

Donald Seto

List of Publications by Year in descending order

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39
papers

1,839
citations

304743

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289244

40
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docs citations

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times ranked

1499
citing authors

#	ARTICLE	IF	CITATIONS
1	Evidence of Molecular Evolution Driven by Recombination Events Influencing Tropism in a Novel Human Adenovirus that Causes Epidemic Keratoconjunctivitis. <i>PLoS ONE</i> , 2009, 4, e5635.	2.5	201
2	Computational Analysis Identifies Human Adenovirus Type 55 as a Re-Emergent Acute Respiratory Disease Pathogen. <i>Journal of Clinical Microbiology</i> , 2010, 48, 991-993.	3.9	198
3	Using the Whole-Genome Sequence To Characterize and Name Human Adenoviruses. <i>Journal of Virology</i> , 2011, 85, 5701-5702.	3.4	163
4	Tracking SARS-CoV-2 Omicron diverse spike gene mutations identifies multiple inter-variant recombination events. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 138.	17.1	140
5	Computational analysis and identification of an emergent human adenovirus pathogen implicated in a respiratory fatality. <i>Virology</i> , 2011, 409, 141-147.	2.4	135
6	V367F Mutation in SARS-CoV-2 Spike RBD Emerging during the Early Transmission Phase Enhances Viral Infectivity through Increased Human ACE2 Receptor Binding Affinity. <i>Journal of Virology</i> , 2021, 95, e0061721.	3.4	90
7	Re-emergent Human Adenovirus Genome Type 7d Caused an Acute Respiratory Disease Outbreak in Southern China After a Twenty-one Year Absence. <i>Scientific Reports</i> , 2014, 4, 7365.	3.3	73
8	Computational analysis of four human adenovirus type 4 genomes reveals molecular evolution through two interspecies recombination events. <i>Virology</i> , 2013, 443, 197-207.	2.4	66
9	Genomic and Bioinformatics Analysis of HAdV-4, a Human Adenovirus Causing Acute Respiratory Disease: Implications for Gene Therapy and Vaccine Vector Development. <i>Journal of Virology</i> , 2005, 79, 2559-2572.	3.4	57
10	Integration of genomic and proteomic analyses in the classification of the Siphoviridae family. <i>Virology</i> , 2015, 477, 144-154.	2.4	52
11	Overreliance on the Hexon Gene, Leading to Misclassification of Human Adenoviruses. <i>Journal of Virology</i> , 2012, 86, 4693-4695.	3.4	49
12	Predicting the Next Eye Pathogen: Analysis of a Novel Adenovirus. <i>MBio</i> , 2013, 4, e00595-12.	4.1	44
13	Genomic characterization of human adenovirus 36, a putative obesity agent. <i>Virus Research</i> , 2010, 149, 152-161.	2.2	42
14	A Survey of Recent Adenoviral Respiratory Pathogens in Hong Kong Reveals Emergent and Recombinant Human Adenovirus Type 4 (HAdV-E4) Circulating in Civilian Populations. <i>Viruses</i> , 2019, 11, 129.	3.3	40
15	Genomic analysis of a large set of currently and historically important human adenovirus pathogens. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-22.	6.5	39
16	Are adenoviruses zoonotic? A systematic review of the evidence. <i>Emerging Microbes and Infections</i> , 2019, 8, 1679-1687.	6.5	39
17	Characterizing, typing, and naming human adenovirus type 55 in the era of whole genome data. <i>Journal of Clinical Virology</i> , 2013, 58, 741-742.	3.1	36
18	Adenoviromics: Mining the Human Adenovirus Species D Genome. <i>Frontiers in Microbiology</i> , 2018, 9, 2178.	3.5	34

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19	Genomic and Bioinformatics Analyses of HAdV-4vac and HAdV-7vac, Two Human Adenovirus (HAdV) Strains That Constituted Original Prophylaxis against HAdV-Related Acute Respiratory Disease, a Reemerging Epidemic Disease. <i>Journal of Clinical Microbiology</i> , 2005, 43, 3083-3094.	3.9	33
20	Genomic foundations of evolution and ocular pathogenesis in human adenovirus species D. <i>FEBS Letters</i> , 2019, 593, 3583-3608.	2.8	33
21	A Zoonotic Adenoviral Human Pathogen Emerged through Genomic Recombination among Human and Nonhuman Simian Hosts. <i>Journal of Virology</i> , 2019, 93, .	3.4	31
22	Recombination of the epsilon determinant and corneal tropism: Human adenovirus species D types 15, 29, 56, and 69. <i>Virology</i> , 2015, 485, 452-459.	2.4	25
23	Applying Genomic and Bioinformatic Resources to Human Adenovirus Genomes for Use in Vaccine Development and for Applications in Vector Development for Gene Delivery. <i>Viruses</i> , 2010, 2, 1-26.	3.3	24
24	Simian adenovirus type 35 has a recombinant genome comprising human and simian adenovirus sequences, which predicts its potential emergence as a human respiratory pathogen. <i>Virology</i> , 2013, 447, 265-273.	2.4	24
25	Comparative genomic analysis of two emergent human adenovirus type 14 respiratory pathogen isolates in China reveals similar yet divergent genomes. <i>Emerging Microbes and Infections</i> , 2017, 6, 1-12.	6.5	21
26	Genomic and bioinformatics analyses of HAdV-14p, reference strain of a re-emerging respiratory pathogen and analysis of B1/B2. <i>Virus Research</i> , 2009, 143, 94-105.	2.2	18
27	Selection Pressure in the Human Adenovirus Fiber Knob Drives Cell Specificity in Epidemic Keratoconjunctivitis. <i>Journal of Virology</i> , 2016, 90, 9598-9607.	3.4	18
28	The 5'UTR in human adenoviruses: leader diversity in late gene expression. <i>Scientific Reports</i> , 2017, 7, 618.	3.3	13
29	Adenoviral Infections in Singapore: Should New Antiviral Therapies and Vaccines Be Adopted?. <i>Journal of Infectious Diseases</i> , 2019, 221, 566-577.	4.0	13
30	Construction and Characterization of a Novel Recombinant Attenuated and Replication-Deficient Candidate Human Adenovirus Type 3 Vaccine: Adenovirus Vaccine Within an Adenovirus Vector. <i>Virologica Sinica</i> , 2021, 36, 354-364.	3.0	12
31	Bacterial RecA Protein Promotes Adenoviral Recombination during <i>In Vitro</i> Infection. <i>MSphere</i> , 2018, 3, .	2.9	11
32	Emergence and characterization of a putative novel human adenovirus recombinant HAdV-C104 causing pneumonia in Southern China. <i>Virus Evolution</i> , 2021, 7, veab018.	4.9	11
33	Pitfalls of restriction enzyme analysis in identifying, characterizing, typing, and naming viral pathogens in the era of whole genome data, as illustrated by HAdV type 55. <i>Virologica Sinica</i> , 2016, 31, 448-453.	3.0	10
34	Genomics-based re-examination of the taxonomy and phylogeny of human and simian Mastadenoviruses: an evolving whole genomes approach, revealing putative zoonosis, anthroponosis, and amphizoonosis. <i>Cladistics</i> , 2020, 36, 358-373.	3.3	10
35	Characterization of Influenza A and B Viruses Circulating in Southern China During the 2017-2018 Season. <i>Frontiers in Microbiology</i> , 2020, 11, 1079.	3.5	10
36	Viral Genomics and Bioinformatics. <i>Viruses</i> , 2010, 2, 2587-2593.	3.3	6

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37	Genome Sequence of a Cynomolgus Macaque Adenovirus (CynAdV-1) Isolate from a Primate Colony in the United Kingdom. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
38	Divergent Evolution of E1A CR3 in Human Adenovirus Species D. <i>Viruses</i> , 2019, 11, 143.	3.3	3
39	In silico bioinformatic tools for determining core genes from sets of genomes. <i>Drug Development Research</i> , 2011, 72, 147-152.	2.9	0