

Julie M Allen

List of Publications by Year in descending order

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42
papers

1,546
citations

430874

18
h-index

345221

36
g-index

45
all docs

45
docs citations

45
times ranked

1893
citing authors

#	ARTICLE	IF	CITATIONS
1	Population genomics of <i>Monadenia</i> (Gastropoda: Stylommatophora: Xanthonychidae) land snails reveals structuring but gene-flow across distinct species and morphotypes. <i>Conservation Genetics</i> , 2022, 23, 299-311.	1.5	1
2	Phylogenetics and host-specificity of the mega-diverse louse genus <i>Myrsidea</i> (Amblycera: Tj ETQq0 0 0 rBT /Overlock 10 Tf	3.9	5
3	Long-distance dispersal of pigeons and doves generated new ecological opportunities for host-switching and adaptive radiation by their parasites. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, 20220042.	2.6	13
4	Disentangling lousy relationships: Comparative phylogenomics of two sucking louse lineages parasitizing chipmunks. <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 106998.	2.7	3
5	Integrative analysis of DNA, macroscopic remains and stable isotopes of dog coprolites to reconstruct community diet. <i>Scientific Reports</i> , 2021, 11, 3113.	3.3	12
6	Ancient DNA from the extinct Haitian cave-rail (<i>Nesotrochis steganinos</i>) suggests a biogeographic connection between the Caribbean and Old World. <i>Biology Letters</i> , 2021, 17, 20200760.	2.3	11
7	Spatial phylogenetics of butterflies in relation to environmental drivers and angiosperm diversity across North America. <i>IScience</i> , 2021, 24, 102239.	4.1	22
8	Systematics and conservation of an endemic radiation of <i>Accipiter</i> hawks in the Caribbean islands. <i>Auk</i> , 2021, 138, .	1.4	9
9	Human Health, Interagency Coordination, and the Need for Biodiversity Data. <i>BioScience</i> , 2020, 70, 527-527.	4.9	2
10	Ancient DNA and high-resolution chronometry reveal a long-term human role in the historical diversity and biogeography of the Bahamian hutia. <i>Scientific Reports</i> , 2020, 10, 1373.	3.3	20
11	Transcriptomics illuminate the phylogenetic backbone of tiger beetles. <i>Biological Journal of the Linnean Society</i> , 2020, 129, 740-751.	1.6	16
12	Spatial phylogenetics of the North American flora. <i>Journal of Systematics and Evolution</i> , 2020, 58, 393-405.	3.1	39
13	Extensive in situ radiation of feather lice on tinamous. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20193005.	2.6	5
14	For common community phylogenetic analyses, go ahead and use synthesis phylogenies. <i>Ecology</i> , 2019, 100, e02788.	3.2	80
15	Rates of niche and phenotype evolution lag behind diversification in a temperate radiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10874-10882.	7.1	115
16	Extensive host-switching of avian feather lice following the Cretaceous-Paleogene mass extinction event. <i>Communications Biology</i> , 2019, 2, 445.	4.4	20
17	Impacts of Inference Method and Data set Filtering on Phylogenomic Resolution in a Rapid Radiation of Ground Squirrels (Xerinae: Marmotini). <i>Systematic Biology</i> , 2019, 68, 298-316.	5.6	33
18	Genomic sequence capture of haemosporidian parasites: Methods and prospects for enhanced study of host-parasite evolution. <i>Molecular Ecology Resources</i> , 2019, 19, 400-410.	4.8	16

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19	Biodiversity synthesis across the green branches of the tree of life. <i>Nature Plants</i> , 2019, 5, 11-13.	9.3	19
20	Spatial Phylogenetics of Florida Vascular Plants: The Effects of Calibration and Uncertainty on Diversity Estimates. <i>IScience</i> , 2019, 11, 57-70.	4.1	41
21	Fully automated sequence alignment methods are comparable to, and much faster than, traditional methods in large data sets: an example with hepatitis B virus. <i>PeerJ</i> , 2019, 7, e6142.	2.0	3
22	Host and parasite morphology influence congruence between host and parasite phylogenies. <i>International Journal for Parasitology</i> , 2018, 48, 641-648.	3.1	12
23	Integrating phylogenomic and population genomic patterns in avian lice provides a more complete picture of parasite evolution. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 95-112.	2.3	22
24	Phylogenomics and the evolution of hemipteroid insects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12775-12780.	7.1	275
25	Simultaneous radiation of bird and mammal lice following the K-Pg boundary. <i>Biology Letters</i> , 2018, 14, 20180141.	2.3	33
26	aTRAM 2.0: An Improved, Flexible Locus Assembler for NGS Data. <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431877454.	1.2	68
27	Composition and distribution of lice (Insecta: Phthiraptera) on Colombian and Peruvian birds: New data on louse-host association in the Neotropics. <i>Biodiversity Data Journal</i> , 2018, 6, e21635.	0.8	8
28	Primates, Lice and Bacteria: Speciation and Genome Evolution in the Symbionts of Hominid Lice. <i>Molecular Biology and Evolution</i> , 2017, 34, 1743-1757.	8.9	51
29	Phylogenomics from Whole Genome Sequences Using aTRAM. <i>Systematic Biology</i> , 2017, 66, syw105.	5.6	47
30	Phylogenomics using Target-restricted Assembly Resolves Intra-generic Relationships of Parasitic Lice (Phthiraptera: <i>Columbicola</i>). <i>Systematic Biology</i> , 2017, 66, syx027.	5.6	22
31	Anchored Hybrid Enrichment-Based Phylogenomics of Leafhoppers and Treehoppers (Hemiptera: Tj ETQq1 1 0.784314 rgBT /Overloc 1.7 110		
32	Two Bacterial Genera, <i>Sodalis</i> and <i>Rickettsia</i> , Associated with the Seal Louse <i>Proechinophthirus fluctus</i> (Phthiraptera: Anoplura). <i>Applied and Environmental Microbiology</i> , 2016, 82, 3185-3197.	3.1	63
33	Unlocking the black box of feather louse diversity: A molecular phylogeny of the hyper-diverse genus <i>Brueelia</i> . <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 737-751.	2.7	62
34	Effects of 16S rDNA sampling on estimates of the number of endosymbiont lineages in sucking lice. <i>PeerJ</i> , 2016, 4, e2187.	2.0	14
35	Data supporting a molecular phylogeny of the hyper-diverse genus <i>Brueelia</i> . <i>Data in Brief</i> , 2015, 5, 1078-1091.	1.0	6
36	aTRAM - automated target restricted assembly method: a fast method for assembling loci across divergent taxa from next-generation sequencing data. <i>BMC Bioinformatics</i> , 2015, 16, 98.	2.6	78

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37	Novel Primers From Informative Nuclear Loci for Louse Molecular Phylogenetics (Insecta:) Tj ETQq1 1 0.784314 rgBT/Overlock 10 Tf 50	1.8	11
38	Genome Sequence of <i>Candidatus</i> <i>Riesia pediculischaeffi</i> , Endosymbiont of Chimpanzee Lice, and Genomic Comparison of Recently Acquired Endosymbionts from Human and Chimpanzee Lice. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2189-2195.	1.8	30
39	Primate <i>scp</i> DNA suggests long-term stability of an African rainforest. <i>Ecology and Evolution</i> , 2012, 2, 2829-2842.	1.9	13
40	Microsatellite loci for testing temporal changes in the population genetics of the Florida mouse (<i>Podomys floridanus</i>). <i>Conservation Genetics Resources</i> , 2011, 3, 135-139.	0.8	1
41	Mutational Meltdown in Primary Endosymbionts: Selection Limits Muller's Ratchet. <i>PLoS ONE</i> , 2009, 4, e4969.	2.5	43
42	Evolutionary Relationships of <i>Candidatus</i> <i>Riesia</i> spp., Endosymbiotic Enterobacteriaceae Living within Hematophagous Primate Lice. <i>Applied and Environmental Microbiology</i> , 2007, 73, 1659-1664.	3.1	90