007008	6	13
134	Proteogenomic Investigation of Strain Variation in Clinical Mycobacterium tuberculosis Isolates. <i>Journal of Proteome Research</i> , 2017 , 16, 3841-3851	5.6	15
133	Microfibrous silver-coated polymeric scaffolds with tunable mechanical properties. <i>RSC Advances</i> , 2017 , 7, 34331-34338	3.7	17
132	Enteric Infections Circulating during Hajj Seasons, 2011-2013. <i>Emerging Infectious Diseases</i> , 2017 , 23,	10.2	23

131	A multiple genome analysis of Mycobacterium tuberculosis reveals specific novel genes and mutations associated with pyrazinamide resistance. <i>BMC Genomics</i> , 2017 , 18, 769	4.5	15
130	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	35.1	80
129	Genome-scale comparison of expanded gene families in Plasmodium ovale wallikeri and Plasmodium ovale curtisi with Plasmodium malariae and with other Plasmodium species. <i>International Journal for Parasitology</i> , 2016 , 46, 685-96	4.3	43
128	Turkish and Japanese Mycobacterium tuberculosis sublineages share a remote common ancestor. <i>Infection, Genetics and Evolution</i> , 2016 , 45, 461-473	4.5	5
127	Translational repression of the cpw-wpc gene family in the malaria parasite Plasmodium. <i>Parasitology International</i> , 2016 , 65, 463-71	2.1	13
126	Genomic and Phenotypic Analyses Reveal the Emergence of an Atypical Salmonella enterica Serovar Senftenberg Variant in China. <i>Journal of Clinical Microbiology</i> , 2016 , 54, 2014-22	9.7	12
125	Identification of the genes involved in odorant reception and detection in the palm weevil Rhynchophorus ferrugineus, an important quarantine pest, by antennal transcriptome analysis. <i>BMC Genomics</i> , 2016 , 17, 69	4.5	55
124	Normocyte-binding protein required for human erythrocyte invasion by the zoonotic malaria parasite Plasmodium knowlesi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 7231-6	11.5	40
123	Metabolic pathway redundancy within the apicomplexan-dinoflagellate radiation argues against an ancient chromalveolate plastid. <i>Communicative and Integrative Biology</i> , 2016 , 9, e1116653	1.7	22
122	Candidate Essential Genes in Burkholderia cenocepacia J2315 Identified by Genome-Wide TraDIS. <i>Frontiers in Microbiology</i> , 2016 , 7, 1288	5.7	32
121	Proteomic Investigation of Rhizoctonia solani 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, 3101-10	5.7	9
120	Diversity of extracellular proteins during the transition from the 'proto-apicomplexan' alveolates to the apicomplexan obligate parasites. <i>Parasitology</i> , 2016 , 143, 1-17	2.7	26
119	Mycobacterium tuberculosis whole genome sequencing and protein structure modelling provides insights into anti-tuberculosis drug resistance. <i>BMC Medicine</i> , 2016 , 14, 31	11.4	77
118	Recombination in pe/ppe genes contributes to genetic variation in Mycobacterium tuberculosis lineages. <i>BMC Genomics</i> , 2016 , 17, 151	4.5	43
117	A proportion of mutations fixed in the genomes of in vitro selected isogenic drug-resistant Mycobacterium tuberculosis mutants can be detected as minority variants in the parent culture. <i>FEMS Microbiology Letters</i> , 2015 , 362, 1-7	2.9	5
116	The draft genome of Mycobacterium aurum, a potential model organism for investigating drugs against Mycobacterium tuberculosis and Mycobacterium leprae. <i>International Journal of Mycobacteriology</i> , 2015 , 4, 207-16	0.9	14
115	Exome and transcriptome sequencing of Aedes aegypti identifies a locus that confers resistance to Brugia malayi and alters the immune response. <i>PLoS Pathogens</i> , 2015 , 11, e1004765	7.6	25
114	Essential Role of the ESX-5 Secretion System in Outer Membrane Permeability of Pathogenic Mycobacteria. <i>PLoS Genetics</i> , 2015 , 11, e1005190	6	105

113	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, 5767-72	11.5	60
112	Multidrug-Resistant Mycobacterium tuberculosis of the Latin American Mediterranean Lineage, Wrongly Identified as Mycobacterium pinnipedii (Spoligotype International Type 863 [SIT863]), Causing Active Tuberculosis in South Brazil. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 3805-11	9.7	11
111	Genes involved in sex pheromone biosynthesis of Ephestia cautella, an important food storage pest, are determined by transcriptome sequencing. <i>BMC Genomics</i> , 2015 , 16, 532	4.5	29
110	Whole genome sequence analysis of Mycobacterium suricattae. <i>Tuberculosis</i> , 2015 , 95, 682-688	2.6	34
109	Genome Sequence of a Multidrug-Resistant Strain of Stenotrophomonas maltophilia with Carbapenem Resistance, Isolated from King Abdullah Medical City, Makkah, Saudi Arabia. <i>Genome Announcements</i> , 2015 , 3,		1
108	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	4.9	57
107	Draft genome of the most devastating insect pest of coffee worldwide: the coffee berry borer, Hypothenemus hampei. <i>Scientific Reports</i> , 2015 , 5, 12525	4.9	44
106	Comprehensive evaluation of Toxoplasma gondii VEG and Neospora caninum LIV genomes with tachyzoite stage transcriptome and proteome defines novel transcript features. <i>PLoS ONE</i> , 2015 , 10, e0124473	3.7	25
105	Plasmodium P-Type Cyclin CYC3 Modulates Endomitotic Growth during Oocyst Development in Mosquitoes. <i>PLoS Pathogens</i> , 2015 , 11, e1005273	7.6	42
104	Chromerid genomes reveal the evolutionary path from photosynthetic algae to obligate intracellular parasites. <i>ELife</i> , 2015 , 4, e06974	8.9	138
103	PhyTB: Phylogenetic tree visualisation and sample positioning for M. tuberculosis. <i>BMC Bioinformatics</i> , 2015 , 16, 155	3.6	16
102	Rapid determination of anti-tuberculosis drug resistance from whole-genome sequences. <i>Genome Medicine</i> , 2015 , 7, 51	14.4	234
101	Population genomic structure and adaptation in the zoonotic malaria parasite Plasmodium knowlesi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 13027-32	11.5	62
100	Divergent mitochondrial respiratory chains in phototrophic relatives of apicomplexan parasites. <i>Molecular Biology and Evolution</i> , 2015 , 32, 1115-31	8.3	62
99	Genome-wide transposon mutagenesis indicates that Mycobacterium marinum customizes its virulence mechanisms for survival and replication in different hosts. <i>Infection and Immunity</i> , 2015 , 83, 1778-88	3.7	44
98	Whole genome sequencing based characterization of extensively drug-resistant Mycobacterium tuberculosis isolates from Pakistan. <i>PLoS ONE</i> , 2015 , 10, e0117771	3.7	41
97	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014 , 507, 462-70	50.4	1301
96	Genome-wide functional analysis of Plasmodium protein phosphatases reveals key regulators of parasite development and differentiation. <i>Cell Host and Microbe</i> , 2014 , 16, 128-40	23.4	71

95	The genome and life-stage specific transcriptomes of <i>Globodera pallida</i> elucidate key aspects of plant parasitism by a cyst nematode. <i>Genome Biology</i> , 2014 , 15, R43	18.3	155
94	Genomic analysis of the causative agents of coccidiosis in domestic chickens. <i>Genome Research</i> , 2014 , 24, 1676-85	9.7	121
93	A barcode of organellar genome polymorphisms identifies the geographic origin of <i>Plasmodium falciparum</i> strains. <i>Nature Communications</i> , 2014 , 5, 4052	17.4	83
92	PolyTB: a genomic variation map for <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2014 , 94, 346-54	2.6	64
91	Genome-wide RIP-Chip analysis of translational repressor-bound mRNAs in the <i>Plasmodium</i> gametocyte. <i>Genome Biology</i> , 2014 , 15, 493	18.3	57
90	The evolutionary dynamics of variant antigen genes in <i>Babesia</i> reveal a history of genomic innovation underlying host-parasite interaction. <i>Nucleic Acids Research</i> , 2014 , 42, 7113-31	20.1	66
89	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	4.8	34
88	SVAMP: sequence variation analysis, maps and phylogeny. <i>Bioinformatics</i> , 2014 , 30, 2227-9	7.2	3
87	The population structure of <i>Vibrio cholerae</i> from the Chandigarh Region of Northern India. <i>PLoS Neglected Tropical Diseases</i> , 2014 , 8, e2981	4.8	20
86	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,		3
85	A robust SNP barcode for typing <i>Mycobacterium tuberculosis</i> complex strains. <i>Nature Communications</i> , 2014 , 5, 4812	17.4	355
84	Identification of a novel conjugative plasmid in mycobacteria that requires both type IV and type VII secretion. <i>MBio</i> , 2014 , 5, e01744-14	7.8	50
83	Unraveling <i>Mycobacterium tuberculosis</i> genomic diversity and evolution in Lisbon, Portugal, a highly drug resistant setting. <i>BMC Genomics</i> , 2014 , 15, 991	4.5	45
82	A comprehensive evaluation of rodent malaria parasite genomes and gene expression. <i>BMC Biology</i> , 2014 , 12, 86	7.3	174
81	Genome sequencing of chimpanzee malaria parasites reveals possible pathways of adaptation to human hosts. <i>Nature Communications</i> , 2014 , 5, 4754	17.4	107
80	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	3.7	42
79	A Poisson hierarchical modelling approach to detecting copy number variation in sequence coverage data. <i>BMC Genomics</i> , 2013 , 14, 128	4.5	16
78	The rhoptry proteome of <i>Eimeria tenella</i> sporozoites. <i>International Journal for Parasitology</i> , 2013 , 43, 181-8	4.3	36

77	Light harvesting complexes of <i>Chromera velia</i> , photosynthetic relative of apicomplexan parasites. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2013 , 1827, 723-9	4.6	28
76	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, 2447-62	8.3	47
75	Draft Genome Sequences of <i>Pseudomonas fluorescens</i> BS2 and <i>Pusillimonas noertemannii</i> BS8, Soil Bacteria That Cooperate To Degrade the Poly- β -Glutamic Acid Anthrax Capsule. <i>Genome Announcements</i> , 2013 , 1,		6
74	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	7.6	29
73	READSCAN: a fast and scalable pathogen discovery program with accurate genome relative abundance estimation. <i>Bioinformatics</i> , 2013 , 29, 391-2	7.2	44
72	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, 531-6	11.5	154
71	Defining the protein interaction network of human malaria parasite <i>Plasmodium falciparum</i> . <i>Genomics</i> , 2012 , 99, 69-75	4.3	22
70	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	4.5	19
69	Complete genome sequence of <i>Mycobacterium phlei</i> type strain RIVM601174. <i>Journal of Bacteriology</i> , 2012 , 194, 3284-5	3.5	10
68	Comparative genomics of the apicomplexan parasites <i>Toxoplasma gondii</i> and <i>Neospora caninum</i> : <i>Coccidia</i> differing in host range and transmission strategy. <i>PLoS Pathogens</i> , 2012 , 8, e1002567	7.6	154
67	Complete genome sequence of <i>Mycobacterium xenopi</i> type strain RIVM700367. <i>Journal of Bacteriology</i> , 2012 , 194, 3282-3	3.5	3
66	Re-evaluating the green versus red signal in eukaryotes with secondary plastid of red algal origin. <i>Genome Biology and Evolution</i> , 2012 , 4, 626-35	3.9	58
65	Complete genome sequence of <i>Mycobacterium vaccae</i> type strain ATCC 25954. <i>Journal of Bacteriology</i> , 2012 , 194, 6339-40	3.5	7
64	Complete genome sequence of <i>Mycobacterium fortuitum</i> subsp. <i>fortuitum</i> type strain DSM46621. <i>Journal of Bacteriology</i> , 2012 , 194, 6337-8	3.5	5
63	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	7.8	48
62	A scalable pipeline for highly effective genetic modification of a malaria parasite. <i>Nature Methods</i> , 2011 , 8, 1078-82	21.6	68
61	New Initiatives for Management of Red Palm Weevil Threats to Historical Arabian Date Palms*. <i>Florida Entomologist</i> , 2011 , 94, 733-736	1	20
60	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	7.6	12

59	Transition of Plasmodium sporozoites into liver stage-like forms is regulated by the RNA binding protein Pumilio. <i>PLoS Pathogens</i> , 2011 , 7, e1002046	7.6	64
58	New insights into the blood-stage transcriptome of Plasmodium falciparum using RNA-Seq. <i>Molecular Microbiology</i> , 2010 , 76, 12-24	4.1	283
57	Two nonrecombining sympatric forms of the human malaria parasite Plasmodium ovale occur globally. <i>Journal of Infectious Diseases</i> , 2010 , 201, 1544-50	7	235
56	The systematic functional analysis of Plasmodium protein kinases identifies essential regulators of mosquito transmission. <i>Cell Host and Microbe</i> , 2010 , 8, 377-87	23.4	195
55	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	4.5	56
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12	<i>Plasmodium</i> Kinesin-8X associates with mitotic spindles and is essential for oocyst development during parasite proliferation and transmission		2
11	Functional pangenome analysis suggests inhibition of the protein E as a readily available therapy for COVID-2019		4
10	The genomic variation landscape of globally-circulating clades of SARS-CoV-2 defines a genetic barcoding scheme		12
9	A subcellular atlas of <i>Toxoplasma</i> reveals the functional context of the proteome		9
8	iSCAN: An RT-LAMP-coupled CRISPR-Cas12 module for rapid, sensitive detection of SARS-CoV-2		2
7	Simultaneous Detection and Mutation Surveillance of SARS-CoV-2 and co-infections of multiple respiratory viruses by Rapid field-deployable sequencing		1
6	Pheromone receptor of the globally invasive quarantine pest of the palm tree, the red palm weevil (<i>Rhynchophorus ferrugineus</i>)		3

5	Early Humoral Response Correlates with Disease Severity and Outcomes in COVID-19 Patients	2
4	Disruption of the coordination between host circadian rhythms and malaria parasite development alters the duration of the intraerythrocytic cycle	1
3	The genome of the zoonotic malaria parasite Plasmodium simium reveals adaptations to host-switching	5
2	Saudi Arabian SARS-CoV-2 genomes implicate a mutant Nucleocapsid protein in modulating host interactions and increased viral load in COVID-19 patients	5
1	Protein Phosphatase 1 regulates atypical mitotic and meiotic division in Plasmodium sexual stages	1