

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 | Genomics and the challenging translation into conservation practice. <i>Trends in Ecology and Evolution</i> , 2015, 30, 78-87. | 8.7 | 469 |
| 2 | 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 |
| 3 | Widespread evidence for incipient ecological speciation: a meta-analysis of isolation-by-ecology. <i>Ecology Letters</i> , 2013, 16, 940-950. | 6.4 | 262 |
| 4 | 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 |
| 5 | The Peril of Gene-Targeted Conservation. <i>Trends in Ecology and Evolution</i> , 2018, 33, 827-839. | 8.7 | 104 |
| 6 | 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 |
| 7 | 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 |
| 8 | Habitat selection predicts genetic relatedness in an alpine ungulate. <i>Ecology</i> , 2012, 93, 1317-1329. | 3.2 | 71 |
| 9 | Genomic architecture of phenotypic extremes in a wild cervid. <i>BMC Genomics</i> , 2022, 23, 126. | 2.8 | 59 |
| 10 | 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 |
| 11 | 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 |
| 12 | Determinants of genetic variation across eco-evolutionary scales in pinnipeds. <i>Nature Ecology and Evolution</i> , 2020, 4, 1095-1104. | 7.8 | 47 |
| 13 | 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 |
| 14 | Disruptive selection without genome-wide evolution across a migratory divide. <i>Molecular Ecology</i> , 2016, 25, 2529-2541. | 3.9 | 32 |
| 15 | Genome Sequence of Peacock Reveals the Peculiar Case of a Glittering Bird. <i>Frontiers in Genetics</i> , 2018, 9, 392. | 2.3 | 32 |
| 16 | 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 |
| 17 | Past bottlenecks and current population fragmentation of endangered huemul deer (<i>Hippocamelus</i>) | 1.5 | 29 |
| 18 | Genome-scale sampling suggests cryptic epigenetic structuring and insular divergence in Canada lynx. <i>Molecular Ecology</i> , 2019, 28, 3186-3196. | 3.9 | 25 |

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|----|--|-----|-----------|
| 19 | Reply to Garner et al.. Trends in Ecology and Evolution, 2016, 31, 83-84. | 8.7 | 24 |
| 20 | Fine-scale genetic correlates to condition and migration in a wild cervid. Evolutionary Applications, 2014, 7, 937-948. | 3.1 | 22 |
| 21 | Development of an environmental DNA metabarcoding assay for aquatic vascular plant communities. Environmental DNA, 2021, 3, 372-387. | 5.8 | 22 |
| 22 | Forecasting Ecological Genomics: High-Tech Animal Instrumentation Meets High-Throughput Sequencing. PLoS Biology, 2016, 14, e1002350. | 5.6 | 22 |
| 23 | (Lack of) Genetic Diversity in Immune Genes Predates Glacial Isolation in the North American Mountain Goat (<i>Oreamnos americanus</i>). Journal of Heredity, 2012, 103, 371-379. | 2.4 | 21 |
| 24 | Blood transcriptomics of captive forest musk deer (<i>Moschus berezovskii</i>) and possible associations with the immune response to abscesses. Scientific Reports, 2018, 8, 599. | 3.3 | 17 |
| 25 | Inferring Demographic History Using Genomic Data. Population Genomics, 2017, , 511-537. | 0.5 | 16 |
| 26 | The biogeography of <i>Dromiciops</i> in southern South America: Middle Miocene transgressions, speciation and associations with <i>Nothofagus</i> . Molecular Phylogenetics and Evolution, 2021, 163, 107234. | 2.7 | 16 |
| 27 | 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. Molecular Phylogenetics and Evolution, 2007, 44, 192-203. | 2.7 | 15 |
| 28 | Does reduced heterozygosity influence dispersal? A test using spatially structured populations in an alpine ungulate. Biology Letters, 2011, 7, 433-435. | 2.3 | 15 |
| 29 | Quantifying visible absorbance changes and DNA degradation in aging bloodstains under extreme temperatures. Forensic Science International, 2021, 318, 110627. | 2.2 | 15 |
| 30 | An Exploratory Time Since Deposition Analysis of Whole Blood Using Metrics of DNA Degradation and Visible Absorbance Spectroscopy. Pure and Applied Geophysics, 2021, 178, 735-743. | 1.9 | 14 |
| 31 | Placing the mountain goat: A total evidence approach to testing alternative hypotheses. Molecular Phylogenetics and Evolution, 2010, 55, 18-25. | 2.7 | 13 |
| 32 | Recombination and selection in the major histocompatibility complex of the endangered forest musk deer (<i>Moschus berezovskii</i>). Scientific Reports, 2015, 5, 17285. | 3.3 | 13 |
| 33 | Genetic structure and population history of wintering Asian Great Bustard (<i>Otis tarda dybowskii</i>) in China: implications for conservation. Journal of Ornithology, 2017, 158, 761-772. | 1.1 | 13 |
| 34 | Linking genotype, ecotype, and phenotype in an intensively managed large carnivore. Evolutionary Applications, 2014, 7, 301-312. | 3.1 | 12 |
| 35 | Cross-Species Application of SNP Chips is Not Suitable for Identifying Runs of Homozygosity. Journal of Heredity, 2016, 107, 193-195. | 2.4 | 11 |
| 36 | Genome Assembly and Analysis of the North American Mountain Goat (<i>Oreamnos americanus</i>) Reveals Species-Level Responses to Extreme Environments. G3: Genes, Genomes, Genetics, 2020, 10, 437-442. | 1.8 | 11 |

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|----|---|-----|-----------|
| 37 | Panmictic population genetic structure of northern British Columbia mountain goats (<i>Oreamnos</i>) Tj ETQq1 1 0.784314 rgBT gOverloc | 1.5 | 9 |
| 38 | 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 |
| 39 | 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 |
| 40 | 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 |
| 41 | Gut microbiome composition predicts summer core range size in two divergent ungulates. <i>FEMS Microbiology Ecology</i> , 2021, 97, . | 2.7 | 7 |
| 42 | 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 |
| 43 | 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 |
| 44 | 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 |
| 45 | Genome assembly, annotation, and comparative analysis of the cattail <i>Typha latifolia</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, . | 1.8 | 6 |
| 46 | 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 |
| 47 | 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 |
| 48 | Population Genomics of Ungulates. <i>Population Genomics</i> , 2018, , 185-209. | 0.5 | 4 |
| 49 | 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 |
| 50 | 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 |
| 51 | 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 |
| 52 | 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 |
| 53 | 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 |
| 54 | Population demographic history and adaptability of the vulnerable Lolokou Sucker Frog. <i>Genetica</i> , 2020, 148, 207-213. | 1.1 | 1 |

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|----|--|-----|-----------|
| 55 | Cambronne, A.2013. Deerland: America's Hunt for Ecological Balance and the Essence of Wildness. Lyons Press, Guilford, Connecticut, 272 pp. ISBN 978-0-7627-8027-3, price (paper), \$18.95. Journal of Mammalogy, 2014, 95, 433-433. | 1.3 | 0 |