

Daniel A Janies

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9602306/publications.pdf>

Version: 2024-02-01

72
papers

3,085
citations

293460

24
h-index

198040

52
g-index

80
all docs

80
docs citations

80
times ranked

5169
citing authors

#	ARTICLE	IF	CITATIONS
1	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, .	0.7	22
2	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.	2.1	8
3	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.	1.5	16
4	Exploring Feasibility of Multivariate Deep Learning Models in Predicting COVID-19 Epidemic. <i>Frontiers in Public Health</i> , 2021, 9, 661615.	1.3	7
5	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, .	0.2	5
6	Evolution of endemic and sylvatic lineages of dengue virus. <i>Cladistics</i> , 2020, 36, 115-128.	1.5	2
7	The first complete mitochondrial genome of the sand dollar <i>Sphaechinocyamus mai</i> (Echinoidea: Tj ETQq1 1 0.784314 rgBT /Overlock 16	1.3	16
8	StrainHub: a phylogenetic tool to construct pathogen transmission networks. <i>Bioinformatics</i> , 2020, 36, 945-947.	1.8	30
9	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.	1.3	25
10	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.	0.4	8
11	FLAVi: An Enhanced Annotator for Viral Genomes of Flaviviridae. <i>Viruses</i> , 2020, 12, 892.	1.5	6
12	Active Notch signaling is required for arm regeneration in a brittle star. <i>PLoS ONE</i> , 2020, 15, e0232981.	1.1	16
13	Genetic capitalism and stabilizing selection of antimicrobial resistance genotypes in <i>Escherichia coli</i> . <i>Cladistics</i> , 2020, 36, 348-357.	1.5	4
14	Patch dynamics modeling framework from pathogens perspective: Unified and standardized approach for complicated epidemic systems. <i>PLoS ONE</i> , 2020, 15, e0238186.	1.1	5
15	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.	0.6	6
16	Modeling the life cycle of echinoderm larvae clones. <i>Bulletin of Marine Science</i> , 2020, 96, 221-228.	0.4	2
17	Phylogenetic Concepts and Tools Applied to Epidemiologic Investigations of Infectious Diseases. <i>Microbiology Spectrum</i> , 2019, 7, .	1.2	3
18	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.	1.3	25

#	ARTICLE	IF	CITATIONS
19	Discovery of Adults Linked to Cloning Oceanic Starfish Larvae (<i>Oreaster</i> , Asteroidea) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.7	5
20	An operational machine learning approach to predict mosquito abundance based on socioeconomic and landscape patterns. <i>Landscape Ecology</i> , 2019, 34, 1295-1311.	1.9	21
21	A new strategy to infer circularity applied to four new complete frog mitogenomes. <i>Ecology and Evolution</i> , 2018, 8, 4011-4018.	0.8	15
22	Tracking a serial killer: Integrating phylogenetic relationships, epidemiology, and geography for two invasive meningococcal disease outbreaks. <i>PLoS ONE</i> , 2018, 13, e0202615.	1.1	8
23	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.	0.9	112
24	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.	0.6	10
25	Venomix: a simple bioinformatic pipeline for identifying and characterizing toxin gene candidates from transcriptomic data. <i>PeerJ</i> , 2018, 6, e5361.	0.9	18
26	Integration of phylogenomics and molecular modeling reveals lineage-specific diversification of toxins in scorpions. <i>PeerJ</i> , 2018, 6, e5902.	0.9	21
27	Molecular evolution of Zika virus as it crossed the Pacific to the Americas. <i>Cladistics</i> , 2017, 33, 1-20.	1.5	19
28	First global molecular phylogeny and biogeographical analysis of two arachnid orders (Schizomida) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 <i>Biogeography</i> , 2017, 44, 2660-2672.	1.4	37
29	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.	1.2	40
30	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
31	EchinoDB, an application for comparative transcriptomics of deeply-sampled clades of echinoderms. <i>BMC Bioinformatics</i> , 2016, 17, 48.	1.2	26
32	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.	1.9	145
33	Zika Virus: Medical Countermeasure Development Challenges. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004530.	1.3	159
34	Phylotranscriptomic analysis uncovers a wealth of tissue inhibitor of metalloproteinases variants in echinoderms. <i>Royal Society Open Science</i> , 2015, 2, 150377.	1.1	21
35	A phylogeny of sand flies (<i>Diptera: Phlebotominae</i>), using recent Ethiopian collections and a broad selection of publicly available DNA sequence data. <i>Systematic Entomology</i> , 2015, 40, 733-744.	1.7	15
36	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.	1.3	31

#	ARTICLE	IF	CITATIONS
37	Phylogeny of Echinoderm Hemoglobins. PLoS ONE, 2015, 10, e0129668.	1.1	9
38	Phylogenetic visualization of the spread of H7 influenza A viruses. Cladistics, 2015, 31, 679-691.	1.5	8
39	Cladograms with Path to Event (ClaPTE): A novel algorithm to detect associations between genotypes or phenotypes using phylogenies. Computers in Biology and Medicine, 2015, 58, 1-13.	3.9	1
40	Shallow-Water Holothuroids (Echinodermata) of Yap, Federated States of Micronesia. Pacific Science, 2014, 68, 397-420.	0.2	1
41	Genotypic and Phenotypic Heterogeneity in the U3R Region of HIV Type 1 Subtype C. AIDS Research and Human Retroviruses, 2014, 30, 102-112.	0.5	0
42	Multi-species SIR models from a dynamical Bayesian perspective. Theoretical Ecology, 2013, 6, 457-473.	0.4	6
43	A comparison of supermatrix and supertree methods for multilocus phylogenetics using organismal datasets. Cladistics, 2013, 29, 560-566.	1.5	8
44	Eco-Virological Approach for Assessing the Role of Wild Birds in the Spread of Avian Influenza H5N1 along the Central Asian Flyway. PLoS ONE, 2012, 7, e30636.	1.1	63
45	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. Biodiversity and Conservation, 2012, 21, 1865-1876.	1.2	9
46	Analysis and visualization of H7 influenza using genomic, evolutionary and geographic information in a modular web service. Cladistics, 2012, 28, 483-488.	1.5	3
47	CORE: A Phylogenetically-Curated 16S rDNA Database of the Core Oral Microbiome. PLoS ONE, 2011, 6, e19051.	1.1	154
48	The Supramap project: linking pathogen genomes with geography to fight emergent infectious diseases. Cladistics, 2011, 27, 61-66.	1.5	20
49	Health-care hit or miss?. Nature, 2011, 470, 327-329.	13.7	17
50	Echinoderm Phylogeny Including Xyloplax, a Progenetic Asteroid. Systematic Biology, 2011, 60, 420-438.	2.7	76
51	Different Regions of HIV-1 Subtype C Are Associated with Placental Localization and In Utero Mother-to-Child Transmission. Journal of Virology, 2011, 85, 7142-7152.	1.5	28
52	Selection for resistance to oseltamivir in seasonal and pandemic H1N1 influenza and widespread co-circulation of the lineages. International Journal of Health Geographics, 2010, 9, 13.	1.2	29
53	Tracking the geographical spread of avian influenza (H5N1) with multiple phylogenetic trees. Cladistics, 2010, 26, 1-13.	1.5	115
54	Molecular Analysis of H7 Avian Influenza Viruses from Australia and New Zealand: Genetic Diversity and Relationships from 1976 to 2007. Journal of Virology, 2010, 84, 9957-9966.	1.5	39

#	ARTICLE	IF	CITATIONS
55	Genome informatics of influenza A: from data sharing to shared analytical capabilities. <i>Animal Health Research Reviews</i> , 2010, 11, 73-79.	1.4	9
56	Bacterial 16S Sequence Analysis of Severe Caries in Young Permanent Teeth. <i>Journal of Clinical Microbiology</i> , 2010, 48, 4121-4128.	1.8	315
57	GRASSIUS: A Platform for Comparative Regulatory Genomics across the Grasses. <i>Plant Physiology</i> , 2009, 149, 171-180.	2.3	260
58	Evolution of drug resistance in multiple distinct lineages of H5N1 avian influenza. <i>Infection, Genetics and Evolution</i> , 2009, 9, 169-178.	1.0	42
59	Evolution of genomes, host shifts and the geographic spread of SARS-CoV and related coronaviruses. <i>Cladistics</i> , 2008, 24, 111-130.	1.5	35
60	Large-Scale Phylogenetic Analysis on Current HPC Architectures. <i>Scientific Programming</i> , 2008, 16, 255-270.	0.5	14
61	Genomic Analysis and Geographic Visualization of the Spread of Avian Influenza (H5N1). <i>Systematic Biology</i> , 2007, 56, 321-329.	2.7	63
62	Genome Analysis Linking Recent European and African Influenza (H5N1) Viruses. <i>Emerging Infectious Diseases</i> , 2007, 13, 713-718.	2.0	191
63	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.	1.1	58
64	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.	2.2	8
65	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.	0.6	17
66	Molecular Phylogeny of Coral-Reef Sea Cucumbers (Holothuriidae: Aspidochirotida) Based on 16S Mitochondrial Ribosomal DNA Sequence. <i>Marine Biotechnology</i> , 2005, 7, 53-60.	1.1	41
67	Genetic Diversity and Recombination of Porcine Sapoviruses. <i>Journal of Clinical Microbiology</i> , 2005, 43, 5963-5972.	1.8	74
68	Phylogenetic relationships of extant echinoderm classes. <i>Canadian Journal of Zoology</i> , 2001, 79, 1232-1250.	0.4	91
69	Efficiency of Parallel Direct Optimization. <i>Cladistics</i> , 2001, 17, S71-S82.	1.5	9
70	Multiple Sequence Alignment in Phylogenetic Analysis. <i>Molecular Phylogenetics and Evolution</i> , 2000, 16, 317-330.	1.2	216
71	Evolution of Starfishes: Morphology, Molecules, Development, and Paleobiology. Introduction to the Symposium. <i>American Zoologist</i> , 2000, 40, 311-315.	0.7	3
72	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.	0.7	87