

Troy J Kieran

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4172523/publications.pdf>

Version: 2024-02-01

60
papers

7,126
citations

201674

27
h-index

149698

56
g-index

69
all docs

69
docs citations

69
times ranked

9004
citing authors

#	ARTICLE	IF	CITATIONS
1	Estimating Movement Rates Between Eurasian and North American Birds That Are Vectors of Avian Influenza. <i>Avian Diseases</i> , 2022, 66, .	1.0	0
2	Population genetic divergence of bonnethead sharks <i>Sphyrna tiburo</i> in the western North Atlantic: Implications for conservation. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2021, 31, 83-98.	2.0	12
3	Improved Microbial Community Characterization of 16S rRNA via Metagenome Hybridization Capture Enrichment. <i>Frontiers in Microbiology</i> , 2021, 12, 644662.	3.5	23
4	Ultraconserved elements reconstruct the evolution of Chagas disease vector kissing bugs (Reduviidae: Triatominae). <i>Systematic Entomology</i> , 2021, 46, 725-740.	3.9	24
5	Unveiling the Gut Microbiota and Resistome of Wild Cotton Mice, <i>Peromyscus gossypinus</i> , from Heavy Metal- and Radionuclide-Contaminated Sites in the Southeastern United States. <i>Microbiology Spectrum</i> , 2021, 9, e0009721.	3.0	4
6	Escaping the fate of Sisyphus: assessing resistome hybridization baits for antimicrobial resistance gene capture. <i>Environmental Microbiology</i> , 2021, 23, 7523-7537.	3.8	3
7	A High-Quality Reference Genome Assembly of the Saltwater Crocodile, <i>Crocodylus porosus</i> , Reveals Patterns of Selection in Crocodylidae. <i>Genome Biology and Evolution</i> , 2020, 12, 3635-3646.	2.5	15
8	How microclimatic variables and blood meal sources influence <i>Rhodnius prolixus</i> abundance and <i>Trypanosoma cruzi</i> infection in <i>Attalea butyracea</i> and <i>Elaeis guineensis</i> palms?. <i>Acta Tropica</i> , 2020, 212, 105674.	2.0	4
9	Ultraconserved element bait set for trypanosomatida target enrichment and phylogenetics. <i>Experimental Parasitology</i> , 2020, 219, 108015.	1.2	1
10	Divergence, gene flow, and speciation in eight lineages of trans-Beringian birds. <i>Molecular Ecology</i> , 2020, 29, 3526-3542.	3.9	18
11	Agricultural pests consumed by common bat species in the United States corn belt: The importance of DNA primer choice. <i>Agriculture, Ecosystems and Environment</i> , 2020, 303, 107105.	5.3	17
12	Microbiota of Four Tissue Types in American Alligators (<i>Alligator mississippiensis</i>) Following Extended Dietary Selenomethionine Exposure. <i>Bulletin of Environmental Contamination and Toxicology</i> , 2020, 105, 381-386.	2.7	1
13	Co-occurrence of antibiotic, biocide, and heavy metal resistance genes in bacteria from metal and radionuclide contaminated soils at the Savannah River Site. <i>Microbial Biotechnology</i> , 2020, 13, 1179-1200.	4.2	89
14	Identification and characterization of microRNAs (miRNAs) and their transposable element origins in the saltwater crocodile, <i>Crocodylus porosus</i> . <i>Analytical Biochemistry</i> , 2020, 602, 113781.	2.4	6
15	Mitochondrial, metagenomic, and phylogenetic analysis of the ground beetle <i>Harpalus pensylvanicus</i> (Coleoptera: Carabidae). <i>Gene</i> , 2020, 740, 144540.	2.2	4
16	Genome comparison and transcriptome analysis of the invasive brown root rot pathogen, <i>Phellinus noxius</i> , from different geographic regions reveals potential enzymes associated with degradation of different wood substrates. <i>Fungal Biology</i> , 2020, 124, 144-154.	2.5	11
17	Comparison of the ruminal and fecal microbiotas in beef calves supplemented or not with concentrate. <i>PLoS ONE</i> , 2020, 15, e0231533.	2.5	56
18	Population genetics of two chromatic morphs of the Chagas disease vector <i>Rhodnius pallescens</i> Barber, 1932 in Panama. <i>Infection, Genetics and Evolution</i> , 2020, 84, 104369.	2.3	2

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19	Phylogeny of the North-Central American clade of blood-sucking reduviid bugs of the tribe Triatomini (Hemiptera: Triatominae) based on the mitochondrial genome. <i>Infection, Genetics and Evolution</i> , 2020, 84, 104373.	2.3	14
20	Preservation-Induced Morphological Change in Salamanders and Failed DNA Extraction from a Decades-Old Museum Specimen: Implications for <i>Plethodon ainsworthi</i> . <i>Journal of Herpetology</i> , 2020, 54, 137.	0.5	13
21	Regional biogeography of microbiota composition in the Chagas disease vector <i>Rhodnius pallescens</i> . <i>Parasites and Vectors</i> , 2019, 12, 504.	2.5	17
22	Genomic mutations after multigenerational exposure of <i>Caenorhabditis elegans</i> to pristine and sulfidized silver nanoparticles. <i>Environmental Pollution</i> , 2019, 254, 113078.	7.5	31
23	Bromate-induced Changes in p21 DNA Methylation and Histone Acetylation in Renal Cells. <i>Toxicological Sciences</i> , 2019, 168, 460-473.	3.1	7
24	Generalist host species drive <i>Trypanosoma cruzi</i> vector infection in oil palm plantations in the Orinoco region, Colombia. <i>Parasites and Vectors</i> , 2019, 12, 274.	2.5	16
25	Analysis of the Rumen Microbiota of Beef Calves Supplemented During the Suckling Phase. <i>Frontiers in Microbiology</i> , 2019, 10, 1131.	3.5	15
26	Examining the Effects of Chronic Selenium Exposure on Traditionally Used Stress Parameters in Juvenile American Alligators (<i>Alligator mississippiensis</i>). <i>Archives of Environmental Contamination and Toxicology</i> , 2019, 77, 14-21.	4.1	15
27	Formation of a recent hybrid zone offers insight into the geographic puzzle and maintenance of species boundaries in musk turtles. <i>Molecular Ecology</i> , 2019, 28, 761-771.	3.9	17
28	Insight from an ultraconserved element bait set designed for hemipteran phylogenetics integrated with genomic resources. <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 297-303.	2.7	51
29	Adapterama III: Quadruple-indexed, double/triple-enzyme RADseq libraries (2RAD/3RAD). <i>PeerJ</i> , 2019, 7, e7724.	2.0	96
30	Adapterama I: universal stubs and primers for 384 unique dual-indexed or 147,456 combinatorially-indexed Illumina libraries (iTru & iNext). <i>PeerJ</i> , 2019, 7, e7755.	2.0	243
31	Adapterama II: universal amplicon sequencing on Illumina platforms (TaggiMatrix). <i>PeerJ</i> , 2019, 7, e7786.	2.0	47
32	Mitochondrial genomes of the Pacific sierra mackerel <i>Scomberomorus sierra</i> and the Monterey Spanish mackerel <i>Scomberomorus concolor</i> (Perciformes, Scombridae). <i>Conservation Genetics Resources</i> , 2018, 10, 471-474.	0.8	1
33	Conflicting Evolutionary Histories of the Mitochondrial and Nuclear Genomes in New World Myotis Bats. <i>Systematic Biology</i> , 2018, 67, 236-249.	5.6	56
34	Resolving taxonomic turbulence and uncovering cryptic diversity in the musk turtles (<i>Sternotherus</i>) using robust demographic modeling. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 1-15.	2.7	23
35	A High-Quality Reference Genome for the Invasive Mosquitofish <i>Gambusia affinis</i> Using a Chicago Library. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1855-1861.	1.8	16
36	Dietary Selenomethionine Administration and Its Effects on the American Alligator (<i>Alligator</i>) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 67 T</i> Contamination and Toxicology, 2018, 75, 37-44.	4.1	11

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37	Ultraconserved elements (UCEs) illuminate the population genomics of a recent, high-latitude avian speciation event. <i>PeerJ</i> , 2018, 6, e5735.	2.0	31
38	Dietary Selenomethionine Administration in the American Alligator (<i>Alligator mississippiensis</i>): Hepatic and Renal Se Accumulation and Its Effects on Growth and Body Condition. <i>Archives of Environmental Contamination and Toxicology</i> , 2017, 72, 439-448.	4.1	16
39	Blood Meal Source Characterization Using Illumina Sequencing in the Chagas Disease Vector <i>Rhodnius pallescens</i> (Hemiptera: Reduviidae) in Panamá. <i>Journal of Medical Entomology</i> , 2017, 54, 1786-1789.	1.8	36
40	The Novel Evolution of the Sperm Whale Genome. <i>Genome Biology and Evolution</i> , 2017, 9, 3260-3264.	2.5	33
41	Capturing Darwin's dream. <i>Molecular Ecology Resources</i> , 2016, 16, 1051-1058.	4.8	22
42	<sc>RAD</sc>cap: sequence capture of dual-digest <sc>RAD</sc>seq libraries with identifiable duplicates and reduced missing data. <i>Molecular Ecology Resources</i> , 2016, 16, 1264-1278.	4.8	117
43	Sequence Capture versus Restriction Site Associated DNA Sequencing for Shallow Systematics. <i>Systematic Biology</i> , 2016, 65, 910-924.	5.6	220
44	Targeted DNA Region Re-sequencing. , 2016, , 43-68.		9
45	Detection of an Enigmatic Plethodontid Salamander Using Environmental DNA. <i>Copeia</i> , 2016, 104, 78-82.	1.3	19
46	Analysis of a Rapid Evolutionary Radiation Using Ultraconserved Elements: Evidence for a Bias in Some Multispecies Coalescent Methods. <i>Systematic Biology</i> , 2016, 65, 612-627.	5.6	137
47	Aflatoxin B ₁ Induced Compositional Changes in Gut Microbial Communities of Male F344 Rats. <i>Toxicological Sciences</i> , 2016, 150, 54-63.	3.1	78
48	Avoiding Missing Data Biases in Phylogenomic Inference: An Empirical Study in the Landfowl (Aves: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	8.9	208
49	Impacts of degraded <sc>DNA</sc> on restriction enzyme associated <sc>DNA</sc> sequencing (<sc>RADS</sc>eq). <i>Molecular Ecology Resources</i> , 2015, 15, 1304-1315.	4.8	114
50	A phylogenomic analysis of turtles. <i>Molecular Phylogenetics and Evolution</i> , 2015, 83, 250-257.	2.7	244
51	Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014, 346, 1254449.	12.6	300
52	Target Capture and Massively Parallel Sequencing of Ultraconserved Elements for Comparative Studies at Shallow Evolutionary Time Scales. <i>Systematic Biology</i> , 2014, 63, 83-95.	5.6	286
53	A Phylogeny of Birds Based on Over 1,500 Loci Collected by Target Enrichment and High-Throughput Sequencing. <i>PLoS ONE</i> , 2013, 8, e54848.	2.5	287
54	Not All Sequence Tags Are Created Equal: Designing and Validating Sequence Identification Tags Robust to Indels. <i>PLoS ONE</i> , 2012, 7, e42543.	2.5	267

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55	More than 1000 ultraconserved elements provide evidence that turtles are the sister group of archosaurs. <i>Biology Letters</i> , 2012, 8, 783-786.	2.3	331
56	Ultraconserved Elements Anchor Thousands of Genetic Markers Spanning Multiple Evolutionary Timescales. <i>Systematic Biology</i> , 2012, 61, 717-726.	5.6	983
57	Ultraconserved elements are novel phylogenomic markers that resolve placental mammal phylogeny when combined with species-tree analysis. <i>Genome Research</i> , 2012, 22, 746-754.	5.5	349
58	Field guide to next-generation DNA sequencers. <i>Molecular Ecology Resources</i> , 2011, 11, 759-769.	4.8	940
59	Coselection for microbial resistance to metals and antibiotics in freshwater microcosms. <i>Environmental Microbiology</i> , 2006, 8, 1510-1514.	3.8	258
60	Isolating Microsatellite DNA Loci. <i>Methods in Enzymology</i> , 2005, 395, 202-222.	1.0	758