

# 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	Comparative genomic analysis of three <i>Leishmania</i> species that cause diverse human disease. <i>Nature Genetics</i> , 2007, 39, 839-847.	9.4	648
2	Chromosome and gene copy number variation allow major structural change between species and strains of <i>Leishmania</i> . <i>Genome Research</i> , 2011, 21, 2129-2142.	2.4	380
3	Rapid Whole-Genome Sequencing of <i>Mycobacterium tuberculosis</i> Isolates Directly from Clinical Samples. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2230-2237.	1.8	242
4	Direct RNA sequencing on nanopore arrays redefines the transcriptional complexity of a viral pathogen. <i>Nature Communications</i> , 2019, 10, 754.	5.8	200
5	Specific Capture and Whole-Genome Sequencing of Viruses from Clinical Samples. <i>PLoS ONE</i> , 2011, 6, e27805.	1.1	193
6	RNA m <sup>6</sup> A modification enzymes shape innate responses to DNA by regulating interferon $\beta$ . <i>Genes and Development</i> , 2018, 32, 1472-1484.	2.7	180
7	Viral population analysis and minority-variant detection using short read next-generation sequencing. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120205.	1.8	168
8	Direct RNA sequencing reveals m6A modifications on adenovirus RNA are necessary for efficient splicing. <i>Nature Communications</i> , 2020, 11, 6016.	5.8	111
9	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
10	Deep Sequencing of Viral Genomes Provides Insight into the Evolution and Pathogenesis of Varicella Zoster Virus and Its Vaccine in Humans. <i>Molecular Biology and Evolution</i> , 2014, 31, 397-409.	3.5	91
11	A spliced latency-associated VZV transcript maps antisense to the viral transactivator gene 61. <i>Nature Communications</i> , 2018, 9, 1167.	5.8	89
12	Comparative Expression Profiling of <i>Leishmania</i> : Modulation in Gene Expression between Species and in Different Host Genetic Backgrounds. <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e476.	1.3	86
13	Islands of linkage in an ocean of pervasive recombination reveals two-speed evolution of human cytomegalovirus genomes. <i>Virus Evolution</i> , 2016, 2, vew017.	2.2	83
14	Next-Generation Whole Genome Sequencing Identifies the Direction of Norovirus Transmission in Linked Patients. <i>Clinical Infectious Diseases</i> , 2013, 57, 407-414.	2.9	78
15	ICTV Virus Taxonomy Profile: Herpesviridae 2021. <i>Journal of General Virology</i> , 2021, 102, .	1.3	74
16	Whole-genome enrichment and sequencing of <i>Chlamydia trachomatis</i> directly from clinical samples. <i>BMC Infectious Diseases</i> , 2014, 14, 591.	1.3	71
17	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
18	Targeting the m <sup>6</sup> A RNA modification pathway blocks SARS-CoV-2 and HCoV-OC43 replication. <i>Genes and Development</i> , 2021, 35, 1005-1019.	2.7	70

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19	Recombination of Globally Circulating Varicella-Zoster Virus. <i>Journal of Virology</i> , 2015, 89, 7133-7146.	1.5	68
20	In vitro system using human neurons demonstrates that varicella-zoster vaccine virus is impaired for reactivation, but not latency. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2403-12.	3.3	64
21	Molecular Aspects of Varicella-Zoster Virus Latency. <i>Viruses</i> , 2018, 10, 349.	1.5	50
22	Comparative genomic, transcriptomic, and proteomic reannotation of human herpesvirus 6. <i>BMC Genomics</i> , 2018, 19, 204.	1.2	45
23	Widespread remodeling of the m <sup>6</sup> 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
24	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
25	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
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	Deep Sequencing of Distinct Preparations of the Live Attenuated Varicella-Zoster Virus Vaccine Reveals a Conserved Core of Attenuating Single-Nucleotide Polymorphisms. <i>Journal of Virology</i> , 2016, 90, 8698-8704.	1.5	33
28	Rates of Vaccine Evolution Show Strong Effects of Latency: Implications for Varicella Zoster Virus Epidemiology. <i>Molecular Biology and Evolution</i> , 2015, 32, 1020-1028.	3.5	32
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	Evolution of Cocirculating Varicella-Zoster Virus Genotypes during a Chickenpox Outbreak in Guinea-Bissau. <i>Journal of Virology</i> , 2014, 88, 13936-13946.	1.5	29
31	Decoding the Architecture of the Varicella-Zoster Virus Transcriptome. <i>MBio</i> , 2020, 11, .	1.8	29
32	RepSeq – A database of amino acid repeats present in lower eukaryotic pathogens. <i>BMC Bioinformatics</i> , 2007, 8, 122.	1.2	28
33	Leishmania-Specific Surface Antigens Show Sub-Genus Sequence Variation and Immune Recognition. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e829.	1.3	28
34	DRUMMER – rapid detection of RNA modifications through comparative nanopore sequencing. <i>Bioinformatics</i> , 2022, 38, 3113-3115.	1.8	26
35	Chromatin dynamics and the transcriptional competence of HSV-1 genomes during lytic infections. <i>PLoS Pathogens</i> , 2019, 15, e1008076.	2.1	24
36	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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37	Viral Genome Sequencing Proves Nosocomial Transmission of Fatal Varicella. <i>Journal of Infectious Diseases</i> , 2016, 214, 1399-1402.	1.9	20
38	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
39	Acute Retinal Necrosis Caused by the Zoster Vaccine Virus. <i>Clinical Infectious Diseases</i> , 2017, 65, 2122-2125.	2.9	19
40	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
41	Mode of Virus Rescue Determines the Acquisition of VHS Mutations in VP22-Negative Herpes Simplex Virus 1. <i>Journal of Virology</i> , 2013, 87, 10389-10393.	1.5	17
42	Single-cell transcriptomics identifies Gadd45b as a regulator of herpesvirus-reactivating neurons. <i>EMBO Reports</i> , 2022, 23, e53543.	2.0	16
43	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
44	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
45	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
46	Nanopore-Based Detection of Viral RNA Modifications. <i>MBio</i> , 2022, 13, e0370221.	1.8	12
47	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
48	Using Direct RNA Nanopore Sequencing to Deconvolute Viral Transcriptomes. <i>Current Protocols in Microbiology</i> , 2020, 57, e99.	6.5	11
49	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
50	The influence of human genetic variation on Epstein-Barr virus sequence diversity. <i>Scientific Reports</i> , 2021, 11, 4586.	1.6	8
51	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
52	Analysis of the reiteration regions (R1 to R5) of varicella-zoster virus. <i>Virology</i> , 2020, 546, 38-50.	1.1	7
53	The architecture of the simian varicella virus transcriptome. <i>PLoS Pathogens</i> , 2021, 17, e1010084.	2.1	4
54	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

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55	Varicella-Zoster Virusâ€™ Genetics, Molecular Evolution and Recombination. Current Topics in Microbiology and Immunology, 2021, , 1-23.	0.7	2