

Steven Pullan

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

3,486
citations

279798

23
h-index

265206

42
g-index

52
all docs

52
docs citations

52
times ranked

6437
citing authors

#	ARTICLE	IF	CITATIONS
1	Dose-dependent response to infection with SARS-CoV-2 in the ferret model and evidence of protective immunity. <i>Nature Communications</i> , 2021, 12, 81.	12.8	141
2	â€œKankashaâ€•in Kassala: A prospective observational cohort study of the clinical characteristics, epidemiology, genetic origin, and chronic impact of the 2018 epidemic of Chikungunya virus infection in Kassala, Sudan. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009387.	3.0	13
3	Nanopore metagenomic sequencing of influenza virus directly from respiratory samples: diagnosis, drug resistance and nosocomial transmission, United Kingdom, 2018/19 influenza season. <i>Eurosurveillance</i> , 2021, 26, .	7.0	17
4	Metagenomic identification of a new sarbecovirus from horseshoe bats in Europe. <i>Scientific Reports</i> , 2021, 11, 14723.	3.3	31
5	Resurgence of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks. <i>Nature</i> , 2021, 597, 539-543.	27.8	113
6	Tick-Borne Encephalitis Virus, United Kingdom. <i>Emerging Infectious Diseases</i> , 2020, 26, 90-96.	4.3	82
7	Nanopore metagenomic sequencing to investigate nosocomial transmission of human metapneumovirus from a unique genetic group among haematology patients in the United Kingdom. <i>Journal of Infection</i> , 2020, 80, 571-577.	3.3	15
8	Oropouche virus cases identified in Ecuador using an optimised qRT-PCR informed by metagenomic sequencing. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0007897.	3.0	10
9	Evolutionary Dynamics of Oropouche Virus in South America. <i>Journal of Virology</i> , 2020, 94, .	3.4	17
10	Succession of physiological stages hallmarks the transcriptomic response of the fungus <i>Aspergillus niger</i> to lignocellulose. <i>Biotechnology for Biofuels</i> , 2020, 13, 69.	6.2	4
11	Detection of Crimean-Congo Haemorrhagic Fever cases in a severe undifferentiated febrile illness outbreak in the Federal Republic of Sudan: A retrospective epidemiological and diagnostic cohort study. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007571.	3.0	10
12	Metagenomic Nanopore Sequencing of Influenza Virus Direct from Clinical Respiratory Samples. <i>Journal of Clinical Microbiology</i> , 2019, 58, .	3.9	121
13	Rhombencephalitis and Myeloradiculitis Caused by a European Subtype of Tick-Borne Encephalitis Virus. <i>Emerging Infectious Diseases</i> , 2019, 25, 2317-2319.	4.3	2
14	Metagenomic sequencing at the epicenter of the Nigeria 2018 Lassa fever outbreak. <i>Science</i> , 2019, 363, 74-77.	12.6	201
15	Detection of new endemic focus of tick-borne encephalitis virus (TBEV), Hampshire/Dorset border, England, September 2019. <i>Eurosurveillance</i> , 2019, 24, .	7.0	46
16	Assessment of metagenomic Nanopore and Illumina sequencing for recovering whole genome sequences of chikungunya and dengue viruses directly from clinical samples. <i>Eurosurveillance</i> , 2018, 23, .	7.0	85
17	Closed Genome Sequence Obtained Using Hybrid Nanopore/Illumina Assembly of a <i>Bacillus anthracis</i> Isolate from an Animal-Skin-Drum-Associated Anthrax Case in the United Kingdom. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	0
18	Detection of Viral Pathogens With Multiplex Nanopore MinION Sequencing: Be Careful With Cross-Talk. <i>Frontiers in Microbiology</i> , 2018, 9, 2225.	3.5	75

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19	Isolation of Oropouche Virus from Febrile Patient, Ecuador. <i>Emerging Infectious Diseases</i> , 2018, 24, 935-937.	4.3	21
20	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018, 361, 894-899.	12.6	279
21	Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. <i>Nature Protocols</i> , 2017, 12, 1261-1276.	12.0	898
22	First Complete Genome Sequences of Zika Virus Isolated from Febrile Patient Sera in Ecuador. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
23	The Effect of Nucleic Acid Extraction Platforms and Sample Storage on the Integrity of Viral RNA for Use in Whole Genome Sequencing. <i>Journal of Molecular Diagnostics</i> , 2017, 19, 303-312.	2.8	15
24	A Human Bi-specific Antibody against Zika Virus with High Therapeutic Potential. <i>Cell</i> , 2017, 171, 229-241.e15.	28.9	118
25	Expression of <i>Aspergillus niger</i> CAZymes is determined by compositional changes in wheat straw generated by hydrothermal or ionic liquid pretreatments. <i>Biotechnology for Biofuels</i> , 2017, 10, 35.	6.2	18
26	Complete Genome Sequence of Seoul Virus Strain Tchoupitoulas. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
27	The effect of growth rate on pyrazinamide activity in <i>Mycobacterium tuberculosis</i> - insights for early bactericidal activity?. <i>BMC Infectious Diseases</i> , 2016, 16, 205.	2.9	13
28	Complete Genome Sequence of Zika Virus Isolated from Semen. <i>Genome Announcements</i> , 2016, 4, .	0.8	16
29	<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.	2.5	29
30	Whole Genome Analysis of Injectional Anthrax Identifies Two Disease Clusters Spanning More Than 13 Years. <i>EBioMedicine</i> , 2015, 2, 1613-1618.	6.1	27
31	Whole-genome sequencing investigation of animal-skin-drum-associated UK anthrax cases reveals evidence of mixed populations and relatedness to a US case. <i>Microbial Genomics</i> , 2015, 1, e000039.	2.0	9
32	Exploring fungal biodiversity: organic acid production by 66 strains of filamentous fungi. <i>Fungal Biology and Biotechnology</i> , 2014, 1, 1-14.	5.1	119
33	RNA-sequencing reveals the complexities of the transcriptional response to lignocellulosic biofuel substrates in <i>Aspergillus niger</i> . <i>Fungal Biology and Biotechnology</i> , 2014, 1, 3.	5.1	41
34	The role of carbon starvation in the induction of enzymes that degrade plant-derived carbohydrates in <i>Aspergillus niger</i> . <i>Fungal Genetics and Biology</i> , 2014, 72, 34-47.	2.1	95
35	Development of an Unmarked Gene Deletion System for the Filamentous Fungi <i>Aspergillus niger</i> and <i>Talaromyces versatilis</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 3484-3487.	3.1	22
36	Transcriptional landscape of <i>Aspergillus niger</i> at breaking of conidial dormancy revealed by RNA-sequencing. <i>BMC Genomics</i> , 2013, 14, 246.	2.8	54

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37	Genome-wide transcriptional response of <i>Trichoderma reesei</i> to lignocellulose using RNA sequencing and comparison with <i>Aspergillus niger</i> . <i>BMC Genomics</i> , 2013, 14, 541.	2.8	86
38	Uncovering the Genome-Wide Transcriptional Responses of the Filamentous Fungus <i>Aspergillus niger</i> to Lignocellulose Using RNA Sequencing. <i>PLoS Genetics</i> , 2012, 8, e1002875.	3.5	157
39	Genome-wide analysis of the role of GlnR in <i>Streptomyces venezuelae</i> provides new insights into global nitrogen regulation in actinomycetes. <i>BMC Genomics</i> , 2011, 12, 175.	2.8	127
40	Microbial Responses to Nitric Oxide and Nitrosative Stress: Growth, α -Omic, and Physiological Methods. <i>Methods in Enzymology</i> , 2008, 437, 499-519.	1.0	18
41	Nitric Oxide in Chemostat-Cultured <i>Escherichia coli</i> Is Sensed by Fnr and Other Global Regulators: Unaltered Methionine Biosynthesis Indicates Lack of S Nitrosation. <i>Journal of Bacteriology</i> , 2007, 189, 1845-1855.	2.2	132
42	Transcriptional Responses of <i>Escherichia coli</i> to S-Nitrosoglutathione under Defined Chemostat Conditions Reveal Major Changes in Methionine Biosynthesis. <i>Journal of Biological Chemistry</i> , 2005, 280, 10065-10072.	3.4	113
43	A novel metallo- β -lactamase, Mbl1b, produced by the environmental bacterium <i>Caulobacter crescentus</i> 1. <i>FEBS Letters</i> , 2001, 509, 350-354.	2.8	31