

Brett E Pickett

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

2,430
citations

430874

18
h-index

276875

41
g-index

56
all docs

56
docs citations

56
times ranked

5190
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-Cell RNA Sequencing Characterizes the Molecular Heterogeneity of the Larval Zebrafish Optic Tectum. <i>Frontiers in Molecular Neuroscience</i> , 2022, 15, 818007.	2.9	8
2	Impact of Local and Demographic Factors on Early COVID-19 Vaccine Hesitancy among Health Care Workers in New York City Public Hospitals. <i>Vaccines</i> , 2022, 10, 273.	4.4	7
3	CD5 Deficiency Alters Helper T Cell Metabolic Function and Shifts the Systemic Metabolome. <i>Biomedicines</i> , 2022, 10, 704.	3.2	1
4	Chikungunya virus time course infection of human macrophages reveals intracellular signaling pathways relevant to repurposed therapeutics. <i>PeerJ</i> , 2022, 10, e13090.	2.0	5
5	Characterization of <i>Staphylococcus aureus</i> biofilms via crystal violet binding and biochemical composition assays of isolates from hospitals, raw meat, and biofilm-associated gene mutants. <i>Microbial Pathogenesis</i> , 2022, 167, 105554.	2.9	4
6	Meta-Analysis of Two Human RNA-seq Datasets to Determine Periodontitis Diagnostic Biomarkers and Drug Target Candidates. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5580.	4.1	6
7	Mutation in Hemagglutinin Antigenic Sites in Influenza A pH1N1 Viruses from 2015â€“2019 in the United States Mountain West, Europe, and the Northern Hemisphere. <i>Genes</i> , 2022, 13, 909.	2.4	1
8	A signaling pathway-driven bioinformatics pipeline for predicting therapeutics against emerging infectious diseases. <i>F1000Research</i> , 2021, 10, 330.	1.6	4
9	Genome-wide bioinformatic analyses predict key host and viral factors in SARS-CoV-2 pathogenesis. <i>Communications Biology</i> , 2021, 4, 590.	4.4	38
10	Evaluation of ELISA-Based Multiplex Peptides for the Detection of Human Serum Antibodies Induced by Zika Virus Infection across Various Countries. <i>Viruses</i> , 2021, 13, 1319.	3.3	2
11	Preprocessing of Public RNA-Sequencing Datasets to Facilitate Downstream Analyses of Human Diseases. <i>Data</i> , 2021, 6, 75.	2.3	1
12	Alphaviruses: Host pathogenesis, immune response, and vaccine & treatment updates. <i>Journal of General Virology</i> , 2021, 102, .	2.9	9
13	Collective interactions augment influenza A virus replication in a host-dependent manner. <i>Nature Microbiology</i> , 2020, 5, 1158-1169.	13.3	32
14	Microbiome disturbance and resilience dynamics of the upper respiratory tract during influenza A virus infection. <i>Nature Communications</i> , 2020, 11, 2537.	12.8	72
15	Evolutionary dynamics and molecular epidemiology of West Nile virus in New York State: 1999â€“2015. <i>Virus Evolution</i> , 2019, 5, vez020.	4.9	14
16	Optimization of qRT-PCR assay for zika virus detection in human serum and urine. <i>Virus Research</i> , 2019, 263, 173-178.	2.2	17
17	Peptide arrays of three collections of human sera from patients infected with mosquito-borne viruses. <i>F1000Research</i> , 2019, 8, 1875.	1.6	6
18	Peptide arrays incubated with three collections of human sera from patients infected with mosquito-borne viruses. <i>F1000Research</i> , 2019, 8, 1875.	1.6	9

#	ARTICLE	IF	CITATIONS
19	Whole-Genome Sequences of Zika Virus FLR Strains after Passage in Vero or C6/36 Cells. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
20	Characterizing the Different Effects of Zika Virus Infection in Placenta and Microglia Cells. <i>Viruses</i> , 2018, 10, 649.	3.3	16
21	Growth and adaptation of Zika virus in mammalian and mosquito cells. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006880.	3.0	42
22	Whole genome sequencing, variant analysis, phylogenetics, and deep sequencing of Zika virus strains. <i>Scientific Reports</i> , 2018, 8, 15843.	3.3	20
23	Sequences of Zika Virus Genomes from a Pediatric Cohort in Nicaragua. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
24	Whole-genome sequencing and analyses identify high genetic heterogeneity, diversity and endemicity of rotavirus genotype P[6] strains circulating in Africa. <i>Infection, Genetics and Evolution</i> , 2018, 63, 79-88.	2.3	26
25	Differing epidemiological dynamics of Chikungunya virus in the Americas during the 2014-2015 epidemic. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006670.	3.0	23
26	Bioinformatics Meets Virology: The European Virus Bioinformatics Center's Second Annual Meeting. <i>Viruses</i> , 2018, 10, 256.	3.3	6
27	Influenza Research Database: An integrated bioinformatics resource for influenza virus research. <i>Nucleic Acids Research</i> , 2017, 45, D466-D474.	14.5	293
28	Identification of Dezidougou Virus in a DAK AR 41524 Zika Virus Stock. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
29	Identification of diagnostic peptide regions that distinguish Zika virus from related mosquito-borne Flaviviruses. <i>PLoS ONE</i> , 2017, 12, e0178199.	2.5	26
30	A RESTful API for Access to Phylogenetic Tools via the CIPRES Science Gateway. <i>Evolutionary Bioinformatics</i> , 2015, 11, EBO.S21501.	1.2	390
31	Diversifying Selection Analysis Predicts Antigenic Evolution of 2009 Pandemic H1N1 Influenza A Virus in Humans. <i>Journal of Virology</i> , 2015, 89, 5427-5440.	3.4	21
32	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. <i>PLoS ONE</i> , 2014, 9, e99979.	2.5	34
33	A comprehensive collection of systems biology data characterizing the host response to viral infection. <i>Scientific Data</i> , 2014, 1, 140033.	5.3	62
34	Toward a method for tracking virus evolutionary trajectory applied to the pandemic H1N1 2009 influenza virus. <i>Infection, Genetics and Evolution</i> , 2014, 28, 351-357.	2.3	3
35	Metadata-driven comparative analysis tool for sequences (meta-CATS): An automated process for identifying significant sequence variations that correlate with virus attributes. <i>Virology</i> , 2013, 447, 45-51.	2.4	35
36	Virus Pathogen Database and Analysis Resource (ViPR): A Comprehensive Bioinformatics Database and Analysis Resource for the Coronavirus Research Community. <i>Viruses</i> , 2012, 4, 3209-3226.	3.3	156

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37	ViPR: an open bioinformatics database and analysis resource for virology research. <i>Nucleic Acids Research</i> , 2012, 40, D593-D598.	14.5	610
38	Influenza Virus Sequence Feature Variant Type Analysis: Evidence of a Role for NS1 in Influenza Virus Host Range Restriction. <i>Journal of Virology</i> , 2012, 86, 5857-5866.	3.4	35
39	Influenza Research Database: an integrated bioinformatics resource for influenza research and surveillance. <i>Influenza and Other Respiratory Viruses</i> , 2012, 6, 404-416.	3.4	270
40	Evidence for separation of HCV subtype 1a into two distinct clades. <i>Journal of Viral Hepatitis</i> , 2011, 18, 608-618.	2.0	58
41	Phylogenetic Analysis of Eastern Equine Encephalitis Virus Isolates from Florida. <i>American Journal of Tropical Medicine and Hygiene</i> , 2011, 84, 709-717.	1.4	14
42	Recombination in West Nile Virus: minimal contribution to genomic diversity. <i>Virology Journal</i> , 2009, 6, 165.	3.4	27
43	A signaling pathway-driven bioinformatics pipeline for predicting therapeutics against emerging infectious diseases. <i>F1000Research</i> , 0, 10, 330.	1.6	8
44	Peptide arrays of three collections of human sera from patients infected with mosquito-borne viruses. <i>F1000Research</i> , 0, 8, 1875.	1.6	0
45	Lessons learned in virulence factor identification and data management from a hackathon on microbial virulence. <i>F1000Research</i> , 0, 11, 160.	1.6	1
46	METASnake: a Snakemake workflow to facilitate automated processing of metagenomic data through the metaWRAP pipeline. <i>F1000Research</i> , 0, 11, 265.	1.6	0
47	SnakeWRAP: a Snakemake workflow to facilitate automated processing of metagenomic data through the metaWRAP pipeline. <i>F1000Research</i> , 0, 11, 265.	1.6	2