

Tavis Anderson

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.

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|-------------------|-------------------------|----------------|-----------------|
| 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 | 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 |
| 71 | 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 |
| 70 | 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 |
| 69 | 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 |
| 68 | Machine Learning Prediction and Experimental Validation of Antigenic Drift in H3 Influenza A Viruses in Swine. <i>MSphere</i> , 2021 , 6, | 5 | 1 |
| 67 | Swine Influenza A Viruses and the Tangled Relationship with Humans. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2021 , 11, | 5.4 | 30 |
| 66 | 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 |
| 65 | 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 |
| 64 | octoFLUshow: an Interactive Tool Describing Spatial and Temporal Trends in the Genetic Diversity of Influenza A Virus in U.S. Swine.. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0108121 | 1.3 | 0 |
| 63 | 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 |
| 62 | Influenza A Virus Field Surveillance at a Swine-Human Interface. <i>MSphere</i> , 2020 , 5, | 5 | 14 |
| 61 | 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 |
| 60 | Comparative Virulence and Genomic Analysis of Isolates. <i>Frontiers in Microbiology</i> , 2020 , 11, 620843 | 5.7 | 5 |
| 59 | A Brief Introduction to Influenza A Virus in Swine. <i>Methods in Molecular Biology</i> , 2020 , 2123, 249-271 | 1.4 | 2 |
| 58 | 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 |
| 57 | 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 |
| 56 | Robinson-Foulds Reticulation Networks 2019 , | | 2 |

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| 55 | 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 |
| 54 | 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 |
| 53 | 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 |
| 52 | Antigenic and genetic evolution of contemporary swine H1 influenza viruses in the United States. <i>Virology</i> , 2018 , 518, 45-54 | 3.6 | 41 |
| 51 | 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 |
| 50 | 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 |
| 49 | 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 |
| 48 | 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 |
| 47 | 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 |
| 46 | Influenza A virus vaccines for swine. <i>Veterinary Microbiology</i> , 2017 , 206, 35-44 | 3.3 | 58 |
| 45 | Culex 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 |
| 44 | 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 |
| 43 | Influenza Research Database: An integrated bioinformatics resource for influenza virus research. <i>Nucleic Acids Research</i> , 2017 , 45, D466-D474 | 20.1 | 174 |
| 42 | 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 |
| 41 | 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 |
| 40 | 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 |
| 39 | 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 |
| 38 | Effect of Trapping Methods, Weather, and Landscape on Estimates of the Culex Vector Mosquito Abundance. <i>Environmental Health Insights</i> , 2016 , 10, 93-103 | 1.4 | 8 |

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| 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 | The global antigenic diversity of swine influenza A viruses. <i>ELife</i> , 2016 , 5, e12217 | 8.9 | 106 |
| 35 | The worm's eye view of community ecology 2016 , 110-130 | | 1 |
| 34 | 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 |
| 33 | 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 |
| 32 | 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 |
| 31 | WEST NILE VIRUS ANTIBODY DECAY RATE IN FREE-RANGING BIRDS. <i>Journal of Wildlife Diseases</i> , 2015 , 51, 601-8 | 1.3 | 9 |
| 30 | Comparative virulence of wild-type H1N1pdm09 influenza A isolates in swine. <i>Veterinary Microbiology</i> , 2015 , 176, 40-9 | 3.3 | 7 |
| 29 | 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 |
| 28 | 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 |
| 27 | Pathogenesis and vaccination of influenza A virus in swine. <i>Current Topics in Microbiology and Immunology</i> , 2014 , 385, 307-26 | 3.3 | 31 |
| 26 | 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 |
| 25 | An inverse association between West Nile virus serostatus and avian malaria infection status. <i>Parasites and Vectors</i> , 2014 , 7, 415 | 4 | 20 |
| 24 | 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 |
| 23 | A brief introduction to influenza A virus in swine. <i>Methods in Molecular Biology</i> , 2014 , 1161, 243-58 | 1.4 | 17 |
| 22 | 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 |
| 21 | 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 |
| 20 | Terrestrial vegetation and aquatic chemistry influence larval mosquito abundance in catch basins, Chicago, USA. <i>Parasites and Vectors</i> , 2013 , 6, 9 | 4 | 36 |

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|----|---|------|----|
| 19 | Genotype patterns of contemporary reassorted H3N2 virus in US swine. <i>Journal of General Virology</i> , 2013 , 94, 1236-1241 | 4.9 | 62 |
| 18 | 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 |
| 17 | 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 |
| 16 | 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 |
| 15 | 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 |
| 14 | 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 |
| 13 | Qualitative community stability determines parasite establishment and richness in estuarine marshes. <i>PeerJ</i> , 2013 , 1, e92 | 3.1 | 5 |
| 12 | Genotype patterns of contemporary reassorted H3N2 virus in US swine. <i>Journal of General Virology</i> , 2013 , 94, 1236-41 | 4.9 | 45 |
| 11 | 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 |
| 10 | 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 |
| 9 | <i>Culex</i> 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 |
| 8 | 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 |
| 7 | Host centrality in food web networks determines parasite diversity. <i>PLoS ONE</i> , 2011 , 6, e26798 | 3.7 | 32 |
| 6 | 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 |
| 5 | 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 |
| 4 | 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 |
| 3 | Robinson-Foulds Reticulation Networks | | 1 |
| 2 | Coordinated evolution between N2 neuraminidase and H1 and H3 hemagglutinin genes increased influenza A virus genetic diversity in swine | | 2 |

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| 1 | Mitigating Pandemic Risk with Influenza A Virus Field Surveillance at a Swine-Human Interface | 6 |
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