# Michael K Schwartz

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/8866517/publications.pdf

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| 184 | 13,844 | 50276 | 24982 |
|---|---|---|---|
| papers | citations | 46 h-index | 109 g-index |

| 188 | 188 | 188 | 12329 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Mixedâ€severity wildfire and salvage logging affect the populations of a forestâ€dependent carnivoran and a competitor. Ecosphere, 2022, 13, . | 2.2 | 4 |
| 2 | Wolf Dispersal Patterns in the Italian Alps and Implications for Wildlife Diseases Spreading. Animals, 2022, 12, 1260. | 2.3 | 9 |
| 3 | <scp>eDNAssay</scp>: A machine learning tool that accurately predicts <scp>qPCR</scp> crossâ€amplification. Molecular Ecology Resources, 2022, 22, 2994-3005. | 4.8 | 7 |
| 4 | Certain detection of uncertain taxa: eDNA detection of a cryptic mountain sucker ( Pantosteus jordani) Tj ETQq0 0 0 rgBT /Overlock 10 T | 5.8 | 6 |
| 5 | Allometric scaling of eDNA production in streamâ€dwelling brook trout (Salvelinus fontinalis) inferred from population size structure. Environmental DNA, 2021, 3, 553-560. | 5.8 | 15 |
| 6 | Tools and Technologies for Quantifying Spread and Impacts of Invasive Species. , 2021, , 243-265. | | 1 |
| 7 | Molecular genetic analysis of air, water, and soil to detect big brown bats in North America. Biological Conservation, 2021, 261, 109252. | 4.1 | 16 |
| 8 | Making environmental DNA (eDNA) biodiversity records globally accessible. Environmental DNA, 2021, 3, 699-705. | 5.8 | 38 |
| 9 | Phylogeography of moose in western North America. Journal of Mammalogy, 2020, 101, 10-23. | 1.3 | 11 |
| 10 | Occupancy Patterns in a Reintroduced Fisher Population during Reestablishment. Journal of Wildlife Management, 2020, 84, 344-358. | 1.8 | 9 |
| 11 | Parallel, targeted analysis of environmental samples via highâ€throughput quantitative PCR. Environmental DNA, 2020, 2, 544-553. | 5.8 | 23 |
| 12 | Identifying Candidate Genetic Markers of CDV Cross-Species Pathogenicity in African Lions. Pathogens, 2020, 9, 872. | 2.8 | 9 |
| 13 | Immigration does not offset harvest mortality in groups of a cooperatively breeding carnivore. Animal Conservation, 2020, 23, 750-761. | 2.9 | 13 |
| 14 | Wolverine Occupancy, Spatial Distribution, and Monitoring Design. Journal of Wildlife Management, 2020, 84, 841-851. | 1.8 | 17 |
| 15 | Plioceneâ€“Early Pleistocene Geological Events Structure Pacific Martens (Martes caurina). Journal of Heredity, 2020, 111, 169-181. | 2.4 | 5 |
| 16 | Population Genomics for the Management of Wild Vertebrate Populations. Population Genomics, 2020, , 419-436. | 0.5 | 7 |
| 17 | Environmental DNA Sampling Informs Fish Eradication Efforts: Case Studies and Lessons Learned. North American Journal of Fisheries Management, 2020, 40, 488-508. | 1.0 | 18 |
| 18 | Landscape genetics of wolverines (Gulo gulo): scale-dependent effects of bioclimatic, topographic, and anthropogenic variables. Journal of Mammalogy, 2020, 101, 790-803. | 1.3 | 14 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Crossâ€species transmission and evolutionary dynamics of canine distemper virus during a spillover in African lions of Serengeti National Park. Molecular Ecology, 2020, 29, 4308-4321. | 3.9 | 18 |
| 20 | An Inventory of Springsnails (Pyrgulopsis spp.) in and Adjacent to the Spring Mountains, Nevada. Western North American Naturalist, 2020, 80, 183. | 0.4 | 2 |
| 21 | Exploiting the Winter Trophic Relationship between Weasels (Mustela spp.) and their Microtine Prey as a Survey Method for Weasels in Meadow Ecosystems. Northwest Science, 2020, 93, 185. | 0.2 | 3 |
| 22 | Detection of 4 imperiled western North American freshwater mussel species from environmental DNA with multiplex qPCR assays. Freshwater Science, 2020, 39, 762-772. | 1.8 | 7 |
| 23 | Demographic fragmentation of a protected wolverine population bisected by a major transportation corridor. Biological Conservation, 2019, 236, 616-625. | 4.1 | 23 |
| 24 | Using environmental DNA sampling to monitor the invasion of nonnative Esox lucius (northern pike) in the Columbia River basin, USA. Environmental DNA, 2019, 1, 215-226. | 5.8 | 21 |
| 25 | Identifying predators from saliva at kill sites with limited remains. Wildlife Society Bulletin, 2019, 43, 546-557. | 1.6 | 5 |
| 26 | Integrative taxonomy refutes a species hypothesis: The asymmetric hybrid origin of Arsapnia arapahoe (Plecoptera, Capniidae). Ecology and Evolution, 2019, 9, 1364-1377. | 1.9 | 6 |
| 27 | Estimating abundance of a cryptic social carnivore using spatially explicit captureâ€“recapture. Wildlife Society Bulletin, 2019, 43, 31-41. | 1.6 | 17 |
| 28 | Using environmental DNA methods to improve winter surveys for rare carnivores: DNA from snow and improved noninvasive techniques. Biological Conservation, 2019, 229, 50-58. | 4.1 | 78 |
| 29 | Repurposing Environmental DNA Samples to Verify the Distribution of Rocky Mountain Tailed Frogs in the Warm Springs Creek Basin, Montana. Northwest Science, 2019, 93, 85. | 0.2 | 3 |
| 30 | Status of Pacific Martens (Martes caurina) on the Olympic Peninsula, Washington. Northwest Science, 2019, 93, 122. | 0.2 | 1 |
| 31 | Evolutionary Community Ecology: Time to Think Outside the (Taxonomic) Box. Trends in Ecology and Evolution, 2018, 33, 240-250. | 8.7 | 25 |
| 32 | Repurposing environmental DNA samplesâ€”detecting the western pearlshell ( Margaritifera falcata ) as a proof of concept. Ecology and Evolution, 2018, 8, 2659-2670. | 1.9 | 30 |
| 33 | Dynamic occupancy modelling reveals a hierarchy of competition among fishers, grey foxes and ringtails. Journal of Animal Ecology, 2018, 87, 813-824. | 2.8 | 24 |
| 34 | Crowdâ€sourced Databases as Essential Elements for Forest Service Partnerships and Aquatic Resource Conservation. Fisheries, 2018, 43, 423-430. | 0.8 | 14 |
| 35 | Quantifying functional connectivity: The role of breeding habitat, abundance, and landscape features on rangeâ€wide gene flow in sageâ€grouse. Evolutionary Applications, 2018, 11, 1305-1321. | 3.1 | 24 |
| 36 | Fineâ€scale environmental <scp>DNA</scp> sampling reveals climateâ€mediated interactions between native and invasive trout species. Ecosphere, 2018, 9, e02500. | 2.2 | 29 |

| # | Article | IF | Citations |
|---|---|---|---|
| 37 | qPCR detection of Sturgeon chub (Macrhybopsis gelida) DNA in environmental samples. PLoS ONE, 2018, 13, e0209601. | 2.5 | 5 |
| 38 | An improved environmental DNA assay for bull trout (Salvelinus confluentus) based on the ribosomal internal transcribed spacer I. PLoS ONE, 2018, 13, e0206851. | 2.5 | 28 |
| 39 | Inferring presence of the western toad (Anaxyrus boreas) species complex using environmental DNA. Global Ecology and Conservation, 2018, 15, e00438. | 2.1 | 10 |
| 40 | Capture enrichment of aquatic environmental DNA: A first proof of concept. Molecular Ecology Resources, 2018, 18, 1392-1401. | 4.8 | 42 |
| 41 | A Non-Invasive Sampling Method for Detecting Non-Native Smallmouth Bass (Micropterus) Tj ETQq1 1 0.784314 rgBT /Overlock 1 | 0.2 | 15 |
| 42 | The genetic network of greater sageâ€grouse: Rangeâ€wide identification of keystone hubs of connectivity. Ecology and Evolution, 2018, 8, 5394-5412. | 1.9 | 18 |
| 43 | Comment: The Importance of Sound Methodology in Environmental DNA Sampling. North American Journal of Fisheries Management, 2018, 38, 592-596. | 1.0 | 38 |
| 44 | Molecular Detection of Northern Leatherside Chub (Lepidomeda copei) DNA in Environmental Samples. Western North American Naturalist, 2018, 78, 92. | 0.4 | 1 |
| 45 | Red Fox Ancestry and Connectivity Assessments Reveal Minimal Fur Farm Introgression in Greater Yellowstone Ecosystem. Journal of Fish and Wildlife Management, 2018, 9, 519-530. | 0.9 | 4 |
| 46 | Genetic recapture identifies long-distance breeding dispersal in Greater Sage-Grouse (Centrocercus urophasianus). Condor, 2017, 119, 155-166. | 1.6 | 15 |
| 47 | Ski areas affect Pacific marten movement, habitat use, and density. Journal of Wildlife Management, 2017, 81, 892-904. | 1.8 | 12 |
| 48 | Ecological segregation moderates a climactic conclusion to trout hybridization. Global Change Biology, 2017, 23, 5021-5023. | 9.5 | 7 |
| 49 | Sexâ€biased dispersal and spatial heterogeneity affect landscape resistance to gene flow in fisher. Ecosphere, 2017, 8, e01839. | 2.2 | 17 |
| 50 | Marine mammal subspecies in the age of genetics: Introductory remarks from the Associate Editor and Editorâ€inâ€Chief of Marine Mammal Science. Marine Mammal Science, 2017, 33, 7-11. | 1.8 | 4 |
| 51 | Tradeâ€offs and efficiencies in optimal budgetâ€constrained multispecies corridor networks. Conservation Biology, 2017, 31, 192-202. | 4.7 | 53 |
| 52 | A Noninvasive Tool to Assess the Distribution of Pacific Lamprey (Entosphenus tridentatus) in the Columbia River Basin. PLoS ONE, 2017, 12, e0169334. | 2.5 | 11 |
| 53 | Environmental DNA assays for the sister taxa sauger (Sander canadensis) and walleye (Sander vitreus). PLoS ONE, 2017, 12, e0176459. | 2.5 | 2 |
| 54 | Where the Wild Things Are: A Research Agenda for Studying the Wildlife-Wilderness Relationship. Journal of Forestry, 2016, 114, 311-319. | 1.0 | 2 |

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|---|---|---|---|
| 55 | Environmental DNA Marker Development with Sparse Biological Information: A Case Study on Opossum Shrimp (Mysis diluviana). PLoS ONE, 2016, 11, e0161664. | 2.5 | 17 |
| 56 | <scp>SNP</scp> discovery in candidate adaptive genes using exon capture in a freeâ€ranging alpine ungulate. Molecular Ecology Resources, 2016, 16, 1147-1164. | 4.8 | 21 |
| 57 | Sampling large geographic areas for rare species using environmental <scp>DNA</scp>: a study of bull trout Salvelinus confluentus occupancy in western Montana. Journal of Fish Biology, 2016, 88, 1215-1222. | 1.6 | 84 |
| 58 | Latent spatial models and sampling design for landscape genetics. Annals of Applied Statistics, 2016, 10, . | 1.1 | 11 |
| 59 | An environmental DNA marker for detecting nonnative brown trout (Salmo trutta). Conservation Genetics Resources, 2016, 8, 259-261. | 0.8 | 7 |
| 60 | Long-distance dispersal of a subadult male cougar from South Dakota to Connecticut documented with DNA evidence. Journal of Mammalogy, 2016, 97, 1435-1440. | 1.3 | 30 |
| 61 | Recipient of the 2015 Molecular Ecology Prize: Fred Allendorf. Molecular Ecology, 2016, 25, 450-453. | 3.9 | 0 |
| 62 | Hierarchical population structure in greater sage-grouse provides insight into management boundary delineation. Conservation Genetics, 2016, 17, 1417-1433. | 1.5 | 13 |
| 63 | Identification of landscape features influencing gene flow: How useful are habitat selection models?. Evolutionary Applications, 2016, 9, 805-817. | 3.1 | 36 |
| 64 | Discovery of 20,000 RADâ€“SNPs and development of a 52-SNP array for monitoring river otters. Conservation Genetics Resources, 2016, 8, 299-302. | 0.8 | 9 |
| 65 | An environmental DNA assay for detecting Arctic grayling in the upper Missouri River basin, North America. Conservation Genetics Resources, 2016, 8, 197-199. | 0.8 | 30 |
| 66 | Conservation genomics of natural and managed populations: building a conceptual and practical framework. Molecular Ecology, 2016, 25, 2967-2977. | 3.9 | 141 |
| 67 | Patterns of hybridization among cutthroat trout and rainbow trout in northern Rocky Mountain streams. Ecology and Evolution, 2016, 6, 688-706. | 1.9 | 40 |
| 68 | Understanding environmental DNA detection probabilities: A case study using a stream-dwelling char Salvelinus fontinalis. Biological Conservation, 2016, 194, 209-216. | 4.1 | 307 |
| 69 | Assessing temporal genetic variation in a cougar population: influence of harvest and neighboring populations. Conservation Genetics, 2016, 17, 379-388. | 1.5 | 5 |
| 70 | An eDNA assay for river otter detection: a tool for surveying a semi-aquatic mammal. Conservation Genetics Resources, 2016, 8, 5-7. | 0.8 | 19 |
| 71 | Reply to Garner et al.. Trends in Ecology and Evolution, 2016, 31, 83-84. | 8.7 | 24 |
| 72 | Quantitative PCR Assays for Detecting Loach Minnow (Rhinichthys cobitis) and Spikedace (Meda) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 | 2.5 | 4 |

| # | Article | IF | Citations |
|---|---|---|---|
| 73 | Climate, Demography, and Zoogeography Predict Introgression Thresholds in Salmonid Hybrid Zones in Rocky Mountain Streams. PLoS ONE, 2016, 11, e0163563. | 2.5 | 27 |
| 74 | Estimating Bighorn Sheep (Ovis canadensis) Abundance Using Noninvasive Sampling at a Mineral Lick within a National Park Wilderness Area. Western North American Naturalist, 2015, 75, 181-191. | 0.4 | 10 |
| 75 | The Dual Challenges of Generality and Specificity When Developing Environmental DNA Markers for Species and Subspecies of Oncorhynchus. PLoS ONE, 2015, 10, e0142008. | 2.5 | 72 |
| 76 | <scp>rSPACE</scp>: Spatially based power analysis for conservation and ecology. Methods in Ecology and Evolution, 2015, 6, 621-625. | 5.2 | 19 |
| 77 | Environmental DNA particle size distribution from Brook Trout (Salvelinus fontinalis). Conservation Genetics Resources, 2015, 7, 639-641. | 0.8 | 79 |
| 78 | Forest structure and species traits mediate projected recruitment declines in western <scp>US</scp> tree species. Global Ecology and Biogeography, 2015, 24, 917-927. | 5.8 | 129 |
| 79 | Temporal correlations in population trends: Conservation implications from time-series analysis of diverse animal taxa. Biological Conservation, 2015, 192, 247-257. | 4.1 | 52 |
| 80 | Integrating resource selection into spatial captureâ€recapture models for large carnivores. Ecosphere, 2015, 6, 1-15. | 2.2 | 49 |
| 81 | Genomics and the challenging translation into conservation practice. Trends in Ecology and Evolution, 2015, 30, 78-87. | 8.7 | 469 |
| 82 | Distance, flow and <scp>PCR</scp> inhibition: e<scp>DNA</scp> dynamics in two headwater streams. Molecular Ecology Resources, 2015, 15, 216-227. | 4.8 | 391 |
| 83 | Cottus schitsuumsh, a new species of sculpin (Scorpaeniformes: Cottidae)Âin the Columbia River basin, Idaho-Montana, USA. Zootaxa, 2014, 3755, 241-58. | 0.5 | 9 |
| 84 | Spatially Explicit Power Analyses for Occupancyâ€Based Monitoring of Wolverine in the U.S. Rocky Mountains. Conservation Biology, 2014, 28, 52-62. | 4.7 | 47 |
| 85 | Sampling affects the detection of genetic subdivision and conservation implications for fisher in the Sierra Nevada. Conservation Genetics, 2014, 15, 123-136. | 1.5 | 33 |
| 86 | A blocking primer increases specificity in environmental DNA detection of bull trout (Salvelinus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22 | 0.8 | 21 |
| 87 | Lack of sex-biased dispersal promotes fine-scale genetic structure in alpine ungulates. Conservation Genetics, 2014, 15, 837-851. | 1.5 | 16 |
| 88 | Recovery of wolverines in the Western United States: Recent extirpation and recolonization or range retraction and expansion?. Journal of Wildlife Management, 2014, 78, 325-334. | 1.8 | 15 |
| 89 | Modeling the effects of dispersal and patch size on predicted fisher (Pekania [Martes] pennanti) distribution in the U.S. Rocky Mountains. Biological Conservation, 2014, 169, 89-98. | 4.1 | 19 |
| 90 | Evaluating sample allocation and effort in detecting population differentiation for discrete and continuously distributed individuals. Conservation Genetics, 2014, 15, 981-992. | 1.5 | 32 |

| # | Article | IF | Citations |
|---|---|---|---|
| 91 | Pronounced differences in genetic structure despite overall ecological similarity for two Ambystoma salamanders in the same landscape. Conservation Genetics, 2014, 15, 573-591. | 1.5 | 30 |
| 92 | Sex-Biased Gene Flow Among Elk in the Greater Yellowstone Ecosystem. Journal of Fish and Wildlife Management, 2014, 5, 124-132. | 0.9 | 3 |
| 93 | Meta-analyses of habitat selection by fishers at resting sites in the pacific coastal region. Journal of Wildlife Management, 2013, 77, 965-974. | 1.8 | 45 |
| 94 | Estimating Abundance and Survival in the Endangered Point Arena Mountain Beaver Using Noninvasive Genetic Methods. Northwest Science, 2013, 87, 126-139. | 0.2 | 2 |
| 95 | Stand- and landscape-scale selection of large trees by fishers in the Rocky Mountains of Montana and Idaho. Forest Ecology and Management, 2013, 305, 103-111. | 3.2 | 20 |
| 96 | The climate velocity of the contiguous <scp>U</scp>nited <scp>S</scp>tates during the 20th century. Global Change Biology, 2013, 19, 241-251. | 9.5 | 267 |
| 97 | Spatial regression methods capture prediction uncertainty in species distribution model projections through time. Global Ecology and Biogeography, 2013, 22, 242-251. | 5.8 | 29 |
| 98 | Effects of Weighting Schemes on the Identification of Wildlife Corridors Generated with Leastâ€Cost Methods. Conservation Biology, 2013, 27, 145-154. | 4.7 | 45 |
| 99 | <scp>DNA</scp> barcoding at riverscape scales: assessing biodiversity among fishes of the genus <scp>C</scp>ottus (<scp>T</scp>eleostei) in northern <scp>R</scp>ocky <scp>M</scp>ountain streams. Molecular Ecology Resources, 2013, 13, 583-595. | 4.8 | 35 |
| 100 | Estimation of effective population size in continuously distributed populations: there goes the neighborhood. Heredity, 2013, 111, 189-199. | 2.6 | 112 |
| 101 | Small geographic range but not panmictic: how forests structure the endangered Point Arena mountain beaver (Aplodontia rufa nigra). Conservation Genetics, 2013, 14, 369-383. | 1.5 | 9 |
| 102 | Genetic Sampling of Palmer's Chipmunks in the Spring Mountains, Nevada. Western North American Naturalist, 2013, 73, 198-210. | 0.4 | 1 |
| 103 | Combined use of mark-recapture and genetic analyses reveals response of a black bear population to changes in food productivity. Journal of Wildlife Management, 2013, 77, 1572-1582. | 1.8 | 12 |
| 104 | Robust Detection of Rare Species Using Environmental DNA: The Importance of Primer Specificity. PLoS ONE, 2013, 8, e59520. | 2.5 | 405 |
| 105 | Breed Locally, Disperse Globally: Fine-Scale Genetic Structure Despite Landscape-Scale Panmixia in a Fire-Specialist. PLoS ONE, 2013, 8, e67248. | 2.5 | 20 |
| 106 | Development of a reliable method for determining sex for a primitive rodent, the Point Arena mountain beaver (Aplodontia rufa nigra). Conservation Genetics Resources, 2012, 4, 975-977. | 0.8 | 2 |
| 107 | Detecting population recovery using gametic disequilibrium-based effective population size estimates. Conservation Genetics Resources, 2012, 4, 987-989. | 0.8 | 8 |
| 108 | Conserving genomic variability in large mammals: Effect of population fluctuations and variance in male reproductive success on variability in Yellowstone bison. Biological Conservation, 2012, 150, 159-166. | 4.1 | 4 |

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|---|---|---|---|
| 109 | Red flags: correlates of impaired species recovery. Trends in Ecology and Evolution, 2012, 27, 542-546. | 8.7 | 34 |
| 110 | Historical and Contemporary DNA Indicate Fisher Decline and Isolation Occurred Prior to the European Settlement of California. PLoS ONE, 2012, 7, e52803. | 2.5 | 29 |
| 111 | Estimating abundance of mountain lions from unstructured spatial sampling. Journal of Wildlife Management, 2012, 76, 1551-1561. | 1.8 | 96 |
| 112 | Development and evaluation of 200 novel SNP assays for population genetic studies of westslope cutthroat trout and genetic identification of related taxa. Molecular Ecology Resources, 2012, 12, 942-949. | 4.8 | 20 |
| 113 | Climate change predicted to shift wolverine distributions, connectivity, and dispersal corridors. , 2011, 21, 2882-2897. | | 92 |
| 114 | Why replication is important in landscape genetics: American black bear in the Rocky Mountains. Molecular Ecology, 2011, 20, 1092-1107. | 3.9 | 165 |
| 115 | Understanding and Estimating Effective Population Size for Practical Application in Marine Species Management. Conservation Biology, 2011, 25, 438-449. | 4.7 | 270 |
| 116 | Integrating motionâ€detection cameras and hair snags for wolverine identification. Journal of Wildlife Management, 2011, 75, 731-739. | 1.8 | 41 |
| 117 | Bridging the gaps between non-invasive genetic sampling and population parameter estimation. European Journal of Wildlife Research, 2011, 57, 1-13. | 1.4 | 52 |
| 118 | Mitochondrial genome sequences illuminate maternal lineages of conservation concern in a rare carnivore. BMC Ecology, 2011, 11, 10. | 3.0 | 66 |
| 119 | Individual identification of Sitka black-tailed deer (Odocoileus hemionus sitkensis) using DNA from fecal pellets. Conservation Genetics Resources, 2010, 2, 115-118. | 0.8 | 30 |
| 120 | Effects of time and rainfall on PCR success using DNA extracted from deer fecal pellets. Conservation Genetics, 2010, 11, 1547-1552. | 1.5 | 88 |
| 121 | Estimation of census and effective population sizes: the increasing usefulness of DNA-based approaches. Conservation Genetics, 2010, 11, 355-373. | 1.5 | 444 |
| 122 | Spatial scaling and multi-model inference in landscape genetics: Martes americana in northern Idaho. Landscape Ecology, 2010, 25, 1601-1612. | 4.2 | 138 |
| 123 | Do male and female blackâ€backed woodpeckers respond differently to gaps in habitat?. Evolutionary Applications, 2010, 3, 263-278. | 3.1 | 28 |
| 124 | Neglect of Genetic Diversity in Implementation of the Convention on Biological Diversity. Conservation Biology, 2010, 24, 86-88. | 4.7 | 182 |
| 125 | Scaleâ€dependent genetic structure of the Idaho giant salamander (Dicamptodon aterrimus) in stream networks. Molecular Ecology, 2010, 19, 898-909. | 3.9 | 44 |
| 126 | Quantifying the lag time to detect barriers in landscape genetics. Molecular Ecology, 2010, 19, 4179-4191. | 3.9 | 426 |

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|---|---|---|---|
| 127 | When are genetic methods useful for estimating contemporary abundance and detecting population trends?. Molecular Ecology Resources, 2010, 10, 684-692. | 4.8 | 82 |
| 128 | Compromising genetic diversity in the wild: unmonitored large-scale release of plants and animals. Trends in Ecology and Evolution, 2010, 25, 520-529. | 8.7 | 454 |
| 129 | The bioclimatic envelope of the wolverine (GuloÂgulo): do climatic constraints limit its geographic distribution?. Canadian Journal of Zoology, 2010, 88, 233-246. | 1.0 | 99 |
| 130 | Landscape Genomics: A Brief Perspective. , 2010, , 165-174. | | 24 |
| 131 | Landscape Genetics. , 2010, , 313-328. | | 1 |
| 132 | Why sampling scheme matters: the effect of sampling scheme on landscape genetic results. Conservation Genetics, 2009, 10, 441-452. | 1.5 | 334 |
| 133 | Wolf survival and population trend using nonâ€invasive captureâ€“recapture techniques in the Western Alps. Journal of Applied Ecology, 2009, 46, 1003-1010. | 4.0 | 93 |
| 134 | Molecules and beyond: assessing the distinctness of the Great Lakes wolf. Molecular Ecology, 2009, 18, 2307-2309. | 3.9 | 15 |
| 135 | Use of Empirically Derived Sourceâ€Destination Models to Map Regional Conservation Corridors. Conservation Biology, 2009, 23, 368-376. | 4.7 | 198 |
| 136 | Uniting ecological and genetic data for the conservation of wild ibex. Animal Conservation, 2009, 12, 103-104. | 2.9 | 3 |
| 137 | Wolverine Confirmation in California after Nearly a Century: Native or Long-Distance Immigrant?. Northwest Science, 2009, 83, 154-162. | 0.2 | 32 |
| 138 | Wolverine gene flow across a narrow climatic niche. Ecology, 2009, 90, 3222-3232. | 3.2 | 166 |
| 139 | Advancing ecological understandings through technological transformations in noninvasive genetics. Molecular Ecology Resources, 2009, 9, 1279-1301. | 4.8 | 296 |
| 140 | Candidate gene microsatellite variation is associated with parasitism in wild bighorn sheep. Biology Letters, 2008, 4, 228-231. | 2.3 | 76 |
| 141 | Using Anecdotal Occurrence Data for Rare or Elusive Species: The Illusion of Reality and a Call for Evidentiary Standards. BioScience, 2008, 58, 549-555. | 4.9 | 148 |
| 142 | Canada Lynx-bobcat (lynx canadensis Ã— L. rufus) Hybrids at the Southern Periphery of Lynx range in Maine, Minnesota and New Brunswick. American Midland Naturalist, 2008, 159, 504-508. | 0.4 | 20 |
| 143 | Does a Population of Cougars Exist in Michigan?. American Midland Naturalist, 2007, 158, 467-471. | 0.4 | 5 |
| 144 | Genetic monitoring as a promising tool for conservation and management. Trends in Ecology and Evolution, 2007, 22, 25-33. | 8.7 | 934 |

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|---|---|---|---|
| 145 | DNA Markers for Identifying Individual Snowshoe Hares Using Field-collected Pellets. Northwest Science, 2007, 81, 316-322. | 0.2 | 7 |
| 146 | Ancient Dna Confirms Native Rocky Mountain Fisher (Martes pennanti) Avoided Early 20th Century Extinction. Journal of Mammalogy, 2007, 88, 921-925. | 1.3 | 13 |
| 147 | Sources and Patterns of Wolverine Mortality in Western Montana. Journal of Wildlife Management, 2007, 71, 2213. | 1.8 | 28 |
| 148 | Development of 22 new microsatellite loci for fishers (Martes pennanti) with variability results from across their range. Molecular Ecology Notes, 2007, 7, 797-801. | 1.7 | 24 |
| 149 | Inferring Geographic Isolation of Wolverines in California Using Historical DNA. Journal of Wildlife Management, 2007, 71, 2170-2179. | 1.8 | 36 |
| 150 | Gene Flow in Complex Landscapes: Testing Multiple Hypotheses with Causal Modeling. American Naturalist, 2006, 168, 486-499. | 2.1 | 571 |
| 151 | Genetic consequences of sex-biased dispersal in a solitary carnivore: Yellowstone cougars. Biology Letters, 2006, 2, 312-315. | 2.3 | 39 |
| 152 | The Efficacy of Wire and Glue Hair Snares in Identifying Mesocarnivores. Wildlife Society Bulletin, 2006, 34, 1152-1161. | 1.6 | 32 |
| 153 | WHEN REINTRODUCTIONS ARE AUGMENTATIONS: THE GENETIC LEGACY OF FISHERS (MARTES PENNANTI) IN MONTANA. Journal of Mammalogy, 2006, 87, 265-271. | 1.3 | 20 |
| 154 | DNA Analysis of Hair and Scat Collected Along Snow Tracks to Document the Presence of Canada Lynx. Wildlife Society Bulletin, 2006, 34, 451-455. | 1.6 | 52 |
| 155 | The Efficacy of Obtaining Genetic-Based Identifications from Putative Wolverine Snow Tracks. Wildlife Society Bulletin, 2006, 34, 1326-1332. | 1.6 | 24 |
| 156 | Development and characterization of microsatellite markers in the Point Arena mountain beaver Aplodontia rufa nigra. Molecular Ecology Notes, 2006, 6, 800-802. | 1.7 | 4 |
| 157 | Detecting genotyping errors and describing American black bear movement in northern Idaho. Ursus, 2006, 17, 138-148. | 0.5 | 42 |
| 158 | Felid sex identification based on noninvasive genetic samples. Molecular Ecology Notes, 2005, 5, 60-61. | 1.7 | 133 |
| 159 | dropout: a program to identify problem loci and samples for noninvasive genetic samples in a capture-mark-recapture framework. Molecular Ecology Notes, 2005, 5, 716-718. | 1.7 | 130 |
| 160 | Gene flow among San Joaquin kit fox populations in a severely changed ecosystem. Conservation Genetics, 2005, 6, 25-37. | 1.5 | 18 |
| 161 | Gene flow after inbreeding leads to higher survival in deer mice. Biological Conservation, 2005, 123, 413-420. | 4.1 | 25 |
| 162 | Moa were many. Proceedings of the Royal Society B: Biological Sciences, 2004, 271, S430-2. | 2.6 | 28 |

| # | Article | IF | Citations |
|---|---|---|---|
| 163 | GENETIC ERRORS ASSOCIATED WITH POPULATION ESTIMATION USING NON-INVASIVE MOLECULAR TAGGING: PROBLEMS AND NEW SOLUTIONS. Journal of Wildlife Management, 2004, 68, 439-448. | 1.8 | 138 |
| 164 | PROVIDING RELIABLE AND ACCURATE GENETIC CAPTUREâ€"MARKâ€"RECAPTURE ESTIMATES IN A COST-EFFECTIVE WAY. Journal of Wildlife Management, 2004, 68, 453-456. | 1.8 | 26 |
| 165 | Hybridization Between Canada Lynx and Bobcats: Genetic Results and Management Implications. Conservation Genetics, 2004, 5, 349-355. | 1.5 | 71 |
| 166 | Landscape location affects genetic variation of Canada lynx ( Lynx canadensis ). Molecular Ecology, 2003, 12, 1807-1816. | 3.9 | 116 |
| 167 | Landscape genetics: combining landscape ecology and population genetics. Trends in Ecology and Evolution, 2003, 18, 189-197. | 8.7 | 1,907 |
| 168 | Measuring and interpreting connectivity for mammals in coniferous forests. , 2003, , 587-613. | | 10 |
| 169 | DNA reveals high dispersal synchronizing the population dynamics of Canada lynx. Nature, 2002, 415, 520-522. | 27.8 | 144 |
| 170 | Rearranging the Deck Chairs on the Malthusian Ship: Reply to Phifer and Roebuck. Conservation Biology, 2001, 15, 1812-1813. | 4.7 | 1 |
| 171 | KINSHIP, SOCIAL RELATIONSHIPS, AND DEN SHARING IN KIT FOXES. Journal of Mammalogy, 2001, 82, 858. | 1.3 | 44 |
| 172 | Kinship, Social Relationships, and Den Sharing in Kit Foxes. Journal of Mammalogy, 2001, 82, 858-866. | 1.3 | 8 |
| 173 | The Tyranny of Population Growth. Conservation Biology, 2000, 14, 1918-1919. | 4.7 | 8 |
| 174 | Identifying lynx and other North American felids based on MtDNA analysis. Conservation Genetics, 2000, 1, 285-288. | 1.5 | 72 |
| 175 | ESTIMATING ANIMAL ABUNDANCE USING NONINVASIVE DNA SAMPLING: PROMISE AND PITFALLS. , 2000, 10, 283-294. | | 328 |
| 176 | The Tyranny of Population Growth. Conservation Biology, 2000, 14, 1918-1919. | 4.7 | 7 |
| 177 | Female-solicited extrapair matings in Humboldt penguins fail to produce extrapair fertilizations. Behavioral Ecology, 1999, 10, 242-250. | 2.2 | 46 |
| 178 | Using genetics to estimate the size of wild populations: many methods, much potential, uncertain utility. Animal Conservation, 1999, 2, 321-323. | 2.9 | 30 |
| 179 | Hunting and social behaviour of leopard seals (Hydrurga leptonyx) at Seal Island, South Shetland Islands, Antarctica. Journal of Zoology, 1999, 249, 97-109. | 1.7 | 46 |
| 180 | Using genetics to estimate the size of wild populations: many methods, much potential, uncertain utility. Animal Conservation, 1999, 2, 321-323. | 2.9 | 2 |

| # | Article | IF | Citations |
|---|---|---|---|
| 181 | Review of DNA-based census and effective population size estimators. Animal Conservation, 1998, 1, 293-299. | 2.9 | 120 |
| 182 | POPULATION GROWTH OF ANTARCTIC FUR SEALS: LIMITATION BY A TOP PREDATOR, THE LEOPARD SEAL?. Ecology, 1998, 79, 2863-2877. | 3.2 | 70 |
| 183 | Review of DNA-based census and effective population size estimators. Animal Conservation, 1998, 1, 293-299. | 2.9 | 13 |
| 184 | Population Growth of Antarctic Fur Seals: Limitation by a Top Predator, the Leopard Seal?. Ecology, 1998, 79, 2863. | 3.2 | 3 |