

Daniel P Depledge

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

3,853
citations

185998

28
h-index

155451

55
g-index

69
all docs

69
docs citations

69
times ranked

5335
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-cell transcriptomics identifies Gadd45b as a regulator of herpesvirus-reactivating neurons. <i>EMBO Reports</i> , 2022, 23, e53543.	2.0	16
2	DRUMMER "rapid detection of RNA modifications through comparative nanopore sequencing. <i>Bioinformatics</i> , 2022, 38, 3113-3115.	1.8	26
3	An eIF3d-dependent switch regulates HCMV replication by remodeling the infected cell translation landscape to mimic chronic ER stress. <i>Cell Reports</i> , 2022, 39, 110767.	2.9	8
4	Nanopore-Based Detection of Viral RNA Modifications. <i>MBio</i> , 2022, 13, e0370221.	1.8	12
5	DLK-Dependent Biphasic Reactivation of Herpes Simplex Virus Latency Established in the Absence of Antivirals. <i>Journal of Virology</i> , 2022, 96, .	1.5	12
6	The influence of human genetic variation on Epstein-Barr virus sequence diversity. <i>Scientific Reports</i> , 2021, 11, 4586.	1.6	8
7	Targeting the m ⁶ A RNA modification pathway blocks SARS-CoV-2 and HCoV-OC43 replication. <i>Genes and Development</i> , 2021, 35, 1005-1019.	2.7	70
8	Enteric viruses evoke broad host immune responses resembling those elicited by the bacterial microbiome. <i>Cell Host and Microbe</i> , 2021, 29, 1014-1029.e8.	5.1	35
9	Widespread remodeling of the m ⁶ A RNA-modification landscape by a viral regulator of RNA processing and export. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	39
10	ICTV Virus Taxonomy Profile: Herpesviridae 2021. <i>Journal of General Virology</i> , 2021, 102, .	1.3	74
11	The architecture of the simian varicella virus transcriptome. <i>PLoS Pathogens</i> , 2021, 17, e1010084.	2.1	4
12	Mutagenesis of the Varicella-Zoster Virus Genome Demonstrates That VLT and VLT-ORF63 Proteins Are Dispensable for Lytic Infection. <i>Viruses</i> , 2021, 13, 2289.	1.5	2
13	Varicella-Zoster Virus "Genetics, Molecular Evolution and Recombination. <i>Current Topics in Microbiology and Immunology</i> , 2021, , 1-23.	0.7	2
14	Recurrent herpes zoster in the Shingles Prevention Study: Are second episodes caused by the same varicella-zoster virus strain?. <i>Vaccine</i> , 2020, 38, 150-157.	1.7	8
15	Kallikrein-Mediated Cytokeratin 10 Degradation Is Required for Varicella Zoster Virus Propagation in Skin. <i>Journal of Investigative Dermatology</i> , 2020, 140, 774-784.e11.	0.3	13
16	Decoding the Architecture of the Varicella-Zoster Virus Transcriptome. <i>MBio</i> , 2020, 11, .	1.8	29
17	Direct RNA sequencing reveals m6A modifications on adenovirus RNA are necessary for efficient splicing. <i>Nature Communications</i> , 2020, 11, 6016.	5.8	111
18	Varicella-zoster virus VLT-ORF63 fusion transcript induces broad viral gene expression during reactivation from neuronal latency. <i>Nature Communications</i> , 2020, 11, 6324.	5.8	23

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19	Analysis of the reiteration regions (R1 to R5) of varicella-zoster virus. <i>Virology</i> , 2020, 546, 38-50.	1.1	7
20	Using Direct RNA Nanopore Sequencing to Deconvolute Viral Transcriptomes. <i>Current Protocols in Microbiology</i> , 2020, 57, e99.	6.5	11
21	Whole genome sequencing of Herpes Simplex Virus 1 directly from human cerebrospinal fluid reveals selective constraints in neurotropic viruses. <i>Virus Evolution</i> , 2020, 6, veaa012.	2.2	15
22	Coevolution of Sites under Immune Selection Shapes Epstein-Barr Virus Population Structure. <i>Molecular Biology and Evolution</i> , 2019, 36, 2512-2521.	3.5	20
23	Direct RNA sequencing on nanopore arrays redefines the transcriptional complexity of a viral pathogen. <i>Nature Communications</i> , 2019, 10, 754.	5.8	200
24	Human cytomegalovirus haplotype reconstruction reveals high diversity due to superinfection and evidence of within-host recombination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5693-5698.	3.3	94
25	Chromatin dynamics and the transcriptional competence of HSV-1 genomes during lytic infections. <i>PLoS Pathogens</i> , 2019, 15, e1008076.	2.1	24
26	Going the Distance: Optimizing RNA-Seq Strategies for Transcriptomic Analysis of Complex Viral Genomes. <i>Journal of Virology</i> , 2019, 93, .	1.5	34
27	Genetic and phenotypic intrastrain variation in herpes simplex virus type 1 Glasgow strain 17 syn+ -derived viruses. <i>Journal of General Virology</i> , 2019, 100, 1701-1713.	1.3	13
28	A spliced latency-associated VZV transcript maps antisense to the viral transactivator gene 61. <i>Nature Communications</i> , 2018, 9, 1167.	5.8	89
29	Nuclear-cytoplasmic compartmentalization of the herpes simplex virus 1 infected cell transcriptome is co-ordinated by the viral endoribonuclease vhs and cofactors to facilitate the translation of late proteins. <i>PLoS Pathogens</i> , 2018, 14, e1007331.	2.1	31
30	RNA m ⁶ A modification enzymes shape innate responses to DNA by regulating interferon β . <i>Genes and Development</i> , 2018, 32, 1472-1484.	2.7	180
31	Use of Whole-Genome Sequencing of Adenovirus in Immunocompromised Pediatric Patients to Identify Nosocomial Transmission and Mixed-Genotype Infection. <i>Journal of Infectious Diseases</i> , 2018, 218, 1261-1271.	1.9	38
32	Molecular Aspects of Varicella-Zoster Virus Latency. <i>Viruses</i> , 2018, 10, 349.	1.5	50
33	High Viral Diversity and Mixed Infections in Cerebral Spinal Fluid From Cases of Varicella Zoster Virus Encephalitis. <i>Journal of Infectious Diseases</i> , 2018, 218, 1592-1601.	1.9	18
34	Comparative genomic, transcriptomic, and proteomic reannotation of human herpesvirus 6. <i>BMC Genomics</i> , 2018, 19, 204.	1.2	45
35	Acute Retinal Necrosis Caused by the Zoster Vaccine Virus. <i>Clinical Infectious Diseases</i> , 2017, 65, 2122-2125.	2.9	19
36	Detection of Low Frequency Multi-Drug Resistance and Novel Putative Maribavir Resistance in Immunocompromised Pediatric Patients with Cytomegalovirus. <i>Frontiers in Microbiology</i> , 2016, 7, 1317.	1.5	71

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37	In vitro system using human neurons demonstrates that varicella-zoster vaccine virus is impaired for reactivation, but not latency. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2403-12.	3.3	64
38	Deep Sequencing of Distinct Preparations of the Live Attenuated Varicella-Zoster Virus Vaccine Reveals a Conserved Core of Attenuating Single-Nucleotide Polymorphisms. Journal of Virology, 2016, 90, 8698-8704.	1.5	33
39	Islands of linkage in an ocean of pervasive recombination reveals two-speed evolution of human cytomegalovirus genomes. Virus Evolution, 2016, 2, vew017.	2.2	83
40	Viral Genome Sequencing Proves Nosocomial Transmission of Fatal Varicella. Journal of Infectious Diseases, 2016, 214, 1399-1402.	1.9	20
41	Rapid Whole-Genome Sequencing of Mycobacterium tuberculosis Isolates Directly from Clinical Samples. Journal of Clinical Microbiology, 2015, 53, 2230-2237.	1.8	242
42	Rates of Vaccine Evolution Show Strong Effects of Latency: Implications for Varicella Zoster Virus Epidemiology. Molecular Biology and Evolution, 2015, 32, 1020-1028.	3.5	32
43	Recombination of Globally Circulating Varicella-Zoster Virus. Journal of Virology, 2015, 89, 7133-7146.	1.5	68
44	Whole-genome enrichment and sequencing of Chlamydia trachomatis directly from clinical samples. BMC Infectious Diseases, 2014, 14, 591.	1.3	71
45	Deep Sequencing of Viral Genomes Provides Insight into the Evolution and Pathogenesis of Varicella Zoster Virus and Its Vaccine in Humans. Molecular Biology and Evolution, 2014, 31, 397-409.	3.5	91
46	Evolution of Cocirculating Varicella-Zoster Virus Genotypes during a Chickenpox Outbreak in Guinea-Bissau. Journal of Virology, 2014, 88, 13936-13946.	1.5	29
47	Viral population analysis and minority-variant detection using short read next-generation sequencing. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120205.	1.8	168
48	Mode of Virus Rescue Determines the Acquisition of VHS Mutations in VP22-Negative Herpes Simplex Virus 1. Journal of Virology, 2013, 87, 10389-10393.	1.5	17
49	Next-Generation Whole Genome Sequencing Identifies the Direction of Norovirus Transmission in Linked Patients. Clinical Infectious Diseases, 2013, 57, 407-414.	2.9	78
50	Chromosome and gene copy number variation allow major structural change between species and strains of <i>Leishmania</i> . Genome Research, 2011, 21, 2129-2142.	2.4	380
51	Specific Capture and Whole-Genome Sequencing of Viruses from Clinical Samples. PLoS ONE, 2011, 6, e27805.	1.1	193
52	Leishmania-Specific Surface Antigens Show Sub-Genus Sequence Variation and Immune Recognition. PLoS Neglected Tropical Diseases, 2010, 4, e829.	1.3	28
53	Comparative Expression Profiling of Leishmania: Modulation in Gene Expression between Species and in Different Host Genetic Backgrounds. PLoS Neglected Tropical Diseases, 2009, 3, e476.	1.3	86
54	Comparative genomic analysis of three Leishmania species that cause diverse human disease. Nature Genetics, 2007, 39, 839-847.	9.4	648

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55	RepSeq " A database of amino acid repeats present in lower eukaryotic pathogens. BMC Bioinformatics, 2007, 8, 122.	1.2	28