

John Sebastian Eden

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

94
papers

3,790
citations

29
h-index

60
g-index

109
ext. papers

5,144
ext. citations

8.1
avg, IF

5.36
L-index

#	Paper	IF	Citations
94	Plasma-Derived HIV-1 Virions Contain Considerable Levels of Defective Genomes.. <i>Journal of Virology</i> , 2022 , jvi0201121	6.6	1
93	Extensive characterization of HIV-1 reservoirs reveals links to plasma viremia before and during analytical treatment interruption.. <i>Cell Reports</i> , 2022 , 39, 110739	10.6	0
92	Metagenomic Identification of Viral Sequences in Laboratory Reagents. <i>Viruses</i> , 2021 , 13,	6.2	2
91	Genomic Insights Into the Pathogenicity of a Novel Biofilm-Forming sp. Bacteria () Identified in Reptiles. <i>Frontiers in Microbiology</i> , 2021 , 12, 635208	5.7	1
90	An Amplicon-Based Approach for the Whole-Genome Sequencing of Human Metapneumovirus. <i>Viruses</i> , 2021 , 13,	6.2	3
89	Cellular activation, differentiation and proliferation influence the dynamics of genetically-intact proviruses over time. <i>Journal of Infectious Diseases</i> , 2021 ,	7	2
88	The spatial-temporal dynamics of respiratory syncytial virus infections across the east-west coasts of Australia during 2016-17. <i>Virus Evolution</i> , 2021 , 7, veab068	3.7	1
87	Genome sequencing and its use in public health responses to COVID-19. <i>Microbiology Australia</i> , 2021 , 42, 44	0.8	1
86	Identification of SARS-CoV-2 Nucleocapsid and Spike T-Cell Epitopes for Assessing T-Cell Immunity. <i>Journal of Virology</i> , 2021 , 95,	6.6	18
85	Analytical validity of nanopore sequencing for rapid SARS-CoV-2 genome analysis. <i>Nature Communications</i> , 2020 , 11, 6272	17.4	70
84	Meta-Transcriptomic Identification of Divergent in Fish. <i>Viruses</i> , 2020 , 12,	6.2	2
83	Opportunistic sampling of wild native and invasive birds reveals a rich diversity of adenoviruses in Australia. <i>Virus Evolution</i> , 2020 , 6, veaa024	3.7	8
82	A Divergent in an Australian Gecko Identified Using Meta-Transcriptomics and Protein Structure Comparisons. <i>Viruses</i> , 2020 , 12,	6.2	3
81	Revealing COVID-19 transmission in Australia by SARS-CoV-2 genome sequencing and agent-based modeling. <i>Nature Medicine</i> , 2020 , 26, 1398-1404	50.5	174
80	Metatranscriptomic Analysis of Virus Diversity in Urban Wild Birds with Parectic Disease. <i>Journal of Virology</i> , 2020 , 94,	6.6	11
79	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	14.5	30
78	Genetic diversity of SARS-CoV-2 and clinical, epidemiological characteristics of COVID-19 patients in Hanoi, Vietnam. <i>PLoS ONE</i> , 2020 , 15, e0242537	3.7	12

77	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	3.5	16
76	Human pegivirus in brain tissue of a patient with encephalitis. <i>Diagnostic Microbiology and Infectious Disease</i> , 2020 , 96, 114898	2.9	6
75	Novel hepaci- and pegi-like viruses in native Australian wildlife and non-human primates. <i>Virus Evolution</i> , 2020 , 6, veaa064	3.7	6
74	Meta-Transcriptomic Discovery of a Divergent Circovirus and a Chaphamaparvovirus in Captive Reptiles with Proliferative Respiratory Syndrome. <i>Viruses</i> , 2020 , 12,	6.2	8
73	Response. <i>Journal of Clinical Virology</i> , 2020 , 130, 104484	14.5	
72	Meta-transcriptomic identification of Trypanosoma spp. in native wildlife species from Australia. <i>Parasites and Vectors</i> , 2020 , 13, 447	4	8
71	An emergent clade of SARS-CoV-2 linked to returned travellers from Iran. <i>Virus Evolution</i> , 2020 , 6, veaa037	3.7	93
70	Hepatitis C Virus Genotype 8 Infection-Successful Treatment With Sofosbuvir/Velpatasvir. <i>Journal of Infectious Diseases</i> , 2019 , 220, 720-722	7	1
69	Meta-transcriptomics reveals a diverse antibiotic resistance gene pool in avian microbiomes. <i>BMC Biology</i> , 2019 , 17, 31	7.3	40
68	Punctuated Evolution of Myxoma Virus: Rapid and Disjunct Evolution of a Recent Viral Lineage in Australia. <i>Journal of Virology</i> , 2019 , 93,	6.6	7
67	Metatranscriptomics as a tool to identify fungal species and subspecies in mixed communities - a proof of concept under laboratory conditions. <i>IMA Fungus</i> , 2019 , 10, 12	6.8	12
66	Identification of diverse arthropod associated viruses in native Australian fleas. <i>Virology</i> , 2019 , 535, 189-199	3.09	13
65	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	2.4	9
64	Novel hepatitis D-like agents in vertebrates and invertebrates. <i>Virus Evolution</i> , 2019 , 5, vez021	3.7	34
63	New insights into Sauropsid evolution and epizootiology: discovery of two novel papillomaviruses in native and invasive Island geckos. <i>Virus Evolution</i> , 2019 , 5, vez051	3.7	3
62	Meta-Transcriptomic Comparison of the RNA Viromes of the Mosquito Vectors and in Northern Europe. <i>Viruses</i> , 2019 , 11,	6.2	33
61	Diversity and Evolution of Novel Invertebrate DNA Viruses Revealed by Meta-Transcriptomics. <i>Viruses</i> , 2019 , 11,	6.2	4
60	Novel RNA viruses associated with Plasmodium vivax in human malaria and Leucocytozoon parasites in avian disease. <i>PLoS Pathogens</i> , 2019 , 15, e1008216	7.6	31

59	Metagenomic discovery and co-infection of diverse wobbly possum disease viruses and a novel hepatitis virus in Australian brushtail possums. <i>One Health Outlook</i> , 2019 , 1, 5	5	9
58	Extensive Diversity of RNA Viruses in Australian Ticks. <i>Journal of Virology</i> , 2019 , 93,	6.6	63
57	Novel RNA viruses associated with Plasmodium vivax in human malaria and Leucocytozoon parasites in avian disease 2019 , 15, e1008216		
56	Novel RNA viruses associated with Plasmodium vivax in human malaria and Leucocytozoon parasites in avian disease 2019 , 15, e1008216		
55	Novel RNA viruses associated with Plasmodium vivax in human malaria and Leucocytozoon parasites in avian disease 2019 , 15, e1008216		
54	The evolutionary history of vertebrate RNA viruses. <i>Nature</i> , 2018 , 556, 197-202	50.4	354
53	The transmission dynamics and diversity of human metapneumovirus in Peru. <i>Influenza and Other Respiratory Viruses</i> , 2018 , 12, 508-513	5.6	4
52	Emergence and Adaptation of a Novel Highly Pathogenic H7N9 Influenza Virus in Birds and Humans from a 2013 Human-Infecting Low-Pathogenic Ancestor. <i>Journal of Virology</i> , 2018 , 92,	6.6	72
51	No detectable effect of Mel on the prevalence and abundance of the RNA virome of. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018 , 285,	4.4	37
50	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	3.7	9
49	Virological Sampling of Inaccessible Wildlife with Drones. <i>Viruses</i> , 2018 , 10,	6.2	31
48	Emerging recombinant noroviruses identified by clinical and waste water screening. <i>Emerging Microbes and Infections</i> , 2018 , 7, 50	18.9	31
47	Viral Discovery in the Invasive Australian Cane Toad (<i>Rhinella marina</i>) Using Metatranscriptomic and Genomic Approaches. <i>Journal of Virology</i> , 2018 , 92,	6.6	7
46	The paradox of HBV evolution as revealed from a 16th century mummy. <i>PLoS Pathogens</i> , 2018 , 14, e1006750	6.6	53
45	Amplification of Near Full-length HIV-1 Proviruses for Next-Generation Sequencing. <i>Journal of Visualized Experiments</i> , 2018 ,	1.6	9
44	A Divergent Hepatitis D-Like Agent in Birds. <i>Viruses</i> , 2018 , 10,	6.2	41
43	Virus-virus interactions and host ecology are associated with RNA virome structure in wild birds. <i>Molecular Ecology</i> , 2018 , 27, 5263-5278	5.7	49
42	Evolution of Human Respiratory Syncytial Virus (RSV) over Multiple Seasons in New South Wales, Australia. <i>Viruses</i> , 2018 , 10,	6.2	18

41	Identification of Genetically Intact HIV-1 Proviruses in Specific CD4 T Cells from Effectively Treated Participants. <i>Cell Reports</i> , 2017 , 21, 813-822	10.6	187
40	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,	6.6	5
39	<i>Francisella tularensis</i> ssp. <i>holarctica</i> in Ringtail Possums, Australia. <i>Emerging Infectious Diseases</i> , 2017 , 23, 1198-1201	10.2	28
38	Persistent infections in immunocompromised hosts are rarely sources of new pathogen variants. <i>Virus Evolution</i> , 2017 , 3, vex018	3.7	14
37	High-Resolution Metatranscriptomics Reveals the Ecological Dynamics of Mosquito-Associated RNA Viruses in Western Australia. <i>Journal of Virology</i> , 2017 , 91,	6.6	104
36	Emergent multisystemic <i>Enterococcus</i> infection threatens endangered Christmas Island reptile populations. <i>PLoS ONE</i> , 2017 , 12, e0181240	3.7	9
35	Genomic and phenotypic characterization of myxoma virus from Great Britain reveals multiple evolutionary pathways distinct from those in Australia. <i>PLoS Pathogens</i> , 2017 , 13, e1006252	7.6	14
34	Proposal for a unified classification system and nomenclature of lagoviruses. <i>Journal of General Virology</i> , 2017 , 98, 1658-1666	4.9	91
33	Benign Rabbit Caliciviruses Exhibit Evolutionary Dynamics Similar to Those of Their Virulent Relatives. <i>Journal of Virology</i> , 2016 , 90, 9317-29	6.6	26
32	Redefining the invertebrate RNA virosphere. <i>Nature</i> , 2016 , 540, 539-543	50.4	821
31	A Multi-Site Study of Norovirus Molecular Epidemiology in Australia and New Zealand, 2013-2014. <i>PLoS ONE</i> , 2016 , 11, e0145254	3.7	21
30	Cross-validation to select Bayesian hierarchical models in phylogenetics. <i>BMC Evolutionary Biology</i> , 2016 , 16, 115	3	12
29	Comparative Phylodynamics of Rabbit Hemorrhagic Disease Virus in Australia and New Zealand. <i>Journal of Virology</i> , 2015 , 89, 9548-58	6.6	27
28	Resolving the Origin of Rabbit Hemorrhagic Disease Virus: Insights from an Investigation of the Viral Stocks Released in Australia. <i>Journal of Virology</i> , 2015 , 89, 12217-20	6.6	13
27	Longitudinal Sequence and Functional Evolution within Glycoprotein E2 in Hepatitis C Virus Genotype 3a Infection. <i>PLoS ONE</i> , 2015 , 10, e0126397	3.7	5
26	Nonnucleoside inhibitors of norovirus RNA polymerase: scaffolds for rational drug design. <i>Antimicrobial Agents and Chemotherapy</i> , 2014 , 58, 3115-23	5.9	37
25	The emergence and evolution of the novel epidemic norovirus GII.4 variant Sydney 2012. <i>Virology</i> , 2014 , 450-451, 106-13	3.6	99
24	Molecular epidemiology of norovirus in Singapore, 2004-2011. <i>Journal of Medical Virology</i> , 2013 , 85, 1842-51	5.1	18

23	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, 1027-34		26
22	Recombination within the pandemic norovirus GII.4 lineage. <i>Journal of Virology</i> , 2013 , 87, 6270-82	6.6	209
21	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	6.1	38
20	Contribution of intra- and interhost dynamics to norovirus evolution. <i>Journal of Virology</i> , 2012 , 86, 3219-23	6.6	93
19	Complete genome of the human norovirus GIV.1 strain Lake Macquarie virus. <i>Journal of Virology</i> , 2012 , 86, 10251-2	6.6	12
18	Norovirus RNA-dependent RNA polymerase is phosphorylated by an important survival kinase, Akt. <i>Journal of Virology</i> , 2011 , 85, 10894-8	6.6	18
17	Rapid evolution of pandemic noroviruses of the GII.4 lineage. <i>PLoS Pathogens</i> , 2010 , 6, e1000831	7.6	228
16	Norovirus GII.4 variant 2006b caused epidemics of acute gastroenteritis in Australia during 2007 and 2008. <i>Journal of Clinical Virology</i> , 2010 , 49, 265-71	14.5	69
15	SARS-CoV-2 Genome Sequencing Using Long Pooled Amplicons on Illumina Platforms v1		8
14	Meta-transcriptomic analysis of virus diversity in urban wild birds with peritric disease		1
13	Metatranscriptomics as a tool to identify fungal species and subspecies in mixed communities		1
12	An emergent clade of SARS-CoV-2 linked to returned travellers from Iran		31
11	Revealing COVID-19 Transmission by SARS-CoV-2 Genome Sequencing and Agent Based Modelling		26
10	Metagenomic identification of diverse animal hepaciviruses and pegiviruses		1
9	Analytical validity of nanopore sequencing for rapid SARS-CoV-2 genome analysis		2
8	The spatial-temporal dynamics of respiratory syncytial virus infections across the east-west coasts of Australia during 2016-17		1
7	A divergent hepatitis D-like agent in birds		1
6	High levels of antibiotic resistance gene expression among birds living in a wastewater treatment plant		2

- 5 Punctuated evolution of myxoma virus: rapid and disjunct evolution of a recent viral lineage in Australia 1
- 4 Matryoshka RNA virus 1: a novel RNA virus associated with Plasmodium parasites in human malaria 1
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- 2 Novel Hendra virus variant detected by sentinel surveillance of Australian horses 4
- 1 Off-season RSV epidemics in Australia after easing of COVID-19 restrictions 4