

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	Vaginal microbiota in ethnically diverse young women who did or did not develop pelvic inflammatory disease: community-based prospective study. <i>Sexually Transmitted Infections</i> , 2022, 98, 503-509.	0.8	3
2	Rare Variation in Drug Metabolism and Long QT Genes and the Genetic Susceptibility to Acquired Long QT Syndrome. <i>Circulation Genomic and Precision Medicine</i> , 2022, 15, CIRCGEN121003391.	1.6	7
3	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
4	Metagenomic profiling of placental tissue suggests DNA virus infection of the placenta is rare. <i>Journal of General Virology</i> , 2021, 102, .	1.3	0
5	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
6	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
7	Sudden Death and Left Ventricular Involvement in Arrhythmogenic Cardiomyopathy. <i>Circulation</i> , 2019, 139, 1786-1797.	1.6	122
8	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
9	Identification of <i>Streptococcus suis</i> Meningitis through Population-Based Surveillance, Togo, 2010–2014. <i>Emerging Infectious Diseases</i> , 2016, 22, 1262-1264.	2.0	10
10	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
11	Clinical use of whole genome sequencing for <i>Mycobacterium tuberculosis</i> . <i>BMC Medicine</i> , 2016, 14, 46.	2.3	91
12	A computational strategy for the search of regulatory small RNAs in <i>Actinobacillus pleuropneumoniae</i> . <i>Rna</i> , 2016, 22, 1373-1385.	1.6	13
13	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
14	<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
15	Clinical Application of Whole-Genome Sequencing To Inform Treatment for Multidrug-Resistant Tuberculosis Cases. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1473-1483.	1.8	89
16	Within-host diversity of MRSA antimicrobial resistances. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 2191-2198.	1.3	49
17	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
18	High Prevalence of Antibiotic-Resistant <i>Mycoplasma genitalium</i> in Nongonococcal Urethritis: The Need for Routine Testing and the Inadequacy of Current Treatment Options. <i>Clinical Infectious Diseases</i> , 2014, 58, 631-637.	2.9	142

#	ARTICLE	IF	CITATIONS
19	Extensive Horizontal Gene Transfer during <i>Staphylococcus aureus</i> Co-colonization In Vivo. <i>Genome Biology and Evolution</i> , 2014, 6, 2697-2708.	1.1	119
20	Deciphering the response of <i>Mycobacterium smegmatis</i> to nitrogen stress using bipartite active modules. <i>BMC Genomics</i> , 2013, 14, 436.	1.2	14
21	Transcriptional Analysis of Temporal Gene Expression in Germinating <i>Clostridium difficile</i> 630 Endospores. <i>PLoS ONE</i> , 2013, 8, e64011.	1.1	63
22	BAC@Sbase—a microbial gene expression and comparative genomic database. <i>Nucleic Acids Research</i> , 2012, 40, D605-D609.	6.5	3
23	<i>Staphylococcus aureus</i> Temperate Bacteriophage: Carriage and Horizontal Gene Transfer is Lineage Associated. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012, 2, 6.	1.8	85
24	Genetic Variation in Spatio-Temporal Confined USA300 Community-Associated MRSA Isolates: A Shift from Clonal Dispersion to Genetic Evolution?. <i>PLoS ONE</i> , 2011, 6, e16419.	1.1	15
25	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
26	The Distribution of Mobile Genetic Elements (MGEs) in MRSA CC398 Is Associated with Both Host and Country. <i>Genome Biology and Evolution</i> , 2011, 3, 1164-1174.	1.1	82
27	Evolutionary Genomics of <i>Staphylococcus aureus</i> Reveals Insights into the Origin and Molecular Basis of Ruminant Host Adaptation. <i>Genome Biology and Evolution</i> , 2010, 2, 454-466.	1.1	174
28	Development and application of the active surveillance of pathogens microarray to monitor bacterial gene flux.. <i>BMC Microbiology</i> , 2008, 8, 177.	1.3	7
29	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
30	Microarrays Reveal that Each of the Ten Dominant Lineages of <i>Staphylococcus aureus</i> Has a Unique Combination of Surface-Associated and Regulatory Genes. <i>Journal of Bacteriology</i> , 2006, 188, 669-676.	1.0	303
31	Application of Comparative Phylogenomics To Study the Evolution of <i>Yersinia enterocolitica</i> and To Identify Genetic Differences Relating to Pathogenicity. <i>Journal of Bacteriology</i> , 2006, 188, 3645-3653.	1.0	78
32	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
33	Comparative phylogenomics of the food-borne pathogen <i>Campylobacter jejuni</i> reveals genetic markers predictive of infection source. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 16043-16048.	3.3	158
34	Identification of pathogen-specific genes through microarray analysis of pathogenic and commensal <i>Neisseria</i> species. <i>Microbiology (United Kingdom)</i> , 2005, 151, 2907-2922.	0.7	80
35	Design, Validation, and Application of a Seven-Strain <i>Staphylococcus aureus</i> PCR Product Microarray for Comparative Genomics. <i>Applied and Environmental Microbiology</i> , 2005, 71, 7504-7514.	1.4	77
36	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

#	ARTICLE	IF	CITATIONS
37	High-Throughput Generation of <i>P. falciparum</i> Functional Molecules by Recombinational Cloning. <i>Genome Research</i> , 2004, 14, 2076-2082.	2.4	58
38	Identification of <i>Plasmodium falciparum</i> antigens by antigenic analysis of genomic and proteomic data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 9952-9957.	3.3	227
39	Transcripts of developmentally regulated <i>Plasmodium falciparum</i> genes quantified by real-time RT-PCR. <i>Nucleic Acids Research</i> , 2002, 30, 2224-2231.	6.5	70
40	Quantitation of Liver-Stage Parasites by Automated TaqMan [®] Real-Time PCR. , 2002, 72, 137-140.		1
41	Microarray design for bacterial genomes. <i>Methods in Microbiology</i> , 2002, 33, 67-82.	0.4	16
42	BIG@Sbase™ a Microarray Database and Analysis Tool. <i>Comparative and Functional Genomics</i> , 2002, 3, 369-371.	2.0	1
43	A proteomic view of the <i>Plasmodium falciparum</i> life cycle. <i>Nature</i> , 2002, 419, 520-526.	13.7	1,184
44	Determining liver stage parasite burden by real time quantitative PCR as a method for evaluating pre-erythrocytic malaria vaccine efficacy. <i>Molecular and Biochemical Parasitology</i> , 2001, 118, 233-245.	0.5	71
45	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
46	Guanylyl Cyclase Activity Associated with Putative Bifunctional Integral Membrane Proteins in <i>Plasmodium falciparum</i> . <i>Journal of Biological Chemistry</i> , 2000, 275, 22147-22156.	1.6	84
47	IFN- γ T Cells Are a Component of Early Immunity against Preerythrocytic Malaria Parasites. <i>Infection and Immunity</i> , 2000, 68, 2224-2230.	1.0	36