

Adam A Witney

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9365367/publications.pdf>

Version: 2024-02-01

47
papers

3,908
citations

201575

27
h-index

233338

45
g-index

47
all docs

47
docs citations

47
times ranked

5327
citing authors

#	ARTICLE	IF	CITATIONS
1	A proteomic view of the Plasmodium falciparum life cycle. Nature, 2002, 419, 520-526.	13.7	1,184
2	Microarrays Reveal that Each of the Ten Dominant Lineages of Staphylococcus aureus Has a Unique Combination of Surface-Associated and Regulatory Genes. Journal of Bacteriology, 2006, 188, 669-676.	1.0	303
3	Identification of Plasmodium falciparum antigens by antigenic analysis of genomic and proteomic data. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 9952-9957.	3.3	227
4	Evolutionary Genomics of Staphylococcus aureus Reveals Insights into the Origin and Molecular Basis of Ruminant Host Adaptation. Genome Biology and Evolution, 2010, 2, 454-466.	1.1	174
5	Comparative phylogenomics of the food-borne pathogen Campylobacter jejuni reveals genetic markers predictive of infection source. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 16043-16048.	3.3	158
6	High Prevalence of Antibiotic-Resistant Mycoplasma genitalium in Nongonococcal Urethritis: The Need for Routine Testing and the Inadequacy of Current Treatment Options. Clinical Infectious Diseases, 2014, 58, 631-637.	2.9	142
7	Sudden Death and Left Ventricular Involvement in Arrhythmogenic Cardiomyopathy. Circulation, 2019, 139, 1786-1797.	1.6	122
8	Extensive Horizontal Gene Transfer during Staphylococcus aureus Co-colonization In Vivo. Genome Biology and Evolution, 2014, 6, 2697-2708.	1.1	119
9	Clinical use of whole genome sequencing for Mycobacterium tuberculosis. BMC Medicine, 2016, 14, 46.	2.3	91
10	Clinical Application of Whole-Genome Sequencing To Inform Treatment for Multidrug-Resistant Tuberculosis Cases. Journal of Clinical Microbiology, 2015, 53, 1473-1483.	1.8	89
11	Staphylococcus aureus Temperate Bacteriophage: Carriage and Horizontal Gene Transfer is Lineage Associated. Frontiers in Cellular and Infection Microbiology, 2012, 2, 6.	1.8	85
12	Guanylyl Cyclase Activity Associated with Putative Bifunctional Integral Membrane Proteins in Plasmodium falciparum. Journal of Biological Chemistry, 2000, 275, 22147-22156.	1.6	84
13	The Distribution of Mobile Genetic Elements (MGEs) in MRSA CC398 Is Associated with Both Host and Country. Genome Biology and Evolution, 2011, 3, 1164-1174.	1.1	82
14	Identification of pathogen-specific genes through microarray analysis of pathogenic and commensal Neisseria species. Microbiology (United Kingdom), 2005, 151, 2907-2922.	0.7	80
15	Application of Comparative Phylogenomics To Study the Evolution of Yersinia enterocolitica and To Identify Genetic Differences Relating to Pathogenicity. Journal of Bacteriology, 2006, 188, 3645-3653.	1.0	78
16	Design, Validation, and Application of a Seven-Strain Staphylococcus aureus PCR Product Microarray for Comparative Genomics. Applied and Environmental Microbiology, 2005, 71, 7504-7514.	1.4	77
17	Determining liver stage parasite burden by real time quantitative PCR as a method for evaluating pre-erythrocytic malaria vaccine efficacy. Molecular and Biochemical Parasitology, 2001, 118, 233-245.	0.5	71
18	Transcripts of developmentally regulated Plasmodium falciparum genes quantified by real-time RT-PCR. Nucleic Acids Research, 2002, 30, 2224-2231.	6.5	70

#	ARTICLE	IF	CITATIONS
19	Transcriptional Analysis of Temporal Gene Expression in Germinating <i>Clostridium difficile</i> 630 Endospores. <i>PLoS ONE</i> , 2013, 8, e64011.	1.1	63
20	High-Throughput Generation of <i>P. falciparum</i> Functional Molecules by Recombinational Cloning. <i>Genome Research</i> , 2004, 14, 2076-2082.	2.4	58
21	Genomic variations define divergence of water/wildlife-associated <i>Campylobacter jejuni</i> niche specialists from common clonal complexes. <i>Environmental Microbiology</i> , 2011, 13, 1549-1560.	1.8	52
22	High-Resolution Analysis by Whole-Genome Sequencing of an International Lineage (Sequence Type 111) of <i>Pseudomonas aeruginosa</i> Associated with Metallo-Carbapenemases in the United Kingdom. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2622-2631.	1.8	50
23	Within-host diversity of MRSA antimicrobial resistances. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 2191-2198.	1.3	49
24	Transcriptional analysis of in vivo <i>Plasmodium yoelii</i> liver stage gene expression. <i>Molecular and Biochemical Parasitology</i> , 2005, 142, 177-183.	0.5	41
25	Î³ T Cells Are a Component of Early Immunity against Preerythrocytic Malaria Parasites. <i>Infection and Immunity</i> , 2000, 68, 2224-2230.	1.0	36
26	<i>Mycobacterium tuberculosis</i> Is Resistant to Isoniazid at a Slow Growth Rate by Single Nucleotide Polymorphisms in <i>katG</i> Codon Ser315. <i>PLoS ONE</i> , 2015, 10, e0138253.	1.1	29
27	Novel Antigen Identification Method for Discovery of Protective Malaria Antigens by Rapid Testing of DNA Vaccines Encoding Exons from the Parasite Genome. <i>Infection and Immunity</i> , 2004, 72, 1594-1602.	1.0	28
28	XDR-TB transmission in London: Case management and contact tracing investigation assisted by early whole genome sequencing. <i>Journal of Infection</i> , 2016, 73, 210-218.	1.7	28
29	Whole-genome sequencing illuminates the evolution and spread of multidrug-resistant tuberculosis in Southwest Nigeria. <i>PLoS ONE</i> , 2017, 12, e0184510.	1.1	27
30	Posttranscriptional Regulation of Flagellin Synthesis in <i>Helicobacter pylori</i> by the RpoN Chaperone HP0958. <i>Journal of Bacteriology</i> , 2008, 190, 7975-7984.	1.0	26
31	Immunogenicity and Protective Efficacy of a <i>Plasmodium yoelii</i> Hsp60 DNA Vaccine in BALB/c Mice. <i>Infection and Immunity</i> , 2001, 69, 3897-3905.	1.0	23
32	Diagnostic yield of hypertrophic cardiomyopathy in first-degree relatives of decedents with idiopathic left ventricular hypertrophy. <i>Europace</i> , 2020, 22, 632-642.	0.7	20
33	Protein kinase B controls <i>Mycobacterium tuberculosis</i> growth via phosphorylation of the transcriptional regulator Lsr2 at threonine 112. <i>Molecular Microbiology</i> , 2019, 112, 1847-1862.	1.2	18
34	Future-proofing and maximizing the utility of metadata: The PHA4GE SARS-CoV-2 contextual data specification package. <i>GigaScience</i> , 2022, 11, .	3.3	18
35	Microarray design for bacterial genomes. <i>Methods in Microbiology</i> , 2002, 33, 67-82.	0.4	16
36	Genetic variation in <i>Mycobacterium tuberculosis</i> isolates from a London outbreak associated with isoniazid resistance. <i>BMC Medicine</i> , 2016, 14, 117.	2.3	16

#	ARTICLE	IF	CITATIONS
37	Genetic Variation in Spatio-Temporal Confined USA300 Community-Associated MRSA Isolates: A Shift from Clonal Dispersion to Genetic Evolution?. PLoS ONE, 2011, 6, e16419.	1.1	15
38	Deciphering the response of Mycobacterium smegmatis to nitrogen stress using bipartite active modules. BMC Genomics, 2013, 14, 436.	1.2	14
39	A computational strategy for the search of regulatory small RNAs in <i>Actinobacillus pleuropneumoniae</i>. Rna, 2016, 22, 1373-1385.	1.6	13
40	Identification of <i>Streptococcus suis</i> Meningitis through Population-Based Surveillance, Togo, 2010â€“2014. Emerging Infectious Diseases, 2016, 22, 1262-1264.	2.0	10
41	Development and application of the active surveillance of pathogens microarray to monitor bacterial gene flux.. BMC Microbiology, 2008, 8, 177.	1.3	7
42	Rare Variation in Drug Metabolism and Long QT Genes and the Genetic Susceptibility to Acquired Long QT Syndrome. Circulation Genomic and Precision Medicine, 2022, 15, CIRCGEN121003391.	1.6	7
43	BÂ€@Sbaseâ€“a microbial gene expression and comparative genomic database. Nucleic Acids Research, 2012, 40, D605-D609.	6.5	3
44	Vaginal microbiota in ethnically diverse young women who did or did not develop pelvic inflammatory disease: community-based prospective study. Sexually Transmitted Infections, 2022, 98, 503-509.	0.8	3
45	Quantitation of Liver-Stage Parasites by Automated TaqMan^{Â€@} Real-Time PCR. , 2002, 72, 137-140.		1
46	BÎ¼@Sbaseâ€“a Microarray Database and Analysis Tool. Comparative and Functional Genomics, 2002, 3, 369-371.	2.0	1
47	Metagenomic profiling of placental tissue suggests DNA virus infection of the placenta is rare. Journal of General Virology, 2021, 102, .	1.3	0