

Tavis Anderson

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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.

72 papers	1,949 citations	27 h-index	42 g-index
83 ext. papers	2,546 ext. citations	4.6 avg, IF	4.73 L-index

#	Paper	IF	Citations
72	Influenza Research Database: An integrated bioinformatics resource for influenza virus research. <i>Nucleic Acids Research</i> , 2017 , 45, D466-D474	20.1	174
71	The global antigenic diversity of swine influenza A viruses. <i>ELife</i> , 2016 , 5, e12217	8.9	106
70	Fine-scale variation in vector host use and force of infection drive localized patterns of West Nile virus transmission. <i>PLoS ONE</i> , 2011 , 6, e23767	3.7	94
69	Population dynamics of cocirculating swine influenza A viruses in the United States from 2009 to 2012. <i>Influenza and Other Respiratory Viruses</i> , 2013 , 7 Suppl 4, 42-51	5.6	90
68	Culex flavivirus and West Nile virus mosquito coinfection and positive ecological association in Chicago, United States. <i>Vector-Borne and Zoonotic Diseases</i> , 2011 , 11, 1099-105	2.4	90
67	A Phylogeny-Based Global Nomenclature System and Automated Annotation Tool for H1 Hemagglutinin Genes from Swine Influenza A Viruses. <i>MSphere</i> , 2016 , 1,	5	84
66	Wild birds and urban ecology of ticks and tick-borne pathogens, Chicago, Illinois, USA, 2005-2010. <i>Emerging Infectious Diseases</i> , 2012 , 18, 1589-95	10.2	71
65	Efficacy in pigs of inactivated and live attenuated influenza virus vaccines against infection and transmission of an emerging H3N2 similar to the 2011-2012 H3N2v. <i>Journal of Virology</i> , 2013 , 87, 9895-903	6.6	68
64	Substitutions near the hemagglutinin receptor-binding site determine the antigenic evolution of influenza A H3N2 viruses in U.S. swine. <i>Journal of Virology</i> , 2014 , 88, 4752-63	6.6	66
63	Genotype patterns of contemporary reassorted H3N2 virus in US swine. <i>Journal of General Virology</i> , 2013 , 94, 1236-1241	4.9	62
62	Influenza A virus vaccines for swine. <i>Veterinary Microbiology</i> , 2017 , 206, 35-44	3.3	58
61	Novel Reassortant Human-Like H3N2 and H3N1 Influenza A Viruses Detected in Pigs Are Virulent and Antigenically Distinct from Swine Viruses Endemic to the United States. <i>Journal of Virology</i> , 2015 , 89, 11213-22	6.6	57
60	Influenza A(H3N2) Virus in Swine at Agricultural Fairs and Transmission to Humans, Michigan and Ohio, USA, 2016. <i>Emerging Infectious Diseases</i> , 2017 , 23, 1551-1555	10.2	50
59	Characterization of co-circulating swine influenza A viruses in North America and the identification of a novel H1 genetic clade with antigenic significance. <i>Virus Research</i> , 2015 , 201, 24-31	6.4	45
58	Genotype patterns of contemporary reassorted H3N2 virus in US swine. <i>Journal of General Virology</i> , 2013 , 94, 1236-41	4.9	45
57	Antigenic and genetic evolution of contemporary swine H1 influenza viruses in the United States. <i>Virology</i> , 2018 , 518, 45-54	3.6	41
56	Porcine reproductive and respiratory disease virus: Evolution and recombination yields distinct ORF5 RFLP 1-7-4 viruses with individual pathogenicity. <i>Virology</i> , 2018 , 513, 168-179	3.6	38

55	Dispersal of adult culex mosquitoes in an urban west nile virus hotspot: a mark-capture study incorporating stable isotope enrichment of natural larval habitats. <i>PLoS Neglected Tropical Diseases</i> , 2014 , 8, e2768	4.8	37
54	The genomic evolution of H1 influenza A viruses from swine detected in the United States between 2009 and 2016. <i>Journal of General Virology</i> , 2017 , 98, 2001-2010	4.9	37
53	Terrestrial vegetation and aquatic chemistry influence larval mosquito abundance in catch basins, Chicago, USA. <i>Parasites and Vectors</i> , 2013 , 6, 9	4	36
52	Broad protection against avian influenza virus by using a modified vaccinia Ankara virus expressing a mosaic hemagglutinin gene. <i>Journal of Virology</i> , 2014 , 88, 13300-9	6.6	34
51	Regional patterns of genetic diversity in swine influenza A viruses in the United States from 2010 to 2016. <i>Influenza and Other Respiratory Viruses</i> , 2019 , 13, 262-273	5.6	34
50	Host centrality in food web networks determines parasite diversity. <i>PLoS ONE</i> , 2011 , 6, e26798	3.7	32
49	The Molecular Determinants of Antibody Recognition and Antigenic Drift in the H3 Hemagglutinin of Swine Influenza A Virus. <i>Journal of Virology</i> , 2016 , 90, 8266-80	6.6	31
48	Pathogenesis and vaccination of influenza A virus in swine. <i>Current Topics in Microbiology and Immunology</i> , 2014 , 385, 307-26	3.3	31
47	Swine Influenza A Viruses and the Tangled Relationship with Humans. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2021 , 11,	5.4	30
46	Swine influenza virus vaccine serologic cross-reactivity to contemporary US swine H3N2 and efficacy in pigs infected with an H3N2 similar to 2011-2012 H3N2v. <i>Influenza and Other Respiratory Viruses</i> , 2013 , 7 Suppl 4, 32-41	5.6	27
45	ISU FLUture: a veterinary diagnostic laboratory web-based platform to monitor the temporal genetic patterns of Influenza A virus in swine. <i>BMC Bioinformatics</i> , 2018 , 19, 397	3.6	25
44	Prevalence of filarioid nematodes and trypanosomes in American robins and house sparrows, Chicago USA. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2013 , 2, 42-9	2.6	21
43	The emergence of novel sparrow deltacoronaviruses in the United States more closely related to porcine deltacoronaviruses than sparrow deltacoronavirus HKU17. <i>Emerging Microbes and Infections</i> , 2018 , 7, 105	18.9	21
42	An inverse association between West Nile virus serostatus and avian malaria infection status. <i>Parasites and Vectors</i> , 2014 , 7, 415	4	20
41	Antigenic evolution of H3N2 influenza A viruses in swine in the United States from 2012 to 2016. <i>Influenza and Other Respiratory Viruses</i> , 2019 , 13, 83-90	5.6	18
40	A brief introduction to influenza A virus in swine. <i>Methods in Molecular Biology</i> , 2014 , 1161, 243-58	1.4	17
39	Host group formation decreases exposure to vector-borne disease: a field experiment in a hotspot of West Nile virus transmission. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014 , 281, 20141586	4.4	16
38	Influenza A Virus Field Surveillance at a Swine-Human Interface. <i>MSphere</i> , 2020 , 5,	5	14

37	Decreased Flight Activity in <i>Culex pipiens</i> (Diptera: Culicidae) Naturally Infected With <i>Culex</i> flavivirus. <i>Journal of Medical Entomology</i> , 2016 , 53, 233-6	2.2	14
36	octoFLU: Automated Classification for the Evolutionary Origin of Influenza A Virus Gene Sequences Detected in U.S. Swine. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	14
35	Ranking viruses: measures of positional importance within networks define core viruses for rational polyvalent vaccine development. <i>Bioinformatics</i> , 2012 , 28, 1624-32	7.2	13
34	<i>Culex</i> Flavivirus During West Nile Virus Epidemic and Interepidemic Years in Chicago, United States. <i>Vector-Borne and Zoonotic Diseases</i> , 2017 , 17, 567-575	2.4	12
33	Selective constraint and adaptive potential of West Nile virus within and among naturally infected avian hosts and mosquito vectors. <i>Virus Evolution</i> , 2018 , 4, vey013	3.7	12
32	Detection of live attenuated influenza vaccine virus and evidence of reassortment in the U.S. swine population. <i>Journal of Veterinary Diagnostic Investigation</i> , 2020 , 32, 301-311	1.5	11
31	Complete Genome Sequences of Two Novel Human-Like H3N2 Influenza A Viruses, A/swine/Oklahoma/65980/2017 (H3N2) and A/Swine/Oklahoma/65260/2017 (H3N2), Detected in Swine in the United States. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1.3	11
30	The relationship between community species richness and the richness of the parasite community in <i>Fundulus heteroclitus</i> . <i>Journal of Parasitology</i> , 2013 , 99, 391-6	0.9	10
29	A new species of <i>Hysterothylacium</i> (Nematoda: Anisakidae) from the stomach of the red-spotted newt, <i>Notophthalmus viridescens</i> , from Pennsylvania fishless ponds. <i>Journal of Parasitology</i> , 2009 , 95, 1503-6	0.9	10
28	WEST NILE VIRUS ANTIBODY DECAY RATE IN FREE-RANGING BIRDS. <i>Journal of Wildlife Diseases</i> , 2015 , 51, 601-8	1.3	9
27	West Nile virus may have hitched a ride across the Western United States on <i>Culex tarsalis</i> mosquitoes. <i>Molecular Ecology</i> , 2010 , 19, 1518-9	5.7	9
26	Evidence for the influence of weeds on corky ringspot persistence in alfalfa and Scotch spearmint rotations. <i>American Journal of Potato Research</i> , 2004 , 81, 215-225	2.1	9
25	A highly pathogenic avian-derived influenza virus H5N1 with 2009 pandemic H1N1 internal genes demonstrates increased replication and transmission in pigs. <i>Journal of General Virology</i> , 2017 , 98, 18-30	4.9	9
24	Aerosol Transmission from Infected Swine to Ferrets of an H3N2 Virus Collected from an Agricultural Fair and Associated with Human Variant Infections. <i>Journal of Virology</i> , 2020 , 94,	6.6	8
23	Effect of Trapping Methods, Weather, and Landscape on Estimates of the <i>Culex</i> Vector Mosquito Abundance. <i>Environmental Health Insights</i> , 2016 , 10, 93-103	1.4	8
22	In silico analysis of the fucosylation-associated genome of the human blood fluke <i>Schistosoma mansoni</i> : cloning and characterization of the fucosyltransferase multigene family. <i>PLoS ONE</i> , 2013 , 8, e63299	3.7	8
21	The avian-origin H3N2 canine influenza virus that recently emerged in the United States has limited replication in swine. <i>Influenza and Other Respiratory Viruses</i> , 2016 , 10, 429-32	5.6	7
20	Comparative virulence of wild-type H1N1pdm09 influenza A isolates in swine. <i>Veterinary Microbiology</i> , 2015 , 176, 40-9	3.3	7

19	Comparison of multilocus sequence types found among North American isolates of from cattle, bison, and deer, 2007-2017. <i>Journal of Veterinary Diagnostic Investigation</i> , 2019 , 31, 899-904	1.5	6
18	Mitigating Pandemic Risk with Influenza A Virus Field Surveillance at a Swine-Human Interface		6
17	In silico analysis of the fucosylation-associated genome of the human blood fluke <i>Schistosoma mansoni</i> : cloning and characterization of the enzymes involved in GDP-L-fucose synthesis and Golgi import. <i>Parasites and Vectors</i> , 2013 , 6, 201	4	5
16	Qualitative community stability determines parasite establishment and richness in estuarine marshes. <i>PeerJ</i> , 2013 , 1, e92	3.1	5
15	Comparative Virulence and Genomic Analysis of Isolates. <i>Frontiers in Microbiology</i> , 2020 , 11, 620843	5.7	5
14	Evolution and Antigenic Advancement of N2 Neuraminidase of Swine Influenza A Viruses Circulating in the United States following Two Separate Introductions from Human Seasonal Viruses. <i>Journal of Virology</i> , 2021 , 95, e0063221	6.6	3
13	Characterization of a 2016-2017 Human Seasonal H3 Influenza A Virus Spillover Now Endemic to U.S. Swine.. <i>MSphere</i> , 2022 , e0080921	5	2
12	Robinson-Foulds Reticulation Networks 2019 ,		2
11	Coordinated evolution between N2 neuraminidase and H1 and H3 hemagglutinin genes increased influenza A virus genetic diversity in swine		2
10	Characterization of contemporary 2010.1 H3N2 swine influenza A viruses circulating in United States pigs. <i>Virology</i> , 2021 , 553, 94-101	3.6	2
9	A Brief Introduction to Influenza A Virus in Swine. <i>Methods in Molecular Biology</i> , 2020 , 2123, 249-271	1.4	2
8	Consensus of All Solutions for Intractable Phylogenetic Tree Inference. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 149-161	3	1
7	Antigenic distance between North American swine and human seasonal H3N2 influenza A viruses as an indication of zoonotic risk to humans. <i>Journal of Virology</i> , 2021 , JVI0137421	6.6	1
6	Spatial and temporal coevolution of N2 neuraminidase and H1 and H3 hemagglutinin genes of influenza A virus in US swine.. <i>Virus Evolution</i> , 2021 , 7, veab090	3.7	1
5	Robinson-Foulds Reticulation Networks		1
4	Machine Learning Prediction and Experimental Validation of Antigenic Drift in H3 Influenza A Viruses in Swine. <i>MSphere</i> , 2021 , 6,	5	1
3	The worm's eye view of community ecology 2016 , 110-130		1
2	Life-cycle mediated effects of urbanization on parasite communities in the estuarine fish, <i>Fundulus heteroclitus</i> . <i>PLoS ONE</i> , 2019 , 14, e0225896	3.7	0

- 1 octoFLUshow: an Interactive Tool Describing Spatial and Temporal Trends in the Genetic Diversity of Influenza A Virus in U.S. Swine.. *Microbiology Resource Announcements*, **2021**, 10, e0108121 1.3 0