

Daniel A Janies

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

3,085
citations

257450

24
h-index

175258

52
g-index

80
all docs

80
docs citations

80
times ranked

4669
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Bacterial 16S Sequence Analysis of Severe Caries in Young Permanent Teeth. <i>Journal of Clinical Microbiology</i> , 2010, 48, 4121-4128. | 3.9 | 315 |
| 2 | GRASSIUS: A Platform for Comparative Regulatory Genomics across the Grasses. <i>Plant Physiology</i> , 2009, 149, 171-180. | 4.8 | 260 |
| 3 | Multiple Sequence Alignment in Phylogenetic Analysis. <i>Molecular Phylogenetics and Evolution</i> , 2000, 16, 317-330. | 2.7 | 216 |
| 4 | Genome Analysis Linking Recent European and African Influenza (H5N1) Viruses. <i>Emerging Infectious Diseases</i> , 2007, 13, 713-718. | 4.3 | 191 |
| 5 | Zika Virus: Medical Countermeasure Development Challenges. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004530. | 3.0 | 159 |
| 6 | CORE: A Phylogenetically-Curated 16S rDNA Database of the Core Oral Microbiome. <i>PLoS ONE</i> , 2011, 6, e19051. | 2.5 | 154 |
| 7 | Tracing Origins of the <i>Salmonella</i> Bareilly Strain Causing a Food-borne Outbreak in the United States. <i>Journal of Infectious Diseases</i> , 2016, 213, 502-508. | 4.0 | 145 |
| 8 | Tracking the geographical spread of avian influenza (H5N1) with multiple phylogenetic trees. <i>Cladistics</i> , 2010, 26, 1-13. | 3.3 | 115 |
| 9 | First detection of <i>Anopheles stephensi</i> Liston, 1901 (Diptera: culicidae) in Ethiopia using molecular and morphological approaches. <i>Acta Tropica</i> , 2018, 188, 180-186. | 2.0 | 112 |
| 10 | Phylogenetic relationships of extant echinoderm classes. <i>Canadian Journal of Zoology</i> , 2001, 79, 1232-1250. | 1.0 | 91 |
| 11 | Relationships among development, ecology, and morphology in the evolution of Echinoderm larvae and life cycles. <i>Biological Journal of the Linnean Society</i> , 1997, 60, 381-400. | 1.6 | 87 |
| 12 | Echinoderm Phylogeny Including <i>Xyloplax</i> , a Progenetic Asteroid. <i>Systematic Biology</i> , 2011, 60, 420-438. | 5.6 | 76 |
| 13 | Genetic Diversity and Recombination of Porcine Sapoviruses. <i>Journal of Clinical Microbiology</i> , 2005, 43, 5963-5972. | 3.9 | 74 |
| 14 | Genomic Analysis and Geographic Visualization of the Spread of Avian Influenza (H5N1). <i>Systematic Biology</i> , 2007, 56, 321-329. | 5.6 | 63 |
| 15 | Eco-Virological Approach for Assessing the Role of Wild Birds in the Spread of Avian Influenza H5N1 along the Central Asian Flyway. <i>PLoS ONE</i> , 2012, 7, e30636. | 2.5 | 63 |
| 16 | Quasispecies of bovine enteric and respiratory coronaviruses based on complete genome sequences and genetic changes after tissue culture adaptation. <i>Virology</i> , 2007, 363, 1-10. | 2.4 | 58 |
| 17 | Evolution of drug resistance in multiple distinct lineages of H5N1 avian influenza. <i>Infection, Genetics and Evolution</i> , 2009, 9, 169-178. | 2.3 | 42 |
| 18 | Molecular Phylogeny of Coral-Reef Sea Cucumbers (Holothuriidae: Aspidochirotida) Based on 16S Mitochondrial Ribosomal DNA Sequence. <i>Marine Biotechnology</i> , 2005, 7, 53-60. | 2.4 | 41 |

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|----|---|-----|-----------|
| 19 | The phylogeny of extant starfish (Asteroidea: Echinodermata) including <i>Xyloplax</i> , based on comparative transcriptomics. <i>Molecular Phylogenetics and Evolution</i> , 2017, 115, 161-170. | 2.7 | 40 |
| 20 | Molecular Analysis of H7 Avian Influenza Viruses from Australia and New Zealand: Genetic Diversity and Relationships from 1976 to 2007. <i>Journal of Virology</i> , 2010, 84, 9957-9966. | 3.4 | 39 |
| 21 | First global molecular phylogeny and biogeographical analysis of two arachnid orders (Schizomida) <i>Tj ETQq1 1 0.784314 rgBT /Overlo</i> <i>Biogeography</i> , 2017, 44, 2660-2672. | 3.0 | 37 |
| 22 | Evolution of genomes, host shifts and the geographic spread of SARS-CoV and related coronaviruses. <i>Cladistics</i> , 2008, 24, 111-130. | 3.3 | 35 |
| 23 | Comparative Phylogenetic Studies on <i>Schistosoma japonicum</i> and Its Snail Intermediate Host <i>Oncomelania hupensis</i> : Origins, Dispersal and Coevolution. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003935. | 3.0 | 31 |
| 24 | StrainHub: a phylogenetic tool to construct pathogen transmission networks. <i>Bioinformatics</i> , 2020, 36, 945-947. | 4.1 | 30 |
| 25 | Selection for resistance to oseltamivir in seasonal and pandemic H1N1 influenza and widespread co-circulation of the lineages. <i>International Journal of Health Geographics</i> , 2010, 9, 13. | 2.5 | 29 |
| 26 | Different Regions of HIV-1 Subtype C Are Associated with Placental Localization and In Utero Mother-to-Child Transmission. <i>Journal of Virology</i> , 2011, 85, 7142-7152. | 3.4 | 28 |
| 27 | EchinoDB, an application for comparative transcriptomics of deeply-sampled clades of echinoderms. <i>BMC Bioinformatics</i> , 2016, 17, 48. | 2.6 | 26 |
| 28 | Frequent expansion of <i>Plasmodium vivax</i> Duffy Binding Protein in Ethiopia and its epidemiological significance. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007222. | 3.0 | 25 |
| 29 | Whole genome sequencing of <i>Plasmodium vivax</i> isolates reveals frequent sequence and structural polymorphisms in erythrocyte binding genes. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008234. | 3.0 | 25 |
| 30 | Predictions of the SARS-CoV-2 Omicron Variant (B.1.1.529) Spike Protein Receptor-Binding Domain Structure and Neutralizing Antibody Interactions. <i>Frontiers in Virology</i> , 2022, 2, . | 1.4 | 22 |
| 31 | Phylotranscriptomic analysis uncovers a wealth of tissue inhibitor of metalloproteinases variants in echinoderms. <i>Royal Society Open Science</i> , 2015, 2, 150377. | 2.4 | 21 |
| 32 | An operational machine learning approach to predict mosquito abundance based on socioeconomic and landscape patterns. <i>Landscape Ecology</i> , 2019, 34, 1295-1311. | 4.2 | 21 |
| 33 | Integration of phylogenomics and molecular modeling reveals lineage-specific diversification of toxins in scorpions. <i>PeerJ</i> , 2018, 6, e5902. | 2.0 | 21 |
| 34 | The Supramap project: linking pathogen genomes with geography to fight emergent infectious diseases. <i>Cladistics</i> , 2011, 27, 61-66. | 3.3 | 20 |
| 35 | Molecular evolution of Zika virus as it crossed the Pacific to the Americas. <i>Cladistics</i> , 2017, 33, 1-20. | 3.3 | 19 |
| 36 | Venomix: a simple bioinformatic pipeline for identifying and characterizing toxin gene candidates from transcriptomic data. <i>PeerJ</i> , 2018, 6, e5361. | 2.0 | 18 |

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|----|--|------|-----------|
| 37 | Resurrection of <i>Bohadschia bivittata</i> from <i>B. marmorata</i> (Holothuroidea: Holothuriidae) based on behavioral, morphological, and mitochondrial DNA evidence. <i>Zoology</i> , 2005, 108, 27-39. | 1.2 | 17 |
| 38 | Health-care hit or miss?. <i>Nature</i> , 2011, 470, 327-329. | 27.8 | 17 |
| 39 | Regeneration in bipinnaria larvae of the bat star <i>Patiria miniata</i> induces rapid and broad new gene expression. <i>Mechanisms of Development</i> , 2016, 142, 10-21. | 1.7 | 16 |
| 40 | The first complete mitochondrial genome of the sand dollar <i>Sinaechinocyamus mai</i> (Echinoidea: Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 6 | 2.9 | 16 |
| 41 | Active Notch signaling is required for arm regeneration in a brittle star. <i>PLoS ONE</i> , 2020, 15, e0232981. | 2.5 | 16 |
| 42 | Fundamental evolution of all <i>Orthocoronavirinae</i> including three deadly lineages descendent from Chiroptera-hosted coronaviruses: SARS-CoV, MERS-CoV and SARS-CoV-2. <i>Cladistics</i> , 2021, 37, 461-488. | 3.3 | 16 |
| 43 | A phylogeny of sand flies (Diptera: Phlebotominae), using recent Ethiopian collections and a broad selection of publicly available DNA sequence data. <i>Systematic Entomology</i> , 2015, 40, 733-744. | 3.9 | 15 |
| 44 | A new strategy to infer circularity applied to four new complete frog mitogenomes. <i>Ecology and Evolution</i> , 2018, 8, 4011-4018. | 1.9 | 15 |
| 45 | Large-Scale Phylogenetic Analysis on Current HPC Architectures. <i>Scientific Programming</i> , 2008, 16, 255-270. | 0.7 | 14 |
| 46 | Glucose-6-Phosphate Dehydrogenase Deficiency Genetic Variants in Malaria Patients in Southwestern Ethiopia. <i>American Journal of Tropical Medicine and Hygiene</i> , 2018, 98, 83-87. | 1.4 | 10 |
| 47 | Genome informatics of influenza A: from data sharing to shared analytical capabilities. <i>Animal Health Research Reviews</i> , 2010, 11, 73-79. | 3.1 | 9 |
| 48 | SpeciesMap: a web-based application for visualizing the overlap of distributions and pollution events, with a list of fishes put at risk by the 2010 Gulf of Mexico oil spill. <i>Biodiversity and Conservation</i> , 2012, 21, 1865-1876. | 2.6 | 9 |
| 49 | Phylogeny of Echinoderm Hemoglobins. <i>PLoS ONE</i> , 2015, 10, e0129668. | 2.5 | 9 |
| 50 | Efficiency of Parallel Direct Optimization. <i>Cladistics</i> , 2001, 17, S71-S82. | 3.3 | 9 |
| 51 | An XML-based System for Synthesis of Data from Disparate Databases. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2006, 13, 289-301. | 4.4 | 8 |
| 52 | A comparison of supermatrix and supertree methods for multilocus phylogenetics using organismal datasets. <i>Cladistics</i> , 2013, 29, 560-566. | 3.3 | 8 |
| 53 | Phylogenetic visualization of the spread of H7 influenza A viruses. <i>Cladistics</i> , 2015, 31, 679-691. | 3.3 | 8 |
| 54 | Tracking a serial killer: Integrating phylogenetic relationships, epidemiology, and geography for two invasive meningococcal disease outbreaks. <i>PLoS ONE</i> , 2018, 13, e0202615. | 2.5 | 8 |

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|----|--|-----|-----------|
| 55 | Four Challenges Associated With Current Mathematical Modeling Paradigm of Infectious Diseases and Call for a Shift. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa333. | 0.9 | 8 |
| 56 | A Novel Machine Learning Framework for Comparison of Viral COVID-19-Related Sina Weibo and Twitter Posts: Workflow Development and Content Analysis. <i>Journal of Medical Internet Research</i> , 2021, 23, e24889. | 4.3 | 8 |
| 57 | Exploring Feasibility of Multivariate Deep Learning Models in Predicting COVID-19 Epidemic. <i>Frontiers in Public Health</i> , 2021, 9, 661615. | 2.7 | 7 |
| 58 | Multi-species SIR models from a dynamical Bayesian perspective. <i>Theoretical Ecology</i> , 2013, 6, 457-473. | 1.0 | 6 |
| 59 | FLAVi: An Enhanced Annotator for Viral Genomes of Flaviviridae. <i>Viruses</i> , 2020, 12, 892. | 3.3 | 6 |
| 60 | Evaluation of PfHRP2 and PfLDH Malaria Rapid Diagnostic Test Performance in Assosa Zone, Ethiopia. <i>American Journal of Tropical Medicine and Hygiene</i> , 2020, 103, 1902-1909. | 1.4 | 6 |
| 61 | Discovery of Adults Linked to Cloning Oceanic Starfish Larvae (<i>Oreaster</i> , Asteroidea.) <i>Tj ETQq1 1 0.784314 rrgBT /Overlock 10 TF</i> | 1.8 | 5 |
| 62 | Patch dynamics modeling framework from pathogensâ€™ perspective: Unified and standardized approach for complicated epidemic systems. <i>PLoS ONE</i> , 2020, 15, e0238186. | 2.5 | 5 |
| 63 | Fundamentals of genomic epidemiology, lessons learned from the coronavirus disease 2019 (COVID-19) pandemic, and new directions. <i>Antimicrobial Stewardship & Healthcare Epidemiology</i> , 2021, 1, . | 0.5 | 5 |
| 64 | Genetic capitalism and stabilizing selection of antimicrobial resistance genotypes in <i>Escherichia coli</i> . <i>Cladistics</i> , 2020, 36, 348-357. | 3.3 | 4 |
| 65 | Evolution of Starfishes: Morphology, Molecules, Development, and Paleobiology. Introduction to the Symposium. <i>American Zoologist</i> , 2000, 40, 311-315. | 0.7 | 3 |
| 66 | Analysis and visualization of H7 influenza using genomic, evolutionary and geographic information in a modular web service. <i>Cladistics</i> , 2012, 28, 483-488. | 3.3 | 3 |
| 67 | Phylogenetic Concepts and Tools Applied to Epidemiologic Investigations of Infectious Diseases. <i>Microbiology Spectrum</i> , 2019, 7, . | 3.0 | 3 |
| 68 | Evolution of endemic and sylvatic lineages of dengue virus. <i>Cladistics</i> , 2020, 36, 115-128. | 3.3 | 2 |
| 69 | Modeling the life cycle of echinoderm larvae clones. <i>Bulletin of Marine Science</i> , 2020, 96, 221-228. | 0.8 | 2 |
| 70 | Shallow-Water Holothuroids (Echinodermata) of Yap, Federated States of Micronesia. <i>Pacific Science</i> , 2014, 68, 397-420. | 0.6 | 1 |
| 71 | Cladograms with Path to Event (ClaPTE): A novel algorithm to detect associations between genotypes or phenotypes using phylogenies. <i>Computers in Biology and Medicine</i> , 2015, 58, 1-13. | 7.0 | 1 |
| 72 | Genotypic and Phenotypic Heterogeneity in the U3R Region of HIV Type 1 Subtype C. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, 102-112. | 1.1 | 0 |