

Aaron B A Shafer

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

2,521
citations

394421

19
h-index

223800

46
g-index

66
all docs

66
docs citations

66
times ranked

4149
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic diversity and demographic history of the <i>Dromiciops</i> genus (Marsupialia: Microbiotheriidae). <i>Molecular Phylogenetics and Evolution</i> , 2022, 168, 107405.	2.7	8
2	Genomic architecture of phenotypic extremes in a wild cervid. <i>BMC Genomics</i> , 2022, 23, 126.	2.8	59
3	Long-term data reveal effects of climate, road access, and latitude on mountain goat horn size. <i>Journal of Wildlife Management</i> , 2022, 86, .	1.8	2
4	Highland forest's environmental complexity drives landscape genomics and connectivity of the rodent <i>Peromyscus melanotis</i> . <i>Landscape Ecology</i> , 2022, 37, 1653-1671.	4.2	5
5	Genome assembly, annotation, and comparative analysis of the cattail <i>Typha latifolia</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	6
6	Using total <i>scp</i> RNA quality metrics for time since deposition estimates in degrading bloodstains. <i>Journal of Forensic Sciences</i> , 2022, 67, 1776-1785.	1.6	2
7	An Exploratory Time Since Deposition Analysis of Whole Blood Using Metrics of DNA Degradation and Visible Absorbance Spectroscopy. <i>Pure and Applied Geophysics</i> , 2021, 178, 735-743.	1.9	14
8	Quantifying visible absorbance changes and DNA degradation in aging bloodstains under extreme temperatures. <i>Forensic Science International</i> , 2021, 318, 110627.	2.2	15
9	Development of an environmental DNA metabarcoding assay for aquatic vascular plant communities. <i>Environmental DNA</i> , 2021, 3, 372-387.	5.8	22
10	Gut microbiome composition predicts summer core range size in two divergent ungulates. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	7
11	Characterizing the demographic history and prion protein variation to infer susceptibility to chronic wasting disease in a naïve population of white-tailed deer (<i>Odocoileus virginianus</i>). <i>Evolutionary Applications</i> , 2021, 14, 1528-1539.	3.1	6
12	Whole bovine blood use in forensic research: Sample preparation and storage considerations. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2021, 61, 214-220.	2.1	8
13	The biogeography of <i>Dromiciops</i> in southern South America: Middle Miocene transgressions, speciation and associations with <i>Nothofagus</i> . <i>Molecular Phylogenetics and Evolution</i> , 2021, 163, 107234.	2.7	16
14	Integrating Genetic Data and Demographic Modeling to Facilitate Conservation of Small, Isolated Mountain Goat Populations. <i>Journal of Wildlife Management</i> , 2021, 85, 271-282.	1.8	7
15	Population demographic history and adaptability of the vulnerable Lolokou Sucker Frog. <i>Genetica</i> , 2020, 148, 207-213.	1.1	1
16	Heritability Estimates of Antler and Body Traits in White-Tailed Deer (<i>Odocoileus virginianus</i>) From Genomic-Relatedness Matrices. <i>Journal of Heredity</i> , 2020, 111, 429-435.	2.4	6
17	Determinants of genetic variation across eco-evolutionary scales in pinnipeds. <i>Nature Ecology and Evolution</i> , 2020, 4, 1095-1104.	7.8	47
18	Panmictic population genetic structure of northern British Columbia mountain goats (<i>Oreamnos</i>)	1.5	9

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19	Genome Assembly and Analysis of the North American Mountain Goat (<i>Oreamnos americanus</i>) Reveals Species-Level Responses to Extreme Environments. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 437-442.	1.8	11
20	The complexity of co-limitation: nutrigenomics reveal non-additive interactions of calcium and phosphorus on gene expression in <i>Daphnia pulex</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20202302.	2.6	4
21	Genome-scale sampling suggests cryptic epigenetic structuring and insular divergence in Canada lynx. <i>Molecular Ecology</i> , 2019, 28, 3186-3196.	3.9	25
22	Blood transcriptomics of captive forest musk deer (<i>Moschus berezovskii</i>) and possible associations with the immune response to abscesses. <i>Scientific Reports</i> , 2018, 8, 599.	3.3	17
23	Demographic histories and genetic diversity across pinnipeds are shaped by human exploitation, ecology and life-history. <i>Nature Communications</i> , 2018, 9, 4836.	12.8	49
24	Genome Sequence of Peacock Reveals the Peculiar Case of a Glittering Bird. <i>Frontiers in Genetics</i> , 2018, 9, 392.	2.3	32
25	The Peril of Gene-Targeted Conservation. <i>Trends in Ecology and Evolution</i> , 2018, 33, 827-839.	8.7	104
26	Population Genomics of Ungulates. <i>Population Genomics</i> , 2018, , 185-209.	0.5	4
27	Genetic structure and population history of wintering Asian Great Bustard (<i>Otis tarda dybowskii</i>) in China: implications for conservation. <i>Journal of Ornithology</i> , 2017, 158, 761-772.	1.1	13
28	Inferring Demographic History Using Genomic Data. <i>Population Genomics</i> , 2017, , 511-537.	0.5	16
29	Bioinformatic processing of RAD-seq data dramatically impacts downstream population genetic inference. <i>Methods in Ecology and Evolution</i> , 2017, 8, 907-917.	5.2	253
30	Comparative Analysis of the Gut Microbial Communities in Forest and Alpine Musk Deer Using High-Throughput Sequencing. <i>Frontiers in Microbiology</i> , 2017, 8, 572.	3.5	73
31	Disruptive selection without genome-wide evolution across a migratory divide. <i>Molecular Ecology</i> , 2016, 25, 2529-2541.	3.9	32
32	Cross-Species Application of SNP Chips is Not Suitable for Identifying Runs of Homozygosity. <i>Journal of Heredity</i> , 2016, 107, 193-195.	2.4	11
33	Reply to Garner et al.. <i>Trends in Ecology and Evolution</i> , 2016, 31, 83-84.	8.7	24
34	Forecasting Ecological Genomics: High-Tech Animal Instrumentation Meets High-Throughput Sequencing. <i>PLoS Biology</i> , 2016, 14, e1002350.	5.6	22
35	Recombination and selection in the major histocompatibility complex of the endangered forest musk deer (<i>Moschus berezovskii</i>). <i>Scientific Reports</i> , 2015, 5, 17285.	3.3	13
36	Genomics and the challenging translation into conservation practice. <i>Trends in Ecology and Evolution</i> , 2015, 30, 78-87.	8.7	469

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37	Demographic inferences using short-read genomic data in an approximate Bayesian computation framework: in silico evaluation of power, biases and proof of concept in Atlantic walrus. <i>Molecular Ecology</i> , 2015, 24, 328-345.	3.9	54
38	Cambronne, A. 2013. <i>Deerland: America's Hunt for Ecological Balance and the Essence of Wildness</i> . Lyons Press, Guilford, Connecticut, 272 pp. ISBN 978-0-7627-8027-3, price (paper), \$18.95. <i>Journal of Mammalogy</i> , 2014, 95, 433-433.	1.3	0
39	Fine-scale genetic correlates to condition and migration in a wild cervid. <i>Evolutionary Applications</i> , 2014, 7, 937-948.	3.1	22
40	Linking genotype, ecotype, and phenotype in an intensively managed large carnivore. <i>Evolutionary Applications</i> , 2014, 7, 301-312.	3.1	12
41	Widespread evidence for incipient ecological speciation: a meta-analysis of isolation-by-ecology. <i>Ecology Letters</i> , 2013, 16, 940-950.	6.4	262
42	(Lack of) Genetic Diversity in Immune Genes Predates Glacial Isolation in the North American Mountain Goat (<i>Oreamnos americanus</i>). <i>Journal of Heredity</i> , 2012, 103, 371-379.	2.4	21
43	Habitat selection predicts genetic relatedness in an alpine ungulate. <i>Ecology</i> , 2012, 93, 1317-1329.	3.2	71
44	Temporal dynamics of genetic variability in a mountain goat (<i>Oreamnos americanus</i>) population. <i>Molecular Ecology</i> , 2011, 20, 1601-1611.	3.9	31
45	HOT SPOTS OF GENETIC DIVERSITY DESCENDED FROM MULTIPLE PLEISTOCENE REFUGIA IN AN ALPINE UNGULATE. <i>Evolution; International Journal of Organic Evolution</i> , 2011, 65, 125-138.	2.3	72
46	Past bottlenecks and current population fragmentation of endangered huemul deer (<i>Hippocamelus</i>) in the Andes. <i>Conservation Genetics</i> , 2011, 12, 1261-1268.	2.5	29
47	Deciphering translocations from relicts in Baranof Island mountain goats: is an endemic genetic lineage at risk?. <i>Conservation Genetics</i> , 2011, 12, 1261-1268.	1.5	8
48	Does reduced heterozygosity influence dispersal? A test using spatially structured populations in an alpine ungulate. <i>Biology Letters</i> , 2011, 7, 433-435.	2.3	15
49	Placing the mountain goat: A total evidence approach to testing alternative hypotheses. <i>Molecular Phylogenetics and Evolution</i> , 2010, 55, 18-25.	2.7	13
50	Of glaciers and refugia: a decade of study sheds new light on the phylogeography of northwestern North America. <i>Molecular Ecology</i> , 2010, 19, 4589-4621.	3.9	435
51	Cophylogeny of <i>Nosema</i> (Microsporidia: Nosematidae) and Bees (Hymenoptera: Apidae) Suggests Both Cospeciation and a Host-switch. <i>Journal of Parasitology</i> , 2009, 95, 198-203.	0.7	33
52	Following the SINEs: A Taxonomic Revision of the Long-Tailed Shrew Complex, <i>Sorex dispar</i> and <i>S. gaspensis</i> . <i>Journal of Mammalogy</i> , 2008, 89, 1421-1427.	1.3	2
53	A Population Crash of the Red-backed Vole (<i>Myodes gapperi</i>) in Nova Scotia Inferred from Bycatch of the Long-tailed Shrew (<i>Sorex dispar</i>). <i>Northeastern Naturalist</i> , 2008, 15, 626-629.	0.3	2
54	Phylogenetic relationships among Nearctic shrews of the genus <i>Sorex</i> (Insectivora, Soricidae) inferred from combined cytochrome b and inter-SINE fingerprint data using Bayesian analysis. <i>Molecular Phylogenetics and Evolution</i> , 2007, 44, 192-203.	2.7	15

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55	A Disjunct Population of <i>Sorex dispar</i> (Long-tailed Shrew) in Nova Scotia. <i>Northeastern Naturalist</i> , 2006, 13, 603-608.	0.3	4