

Alexander William Tucker

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

920
citations

430874

18
h-index

501196

28
g-index

37
all docs

37
docs citations

37
times ranked

1004
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic signatures of human and animal disease in the zoonotic pathogen <i>Streptococcus suis</i> . <i>Nature Communications</i> , 2015, 6, 6740.	12.8	124
2	Development of a Multiplex PCR Assay for Rapid Molecular Serotyping of <i>Haemophilus parasuis</i> . <i>Journal of Clinical Microbiology</i> , 2015, 53, 3812-3821.	3.9	80
3	Proposal of serovars 17 and 18 of <i>Actinobacillus pleuropneumoniae</i> based on serological and genotypic analysis. <i>Veterinary Microbiology</i> , 2018, 217, 1-6.	1.9	64
4	Patterns of antimicrobial resistance in <i>Streptococcus suis</i> isolates from pigs with or without streptococcal disease in England between 2009 and 2014. <i>Veterinary Microbiology</i> , 2017, 207, 117-124.	1.9	53
5	Genome Reduction Is Associated with Bacterial Pathogenicity across Different Scales of Temporal and Ecological Divergence. <i>Molecular Biology and Evolution</i> , 2021, 38, 1570-1579.	8.9	50
6	Comparative sequence analysis of the capsular polysaccharide loci of <i>Actinobacillus pleuropneumoniae</i> serovars 1-18, and development of two multiplex PCRs for comprehensive capsule typing. <i>Veterinary Microbiology</i> , 2018, 220, 83-89.	1.9	49
7	Whole Genome Sequencing for Surveillance of Antimicrobial Resistance in <i>Actinobacillus pleuropneumoniae</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 311.	3.5	42
8	The use of oral fluids to monitor key pathogens in porcine respiratory disease complex. <i>Porcine Health Management</i> , 2017, 3, 7.	2.6	38
9	The use of genome wide association methods to investigate pathogenicity, population structure and serovar in <i>Haemophilus parasuis</i> . <i>BMC Genomics</i> , 2014, 15, 1179.	2.8	34
10	Characterisation of a mobilisable plasmid conferring florfenicol and chloramphenicol resistance in <i>Actinobacillus pleuropneumoniae</i> . <i>Veterinary Microbiology</i> , 2015, 178, 279-282.	1.9	34
11	<i>Streptococcus suis</i> contains multiple phase-variable methyltransferases that show a discrete lineage distribution. <i>Nucleic Acids Research</i> , 2018, 46, 11466-11476.	14.5	31
12	Identification of <i>dfrA14</i> in two distinct plasmids conferring trimethoprim resistance in <i>Actinobacillus pleuropneumoniae</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 2217-2222.	3.0	30
13	The N-linking glycosylation system from <i>Actinobacillus pleuropneumoniae</i> is required for adhesion and has potential use in glycoengineering. <i>Open Biology</i> , 2017, 7, 160212.	3.6	29
14	Pathotyping the Zoonotic Pathogen <i>Streptococcus suis</i> : Novel Genetic Markers To Differentiate Invasive Disease-Associated Isolates from Non-Disease-Associated Isolates from England and Wales. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	29
15	Whole genome investigation of a divergent clade of the pathogen <i>Streptococcus suis</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 1191.	3.5	27
16	Complete Genome Sequence of MIDG2331, a Genetically Tractable Serovar 8 Clinical Isolate of <i>Actinobacillus pleuropneumoniae</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	26
17	The Generation of Successive Unmarked Mutations and Chromosomal Insertion of Heterologous Genes in <i>Actinobacillus pleuropneumoniae</i> Using Natural Transformation. <i>PLoS ONE</i> , 2014, 9, e111252.	2.5	23
18	ICEAp1, an Integrative Conjugative Element Related to ICEHin1056, Identified in the Pig Pathogen <i>Actinobacillus pleuropneumoniae</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 810.	3.5	20

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19	Increased risk of A(H1N1)pdm09 influenza infection in UK pig industry workers compared to a general population cohort. <i>Influenza and Other Respiratory Viruses</i> , 2016, 10, 291-300.	3.4	18
20	â€œPathotypingâ€• Multiplex PCR Assay for <i>Haemophilus parasuis</i> : a Tool for Prediction of Virulence. <i>Journal of Clinical Microbiology</i> , 2017, 55, 2617-2628.	3.9	18
21	Use of Proteins Identified through a Functional Genomic Screen To Develop a Protein Subunit Vaccine That Provides Significant Protection against Virulent <i>Streptococcus suis</i> in Pigs. <i>Infection and Immunity</i> , 2018, 86, .	2.2	16
22	HAM-ART: An optimised culture-free Hi-C metagenomics pipeline for tracking antimicrobial resistance genes in complex microbial communities. <i>PLoS Genetics</i> , 2022, 18, e1009776.	3.5	14
23	Metatranscriptomics reveals metabolic adaptation and induction of virulence factors by <i>Haemophilus parasuis</i> during lung infection. <i>Veterinary Research</i> , 2015, 46, 102.	3.0	13
24	A Survey of Chinese Pig Farms and Human Healthcare Isolates Reveals Separate Human and Animal Methicillinâ€•Resistant <i>Staphylococcus aureus</i> Populations. <i>Advanced Science</i> , 2022, 9, e2103388.	11.2	13
25	Weakly haemolytic variants of <i>Brachyspira hyodysenteriae</i> newly emerged in Europe belong to a distinct subclade with unique genetic properties. <i>Veterinary Research</i> , 2019, 50, 21.	3.0	10
26	Generation and Evaluation of a <i>Glaesserella (Haemophilus) parasuis</i> Capsular Mutant. <i>Infection and Immunity</i> , 2020, 88, .	2.2	7
27	Evaluation of the recombinant proteins RlpB and VacJ as a vaccine for protection against <i>Glaesserella parasuis</i> in pigs. <i>BMC Veterinary Research</i> , 2020, 16, 167.	1.9	5
28	Mutation rate dynamics reflect ecological change in an emerging zoonotic pathogen. <i>PLoS Genetics</i> , 2021, 17, e1009864.	3.5	5
29	Value Chain Governance, Power and Negative Externalities: What Influences Efforts to Control Pig Diseases in Myanmar?. <i>European Journal of Development Research</i> , 2020, 32, 759-780.	2.3	4
30	Rapid Detection of <i>Actinobacillus pleuropneumoniae</i> From Clinical Samples Using Recombinase Polymerase Amplification. <i>Frontiers in Veterinary Science</i> , 2022, 9, 805382.	2.2	3
31	Comparative quasi-static mechanical characterization of fresh and stored porcine trachea specimens. <i>European Physical Journal: Special Topics</i> , 2018, 227, 55-60.	2.6	2
32	Draft Genome Sequences of the Type Strains of <i>Actinobacillus indolicus</i> (46K2C) and <i>Actinobacillus porcinus</i> (NM319), Two NAD-Dependent Bacterial Species Found in the Respiratory Tract of Pigs. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
33	Complete genome for <i>Actinobacillus pleuropneumoniae</i> serovar 8 reference strain 405: comparative analysis with draft genomes for different laboratory stock cultures indicates little genetic variation. <i>Microbial Genomics</i> , 2021, 7, .	2.0	1
34	Rationally designed mariner vectors for functional genomic analysis of <i>Actinobacillus pleuropneumoniae</i> and other Pasteurellaceae species by transposon-directed insertion-site sequencing (TraDIS). <i>Animal Diseases</i> , 2021, 1, 29.	1.4	1
35	The Cipher Code of Simple Sequence Repeats in â€œVampire Pathogensâ€•. <i>Scientific Reports</i> , 2015, 5, 12441.	3.3	0