

John Sebastian Eden

List of Publications by Year in descending order

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Version: 2024-02-01

81
papers

6,040
citations

147801

31
h-index

85541

71
g-index

109
all docs

109
docs citations

109
times ranked

8249
citing authors

#	ARTICLE	IF	CITATIONS
1	Redefining the invertebrate RNA virosphere. Nature, 2016, 540, 539-543.	27.8	1,328
2	The evolutionary history of vertebrate RNA viruses. Nature, 2018, 556, 197-202.	27.8	596
3	Identification of Genetically Intact HIV-1 Proviruses in Specific CD4 + T Cells from Effectively Treated Participants. Cell Reports, 2017, 21, 813-822.	6.4	304
4	Revealing COVID-19 transmission in Australia by SARS-CoV-2 genome sequencing and agent-based modeling. Nature Medicine, 2020, 26, 1398-1404.	30.7	283
5	Rapid Evolution of Pandemic Noroviruses of the GII.4 Lineage. PLoS Pathogens, 2010, 6, e1000831.	4.7	252
6	Recombination within the Pandemic Norovirus GII.4 Lineage. Journal of Virology, 2013, 87, 6270-6282.	3.4	239
7	Analytical validity of nanopore sequencing for rapid SARS-CoV-2 genome analysis. Nature Communications, 2020, 11, 6272.	12.8	183
8	High-Resolution Metatranscriptomics Reveals the Ecological Dynamics of Mosquito-Associated RNA Viruses in Western Australia. Journal of Virology, 2017, 91, .	3.4	149
9	Proposal for a unified classification system and nomenclature of lagoviruses. Journal of General Virology, 2017, 98, 1658-1666.	2.9	148
10	Off-season RSV epidemics in Australia after easing of COVID-19 restrictions. Nature Communications, 2022, 13, .	12.8	135
11	An emergent clade of SARS-CoV-2 linked to returned travellers from Iran. Virus Evolution, 2020, 6, veaa027.	4.9	119
12	Extensive Diversity of RNA Viruses in Australian Ticks. Journal of Virology, 2019, 93, .	3.4	116
13	The emergence and evolution of the novel epidemic norovirus GII.4 variant Sydney 2012. Virology, 2014, 450-451, 106-113.	2.4	111
14	Contribution of Intra- and Interhost Dynamics to Norovirus Evolution. Journal of Virology, 2012, 86, 3219-3229.	3.4	109
15	Emergence and Adaptation of a Novel Highly Pathogenic H7N9 Influenza Virus in Birds and Humans from a 2013 Human-Infecting Low-Pathogenic Ancestor. Journal of Virology, 2018, 92, .	3.4	99
16	Norovirus GII.4 variant 2006b caused epidemics of acute gastroenteritis in Australia during 2007 and 2008. Journal of Clinical Virology, 2010, 49, 265-271.	3.1	77
17	Virus-virus interactions and host ecology are associated with <sc>RNA</sc> virome structure in wild birds. Molecular Ecology, 2018, 27, 5263-5278.	3.9	77
18	Meta-transcriptomics reveals a diverse antibiotic resistance gene pool in avian microbiomes. BMC Biology, 2019, 17, 31.	3.8	76

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19	A Divergent Hepatitis D-Like Agent in Birds. <i>Viruses</i> , 2018, 10, 720.	3.3	69
20	The paradox of HBV evolution as revealed from a 16th century mummy. <i>PLoS Pathogens</i> , 2018, 14, e1006750.	4.7	66
21	Meta-Transcriptomic Comparison of the RNA Viromes of the Mosquito Vectors <i>Culex pipiens</i> and <i>Culex torrentium</i> in Northern Europe. <i>Viruses</i> , 2019, 11, 1033.	3.3	64
22	Novel hepatitis D-like agents in vertebrates and invertebrates. <i>Virus Evolution</i> , 2019, 5, vez021.	4.9	63
23	No detectable effect of <i>Wolbachia w</i> Mel on the prevalence and abundance of the RNA virome of <i>Drosophila melanogaster</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20181165.	2.6	53
24	Novel RNA viruses associated with <i>Plasmodium vivax</i> in human malaria and <i>Leucocytozoon</i> parasites in avian disease. <i>PLoS Pathogens</i> , 2019, 15, e1008216.	4.7	50
25	<i>Francisella tularensis</i> ssp. <i>holarctica</i> in Ringtail Possums, Australia. <i>Emerging Infectious Diseases</i> , 2017, 23, 1198-1201.	4.3	49
26	Virological Sampling of Inaccessible Wildlife with Drones. <i>Viruses</i> , 2018, 10, 300.	3.3	49
27	Identification of SARS-CoV-2 Nucleocapsid and Spike T-Cell Epitopes for Assessing T-Cell Immunity. <i>Journal of Virology</i> , 2021, 95, .	3.4	48
28	Adaptive evolution of bat dipeptidyl peptidase 4 (dpp4): implications for the origin and emergence of Middle East respiratory syndrome coronavirus. <i>Virology Journal</i> , 2013, 10, 304.	3.4	47
29	Interpret with caution: An evaluation of the commercial AusDiagnostics versus in-house developed assays for the detection of SARS-CoV-2 virus. <i>Journal of Clinical Virology</i> , 2020, 127, 104374.	3.1	43
30	Nonnucleoside Inhibitors of Norovirus RNA Polymerase: Scaffolds for Rational Drug Design. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 3115-3123.	3.2	41
31	Emerging recombinant noroviruses identified by clinical and waste water screening. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-14.	6.5	41
32	Benign Rabbit Caliciviruses Exhibit Evolutionary Dynamics Similar to Those of Their Virulent Relatives. <i>Journal of Virology</i> , 2016, 90, 9317-9329.	3.4	36
33	Comparative Phylodynamics of Rabbit Hemorrhagic Disease Virus in Australia and New Zealand. <i>Journal of Virology</i> , 2015, 89, 9548-9558.	3.4	32
34	High levels of genetically intact HIV in HLA-DR+ memory T cells indicates their value for reservoir studies. <i>Aids</i> , 2020, 34, 659-668.	2.2	32
35	A Fluorescence-Based High-Throughput Screen to Identify Small Compound Inhibitors of the Genotype 3a Hepatitis C Virus RNA Polymerase. <i>Journal of Biomolecular Screening</i> , 2013, 18, 1027-1034.	2.6	28
36	Evolution of Human Respiratory Syncytial Virus (RSV) over Multiple Seasons in New South Wales, Australia. <i>Viruses</i> , 2018, 10, 476.	3.3	28

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37	A Multi-Site Study of Norovirus Molecular Epidemiology in Australia and New Zealand, 2013-2014. PLoS ONE, 2016, 11, e0145254.	2.5	27
38	Identification of diverse arthropod associated viruses in native Australian fleas. Virology, 2019, 535, 189-199.	2.4	24
39	Norovirus RNA-Dependent RNA Polymerase Is Phosphorylated by an Important Survival Kinase, Akt. Journal of Virology, 2011, 85, 10894-10898.	3.4	22
40	Genomic and phenotypic characterization of myxoma virus from Great Britain reveals multiple evolutionary pathways distinct from those in Australia. PLoS Pathogens, 2017, 13, e1006252.	4.7	22
41	Persistent infections in immunocompromised hosts are rarely sources of new pathogen variants. Virus Evolution, 2017, 3, vex018.	4.9	21
42	Novel hepaci- and pegi-like viruses in native Australian wildlife and non-human primates. Virus Evolution, 2020, 6, veaa064.	4.9	21
43	Opportunistic sampling of wild native and invasive birds reveals a rich diversity of adenoviruses in Australia. Virus Evolution, 2020, 6, veaa024.	4.9	21
44	Metatranscriptomic Analysis of Virus Diversity in Urban Wild Birds with Paretic Disease. Journal of Virology, 2020, 94, .	3.4	21
45	Metagenomic Identification of Viral Sequences in Laboratory Reagents. Viruses, 2021, 13, 2122.	3.3	21
46	Metatranscriptomics as a tool to identify fungal species and subspecies in mixed communities – a proof of concept under laboratory conditions. IMA Fungus, 2019, 10, 12.	3.8	20
47	Molecular epidemiology of norovirus in Singapore, 2004-2011. Journal of Medical Virology, 2013, 85, 1842-1851.	5.0	19
48	Cross-validation to select Bayesian hierarchical models in phylogenetics. BMC Evolutionary Biology, 2016, 16, 115.	3.2	19
49	A Divergent Articulavirus in an Australian Gecko Identified Using Meta-Transcriptomics and Protein Structure Comparisons. Viruses, 2020, 12, 613.	3.3	19
50	Metagenomic discovery and co-infection of diverse wobbly possum disease viruses and a novel hepacivirus in Australian brushtail possums. One Health Outlook, 2019, 1, 5.	3.4	18
51	Plasma-Derived HIV-1 Virions Contain Considerable Levels of Defective Genomes. Journal of Virology, 2022, 96, jvi0201121.	3.4	18
52	Resolving the Origin of Rabbit Hemorrhagic Disease Virus: Insights from an Investigation of the Viral Stocks Released in Australia. Journal of Virology, 2015, 89, 12217-12220.	3.4	17
53	Punctuated Evolution of Myxoma Virus: Rapid and Disjunct Evolution of a Recent Viral Lineage in Australia. Journal of Virology, 2019, 93, .	3.4	17
54	Genetic diversity of SARS-CoV-2 and clinical, epidemiological characteristics of COVID-19 patients in Hanoi, Vietnam. PLoS ONE, 2020, 15, e0242537.	2.5	17

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55	Diversity and Evolution of Novel Invertebrate DNA Viruses Revealed by Meta-Transcriptomics. <i>Viruses</i> , 2019, 11, 1092.	3.3	16
56	Meta-Transcriptomic Identification of Divergent Amnoonviridae in Fish. <i>Viruses</i> , 2020, 12, 1254.	3.3	16
57	Emergent multisystemic <i>Enterococcus</i> infection threatens endangered Christmas Island reptile populations. <i>PLoS ONE</i> , 2017, 12, e0181240.	2.5	16
58	Extensive characterization of HIV-1 reservoirs reveals links to plasma viremia before and during analytical treatment interruption. <i>Cell Reports</i> , 2022, 39, 110739.	6.4	15
59	Complete Genome of the Human Norovirus GIV.1 Strain Lake Macquarie Virus. <i>Journal of Virology</i> , 2012, 86, 10251-10252.	3.4	14
60	A complex mosaic of enteroviruses shapes community-acquired hand, foot and mouth disease transmission and evolution within a single hospital. <i>Virus Evolution</i> , 2018, 4, vey020.	4.9	14
61	A survey of a mixed species aviary provides new insights into the pathogenicity, diversity, evolution, host range, and distribution of psittacine and passerine adenoviruses. <i>Avian Pathology</i> , 2019, 48, 437-443.	2.0	14
62	Meta-Transcriptomic Discovery of a Divergent Circovirus and a Chaphamaparvovirus in Captive Reptiles with Proliferative Respiratory Syndrome. <i>Viruses</i> , 2020, 12, 1073.	3.3	14
63	Meta-transcriptomic identification of <i>Trypanosoma</i> spp. in native wildlife species from Australia. <i>Parasites and Vectors</i> , 2020, 13, 447.	2.5	14
64	Amplification of Near Full-length HIV-1 Proviruses for Next-Generation Sequencing. <i>Journal of Visualized Experiments</i> , 2018, , .	0.3	13
65	Viral Discovery in the Invasive Australian Cane Toad (<i>Rhinella marina</i>) Using Metatranscriptomic and Genomic Approaches. <i>Journal of Virology</i> , 2018, 92, .	3.4	13
66	Human pegivirus in brain tissue of a patient with encephalitis. <i>Diagnostic Microbiology and Infectious Disease</i> , 2020, 96, 114898.	1.8	11
67	The spatial-temporal dynamics of respiratory syncytial virus infections across the eastâ€“west coasts of Australia during 2016â€“17. <i>Virus Evolution</i> , 2021, 7, veab068.	4.9	11
68	Potent monoclonal antibodyâ€“mediated neutralization of a divergent Hendra virus variant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	11
69	New insights into Sauropsid Papillomaviridae evolution and epizootiology: discovery of two novel papillomaviruses in native and invasive Island geckos. <i>Virus Evolution</i> , 2019, 5, vez051.	4.9	10
70	An Amplicon-Based Approach for the Whole-Genome Sequencing of Human Metapneumovirus. <i>Viruses</i> , 2021, 13, 499.	3.3	10
71	Reverse Engineering Field Isolates of Myxoma Virus Demonstrates that Some Gene Disruptions or Losses of Function Do Not Explain Virulence Changes Observed in the Field. <i>Journal of Virology</i> , 2017, 91, .	3.4	9
72	Cellular Activation, Differentiation, and Proliferation Influence the Dynamics of Genetically Intact Proviruses Over Time. <i>Journal of Infectious Diseases</i> , 2022, 225, 1168-1178.	4.0	9

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73	Longitudinal Sequence and Functional Evolution within Glycoprotein E2 in Hepatitis C Virus Genotype 3a Infection. PLoS ONE, 2015, 10, e0126397.	2.5	6
74	The transmission dynamics and diversity of human metapneumovirus in Peru. Influenza and Other Respiratory Viruses, 2018, 12, 508-513.	3.4	6
75	Genomic Insights Into the Pathogenicity of a Novel Biofilm-Forming Enterococcus sp. Bacteria (Enterococcus lacertideformus) Identified in Reptiles. Frontiers in Microbiology, 2021, 12, 635208.	3.5	6
76	Hepatitis C Virus Genotype 8 Infectionâ€™Successful Treatment With Sofosbuvir/Velpatasvir. Journal of Infectious Diseases, 2019, 220, 720-722.	4.0	2
77	Genome sequencing and its use in public health responses to COVID-19. Microbiology Australia, 2021, 42, 44.	0.4	1
78	Response. Journal of Clinical Virology, 2020, 130, 104484.	3.1	0
79	Title is missing!. , 2019, 15, e1008216.		0
80	Title is missing!. , 2019, 15, e1008216.		0
81	Title is missing!. , 2019, 15, e1008216.		0