Brett E Pickett

List of Publications by Year
in descending order

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	ViPR: an open bioinformatics database and analysis resource for virology research. Nucleic Acids Research, 2012, 40, D593-D598.	14.5	610
2	A RESTful API for Access to Phylogenetic Tools via the CIPRES Science Gateway. Evolutionary Bioinformatics, 2015, 11, EBO.S21501.	1.2	390
3	Influenza Research Database: An integrated bioinformatics resource for influenza virus research. Nucleic Acids Research, 2017, 45, D466-D474.	14.5	293
4	Influenza Research Database: an integrated bioinformatics resource for influenza research and surveillance. Influenza and Other Respiratory Viruses, 2012, 6, 404-416.	3.4	270
5	Virus Pathogen Database and Analysis Resource (ViPR): A Comprehensive Bioinformatics Database and Analysis Resource for the Coronavirus Research Community. Viruses, 2012, 4, 3209-3226.	3.3	156
6	Microbiome disturbance and resilience dynamics of the upper respiratory tract during influenza A virus infection. Nature Communications, 2020, 11, 2537.	12.8	72
7	A comprehensive collection of systems biology data characterizing the host response to viral infection. Scientific Data, 2014, 1, 140033.	5.3	62
8	Evidence for separation of HCV subtype 1a into two distinct clades. Journal of Viral Hepatitis, 2011, 18, 608-618.	2.0	58
9	Growth and adaptation of Zika virus in mammalian and mosquito cells. PLoS Neglected Tropical Diseases, 2018, 12, e0006880.	3.0	42
10	Genome-wide bioinformatic analyses predict key host and viral factors in SARS-CoV-2 pathogenesis. Communications Biology, 2021, 4, 590.	4.4	38
11	Influenza Virus Sequence Feature Variant Type Analysis: Evidence of a Role for NS1 in Influenza Virus Host Range Restriction. Journal of Virology, 2012, 86, 5857-5866.	3.4	35
12	Metadata-driven comparative analysis tool for sequences (meta-CATS): An automated process for identifying significant sequence variations that correlate with virus attributes. Virology, 2013, 447, 45-51.	2.4	35
13	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. PLoS ONE, 2014, 9, e99979.	2.5	34
14	Collective interactions augment influenza A virus replication in a host-dependent manner. Nature Microbiology, 2020, 5, 1158-1169.	13.3	32
15	Recombination in West Nile Virus: minimal contribution to genomic diversity. Virology Journal, 2009, 6, 165.	3.4	27
16	Whole-genome sequencing and analyses identify high genetic heterogeneity, diversity and endemicity of rotavirus genotype P[6] strains circulating in Africa. Infection, Genetics and Evolution, 2018, 63, 79-88.	2.3	26
17	Identification of diagnostic peptide regions that distinguish Zika virus from related mosquito-borne Flaviviruses. PLoS ONE, 2017, 12, e0178199.	2.5	26
18	Differing epidemiological dynamics of Chikungunya virus in the Americas during the 2014-2015 epidemic. PLoS Neglected Tropical Diseases, 2018, 12, e0006670.	3.0	23

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19	Diversifying Selection Analysis Predicts Antigenic Evolution of 2009 Pandemic H1N1 Influenza A Virus in Humans. Journal of Virology, 2015, 89, 5427-5440.	3.4	21
20	Whole genome sequencing, variant analysis, phylogenetics, and deep sequencing of Zika virus strains. Scientific Reports, 2018, 8, 15843.	3.3	20
21	Optimization of qRT-PCR assay for zika virus detection in human serum and urine. Virus Research, 2019, 263, 173-178.	2.2	17
22	Characterizing the Different Effects of Zika Virus Infection in Placenta and Microglia Cells. Viruses, 2018, 10, 649.	3.3	16
23	Phylogenetic Analysis of Eastern Equine Encephalitis Virus Isolates from Florida. American Journal of Tropical Medicine and Hygiene, 2011, 84, 709-717.	1.4	14
24	Evolutionary dynamics and molecular epidemiology of West Nile virus in New York State: 1999â€"2015. Virus Evolution, 2019, 5, vez020.	4.9	14
25	Alphaviruses: Host pathogenesis, immune response, and vaccine & treatment updates. Journal of General Virology, 2021, 102, .	2.9	9
26	Peptide arrays incubated with three collections of human sera from patients infected with mosquito-borne viruses. F1000Research, 2019, 8, 1875.	1.6	9
27	A signaling pathway-driven bioinformatics pipeline for predicting therapeutics against emerging infectious diseases. F1000Research, 0, 10, 330.	1.6	8
28	Single-Cell RNA Sequencing Characterizes the Molecular Heterogeneity of the Larval Zebrafish Optic Tectum. Frontiers in Molecular Neuroscience, 2022, 15, 818007.	2.9	8
29	Impact of Local and Demographic Factors on Early COVID-19 Vaccine Hesitancy among Health Care Workers in New York City Public Hospitals. Vaccines, 2022, 10, 273.	4.4	7
30	Bioinformatics Meets Virology: The European Virus Bioinformatics Centerâ€™s Second Annual Meeting. Viruses, 2018, 10, 256.	3.3	6
31	Peptide arrays of three collections of human sera from patients infected with mosquito-borne viruses. F1000Research, 2019, 8, 1875.	1.6	6
32	Meta-Analysis of Two Human RNA-seq Datasets to Determine Periodontitis Diagnostic Biomarkers and Drug Target Candidates. International Journal of Molecular Sciences, 2022, 23, 5580.	4.1	6
33	Chikungunya virus time course infection of human macrophages reveals intracellular signaling pathways relevant to repurposed therapeutics. PeerJ, 2022, 10, e13090.	2.0	5
34	A signaling pathway-driven bioinformatics pipeline for predicting therapeutics against emerging infectious diseases. F1000Research, 2021, 10, 330.	1.6	4
35	Characterization of Staphylococcus aureus biofilms via crystal violet binding and biochemical composition assays of isolates from hospitals, raw meat, and biofilm-associated gene mutants. Microbial Pathogenesis, 2022, 167, 105554.	2.9	4
36	Toward a method for tracking virus evolutionary trajectory applied to the pandemic H1N1 2009 influenza virus. Infection, Genetics and Evolution, 2014, 28, 351-357.	2.3	3

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37	Whole-Genome Sequences of Zika Virus FLR Strains after Passage in Vero or C6/36 Cells. Genome Announcements, 2018, 6, .	0.8	2
38	Evaluation of ELISA-Based Multiplex Peptides for the Detection of Human Serum Antibodies Induced by Zika Virus Infection across Various Countries. Viruses, 2021, 13, 1319.	3.3	2
39	SnakeWRAP: a Snakemake workflow to facilitate automated processing of metagenomic data through the metaWRAP pipeline. F1000Research, 0, 11, 265.	1.6	2
40	Preprocessing of Public RNA-Sequencing Datasets to Facilitate Downstream Analyses of Human Diseases. Data, 2021, 6, 75.	2.3	1
41	Lessons learned in virulence factor identification and data management from a hackathon on microbial virulence. F1000Research, 0, 11, 160.	1.6	1
42	CD5 Deficiency Alters Helper T Cell Metabolic Function and Shifts the Systemic Metabolome. Biomedicines, 2022, 10, 704.	3.2	1
43	Mutation in Hemagglutinin Antigenic Sites in Influenza A pH1N1 Viruses from 2015â€"2019 in the United States Mountain West, Europe, and the Northern Hemisphere. Genes, 2022, 13, 909.	2.4	1
44	Identification of Dezidougou Virus in a DAK AR 41524 Zika Virus Stock. Genome Announcements, 2017, 5, .	0.8	0
45	Sequences of Zika Virus Genomes from a Pediatric Cohort in Nicaragua. Genome Announcements, 2018, 6, .	0.8	0
46	Peptide arrays of three collections of human sera from patients infected with mosquito-borne viruses. F1000Research, 0, 8, 1875.	1.6	0
47	METASnake: a Snakemake workflow to facilitate automated processing of metagenomic data through the metaWRAP pipeline. F1000Research, 0, 11, 265.	1.6	0