

Lisette P Waits

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3028765/publications.pdf>

Version: 2024-02-01

240
papers

19,002
citations

19657

61
h-index

13771

129
g-index

256
all docs

256
docs citations

256
times ranked

12892
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Genetics, Landscape. , 2024, , 503-523. | | 0 |
| 2 | Applying genomics in assisted migration under climate change: Framework, empirical applications, and case studies. <i>Evolutionary Applications</i> , 2022, 15, 3-21. | 3.1 | 23 |
| 3 | Genetic diversity and population structure for ocelots (<i>Leopardus pardalis</i>) in Costa Rica. <i>Journal of Mammalogy</i> , 2022, 103, 68-81. | 1.3 | 2 |
| 4 | Chromosomal-level reference genome assembly of the North American wolverine (<i>Gulo gulo</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62 | 1.8 | 2 |
| 5 | Reviving ghost alleles: Genetically admixed coyotes along the American Gulf Coast are critical for saving the endangered red wolf. <i>Science Advances</i> , 2022, 8, . | 10.3 | 8 |
| 6 | Estimating Coyote Densities with Local, Discrete Bayesian Capture–Recapture Models. <i>Journal of Wildlife Management</i> , 2021, 85, 73-86. | 1.8 | 3 |
| 7 | Primers to highly conserved elements optimized for qPCR–based telomere length measurement in vertebrates. <i>Molecular Ecology Resources</i> , 2021, 21, 59-67. | 4.8 | 5 |
| 8 | Genomic association with pathogen carriage in bighorn sheep (<i>Ovis canadensis</i>). <i>Ecology and Evolution</i> , 2021, 11, 2488-2502. | 1.9 | 4 |
| 9 | Genetic Diversity and Divergence among Bighorn Sheep from Reintroduced Herds in Washington and Idaho. <i>Journal of Wildlife Management</i> , 2021, 85, 1214-1231. | 1.8 | 3 |
| 10 | The role of neutral and adaptive genomic variation in population diversification and speciation in two ground squirrel species of conservation concern. <i>Molecular Ecology</i> , 2021, 30, 4673-4694. | 3.9 | 5 |
| 11 | Long–term monitoring using DNA sampling reveals the dire demographic status of the critically endangered Gobi bear. <i>Ecosphere</i> , 2021, 12, e03696. | 2.2 | 4 |
| 12 | Detection criteria and post–field sample processing influence results and cost efficiency of occupancy–based monitoring. <i>Ecological Applications</i> , 2021, 31, e02404. | 3.8 | 4 |
| 13 | Molecular evaluation of American black bear prey consumption following diversionary feeding. <i>Ursus</i> , 2021, 2021, . | 0.5 | 0 |
| 14 | Teaching an Old Shell New Tricks: Extracting DNA from Current, Historical, and Ancient Mollusk Shells. <i>BioScience</i> , 2021, 71, 235-248. | 4.9 | 4 |
| 15 | Evaluating otter reintroduction outcomes using genetic spatial capture–recapture modified for dendritic networks. <i>Ecology and Evolution</i> , 2021, 11, 15047-15061. | 1.9 | 6 |
| 16 | Comparing performance of multiple non-invasive genetic capture–recapture methods for abundance estimation: a case study with the Sonoran pronghorn <i>Antilocapra americana sonoriensis</i> . <i>Oryx</i> , 2020, 54, 412-420. | 1.0 | 5 |
| 17 | Combining Harvest and Genetics to Estimate Reproduction in Wolves. <i>Journal of Wildlife Management</i> , 2020, 84, 492-504. | 1.8 | 2 |
| 18 | Does harvest affect genetic diversity in grey wolves?. <i>Molecular Ecology</i> , 2020, 29, 3187-3195. | 3.9 | 10 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | Immigration does not offset harvest mortality in groups of a cooperatively breeding carnivore. <i>Animal Conservation</i> , 2020, 23, 750-761. | 2.9 | 13 |
| 20 | Genetic diversity targets and indicators in the CBD post-2020 Global Biodiversity Framework must be improved. <i>Biological Conservation</i> , 2020, 248, 108654. | 4.1 | 285 |
| 21 | Landscape genetics of wolverines (<i>Gulo gulo</i>): scale-dependent effects of bioclimatic, topographic, and anthropogenic variables. <i>Journal of Mammalogy</i> , 2020, 101, 790-803. | 1.3 | 14 |
| 22 | Optimizing Selection of Brown Bear Hair for Noninvasive Genetic Analysis. <i>Wildlife Society Bulletin</i> , 2020, 44, 94-100. | 1.6 | 4 |
| 23 | Natural re-colonization and admixture of wolves (<i>Canis lupus</i>) in the US Pacific Northwest: challenges for the protection and management of rare and endangered taxa. <i>Heredity</i> , 2019, 122, 133-149. | 2.6 | 13 |
| 24 | Phylogeography, genetic diversity, and connectivity of brown bear populations in Central Asia. <i>PLoS ONE</i> , 2019, 14, e0220746. | 2.5 | 14 |
| 25 | Consideration of sample source for establishing reliable genetic microsatellite data from mammalian carnivore specimens held in natural history collections. <i>Journal of Mammalogy</i> , 2019, 100, 1678-1689. | 1.3 | 5 |
| 26 | Gut microbiota and their putative metabolic functions in fragmented Bengal tiger population of Nepal. <i>PLoS ONE</i> , 2019, 14, e0221868. | 2.5 | 13 |
| 27 | Comparing methods of estimating carnivore diets with uncertainty and imperfect detection. <i>Wildlife Society Bulletin</i> , 2019, 43, 651-660. | 1.6 | 12 |
| 28 | Substantial red wolf genetic ancestry persists in wild canids of southwestern Louisiana. <i>Conservation Letters</i> , 2019, 12, e12621. | 5.7 | 18 |
| 29 | Landscape genetic inferences vary with sampling scenario for a pond-breeding amphibian. <i>Ecology and Evolution</i> , 2019, 9, 5063-5078. | 1.9 | 10 |
| 30 | Feeding ecological knowledge: the underutilised power of faecal DNA approaches for carnivore diet analysis. <i>Mammal Review</i> , 2019, 49, 97-112. | 4.8 | 60 |
| 31 | Introgressive hybridization between native and non-local steelhead (<i>Oncorhynchus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 29, 292-302. | 2.0 | 9 |
| 32 | A spatially-explicit, individual-based demogenetic simulation framework for evaluating hybridization dynamics. <i>Ecological Modelling</i> , 2019, 401, 40-51. | 2.5 | 13 |
| 33 | Stable pack abundance and distribution in a harvested wolf population. <i>Journal of Wildlife Management</i> , 2019, 83, 577-590. | 1.8 | 9 |
| 34 | Intrinsic traits of woodland caribou <i>Rangifer tarandus caribou</i> calves depredated by black bears <i>Ursus americanus</i> and coyotes <i>Canis latrans</i> . <i>Wildlife Biology</i> , 2019, 2019, . | 1.4 | 7 |
| 35 | Empirical comparisons of abundance estimators for two sympatric carnivores using noninvasive genetic sampling. <i>Wildlife Biology</i> , 2019, 2019, . | 1.4 | 2 |
| 36 | Spatiotemporal heterogeneity in prey abundance and vulnerability shapes the foraging tactics of an omnivore. <i>Journal of Animal Ecology</i> , 2018, 87, 874-887. | 2.8 | 50 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 37 | Genetic and genomic monitoring with minimally invasive sampling methods. <i>Evolutionary Applications</i> , 2018, 11, 1094-1119. | 3.1 | 126 |
| 38 | Efficient single-€survey estimation of carnivore density using fecal DNA and spatial capture-€recapture: a bobcat case study. <i>Population Ecology</i> , 2018, 60, 197-209. | 1.2 | 33 |
| 39 | Next-€generation metrics for monitoring genetic erosion within populations of conservation concern. <i>Evolutionary Applications</i> , 2018, 11, 1066-1083. | 3.1 | 93 |
| 40 | Evaluating effective population size and genetic diversity of a declining kit fox population using contemporary and historical specimens. <i>Ecology and Evolution</i> , 2018, 8, 12011-12021. | 1.9 | 16 |
| 41 | Integrating multiple genetic detection methods to estimate population density of social and territorial carnivores. <i>Ecosphere</i> , 2018, 9, e02479. | 2.2 | 13 |
| 42 | Alaskan brown bears (<i>Ursus arctos</i>) aggregate and display fidelity to foraging neighborhoods while preying on Pacific salmon along small streams. <i>Ecology and Evolution</i> , 2018, 8, 9048-9061. | 1.9 | 48 |
| 43 | Advances in Using Non-invasive, Archival, and Environmental Samples for Population Genomic Studies. <i>Population Genomics</i> , 2018, , 63-99. | 0.5 | 24 |
| 44 | Species, sex and geo-location identification of seized tiger (<i>Panthera tigris tigris</i>) parts in Nepal-€A molecular forensic approach. <i>PLoS ONE</i> , 2018, 13, e0201639. | 2.5 | 15 |
| 45 | A bioinformatic pipeline for identifying informative SNP panels for parentage assignment from <i>scRAD</i> seq data. <i>Molecular Ecology Resources</i> , 2018, 18, 1263-1281. | 4.8 | 45 |
| 46 | Assessment of genetic diversity, population structure, and gene flow of tigers (<i>Panthera tigris tigris</i>) across Nepal's Terai Arc Landscape. <i>PLoS ONE</i> , 2018, 13, e0193495. | 2.5 | 25 |
| 47 | Comparing morphological and molecular diet analyses and fecal DNA sampling protocols for a terrestrial carnivore. <i>Wildlife Society Bulletin</i> , 2017, 41, 362-369. | 1.6 | 28 |
| 48 | Harvest and group effects on pup survival in a cooperative breeder. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170580. | 2.6 | 18 |
| 49 | Effects of breeder turnover and harvest on group composition and recruitment in a social carnivore. <i>Journal of Animal Ecology</i> , 2017, 86, 1094-1101. | 2.8 | 15 |
| 50 | The roles of habitat and intraguild predation by coyotes on the spatial dynamics of kit foxes. <i>Ecosphere</i> , 2017, 8, e01749. | 2.2 | 31 |
| 51 | Evidence for sex-specific reproductive senescence in monogamous cooperatively breeding red wolves. <i>Behavioral Ecology and Sociobiology</i> , 2017, 71, 1. | 1.4 | 9 |
| 52 | Examining spatial patterns of selection and use for an altered predator guild. <i>Oecologia</i> , 2017, 185, 725-735. | 2.0 | 6 |
| 53 | Comment on -€Whole-genome sequence analysis shows two endemic species of North American wolf are admixtures of the coyote and gray wolf-€. <i>Science Advances</i> , 2017, 3, e1602250. | 10.3 | 22 |
| 54 | Age-€specific infectious period shapes dynamics of pneumonia in bighorn sheep. <i>Ecology Letters</i> , 2017, 20, 1325-1336. | 6.4 | 39 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 55 | Sampling technique affects detection of habitat factors influencing wild bee communities. <i>Journal of Insect Conservation</i> , 2017, 21, 703-714. | 1.4 | 46 |
| 56 | Comparative landscape genetics of two frugivorous bats in a biological corridor undergoing agricultural intensification. <i>Molecular Ecology</i> , 2017, 26, 4603-4617. | 3.9 | 19 |
| 57 | Panmixia and Limited Interspecific Introgression in Coyotes (<i>Canis latrans</i>) from West Virginia and Virginia, USA. <i>Journal of Heredity</i> , 2017, 108, 608-617. | 2.4 | 3 |
| 58 | Behavioral connectivity among bighorn sheep suggests potential for disease spread. <i>Journal of Wildlife Management</i> , 2017, 81, 38-45. | 1.8 | 16 |
| 59 | Complementary Network-Based Approaches for Exploring Genetic Structure and Functional Connectivity in Two Vulnerable, Endemic Ground Squirrels. <i>Frontiers in Genetics</i> , 2017, 8, 81. | 2.3 | 10 |
| 60 | Genetic health and population monitoring of two small black bear (<i>Ursus americanus</i>) populations in Alabama, with a regional perspective of genetic diversity and exchange. <i>PLoS ONE</i> , 2017, 12, e0186701. | 2.5 | 7 |
| 61 | Genetic monitoring of an endangered species recovery: demographic and genetic trends for reintroduced pygmy rabbits (<i>Brachylagus idahoensis</i>). <i>Journal of Mammalogy</i> , 2017, 98, 350-364. | 1.3 | 19 |
| 62 | A Comparative Analysis of Genetic Diversity and Structure in Jaguars (<i>Panthera onca</i>), Pumas (<i>Puma</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf . Linkage Zone. <i>PLoS ONE</i> , 2016, 11, e0151043. | 2.5 | 41 |
| 63 | Agricultural intensification alters bat assemblage composition and abundance in a dynamic Neotropical landscape. <i>Biotropica</i> , 2016, 48, 667-676. | 1.6 | 24 |
| 64 | Critical considerations for the application of environmental <sc>DNA</sc> methods to detect aquatic species. <i>Methods in Ecology and Evolution</i> , 2016, 7, 1299-1307. | 5.2 | 684 |
| 65 | Estimating Sonoran pronghorn abundance and survival with fecal DNA and capture-recapture methods. <i>Conservation Biology</i> , 2016, 30, 1102-1111. | 4.7 | 22 |
| 66 | Monitoring coyote population dynamics with fecal DNA and spatial capture-recapture. <i>Journal of Wildlife Management</i> , 2016, 80, 824-836. | 1.8 | 43 |
| 67 | Host-adapted aphid populations differ in their migratory patterns and capacity to colonize crops. <i>Journal of Applied Ecology</i> , 2016, 53, 1382-1390. | 4.0 | 9 |
| 68 | Evidence for <i>Bombus occidentalis</i> (Hymenoptera: Apidae) Populations in the Olympic Peninsula, the Palouse Prairie, and Forests of Northern Idaho. <i>Journal of Insect Science</i> , 2016, 16, 20. | 1.5 | 7 |
| 69 | Bias in carnivore diet analysis resulting from misclassification of predator scats based on field identification. <i>Wildlife Society Bulletin</i> , 2016, 40, 669-677. | 1.6 | 56 |
| 70 | Non-invasive genetic sampling reveals diet shifts, but little difference in endoparasite richness and faecal glucocorticoids, in Belizean felids inside and outside protected areas. <i>Journal of Tropical Ecology</i> , 2016, 32, 226-239. | 1.1 | 11 |
| 71 | Identifying gray wolf packs and dispersers using noninvasive genetic samples. <i>Journal of Wildlife Management</i> , 2016, 80, 1408-1419. | 1.8 | 17 |
| 72 | Describing a developing hybrid zone between red wolves and coyotes in eastern North Carolina, <sc>USA</sc>. <i>Evolutionary Applications</i> , 2016, 9, 791-804. | 3.1 | 29 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 73 | Examining the use of fecal pellet morphometry to differentiate age classes in Sonoran pronghorn. <i>Wildlife Biology</i> , 2016, 22, 217-227. | 1.4 | 14 |
| 74 | A Pedagogical Model for Team-Based, Problem-Focused Interdisciplinary Doctoral Education. <i>BioScience</i> , 2016, 66, 477-488. | 4.9 | 41 |
| 75 | Consequences for conservation: population density and genetic effects on reproduction of an endangered lagomorph. <i>Ecological Applications</i> , 2016, 26, 784-795. | 3.8 | 6 |
| 76 | Quantifying and correcting for scat removal in noninvasive carnivore scat surveys. <i>Wildlife Biology</i> , 2016, 22, 45-54. | 1.4 | 14 |
| 77 | A comparison of morphological and molecular diet analyses of predator scats. <i>Journal of Mammalogy</i> , 2016, 97, 112-120. | 1.3 | 38 |
| 78 | Nuclear and Mitochondrial DNA Analyses of Golden Eagles (<i>Aquila chrysaetos canadensis</i>) from Three Areas in Western North America; Initial Results and Conservation Implications. <i>PLoS ONE</i> , 2016, 11, e0164248. | 2.5 | 7 |
| 79 | Development and characterization of fourteen novel microsatellite markers for the chestnut short-tailed fruit bat (<i>Carollia castanea</i>), and cross-amplification to related species. <i>PeerJ</i> , 2016, 4, e2465. | 2.0 | 7 |
| 80 | Managing hybridization of a recovering endangered species: The red wolf <i>Canis rufus</i> as a case study. <i>Environmental Epigenetics</i> , 2015, 61, 191-205. | 1.8 | 63 |
| 81 | Comparing telemetry and fecal dna sampling methods to quantify survival and dispersal of juvenile pygmy rabbits. <i>Wildlife Society Bulletin</i> , 2015, 39, 413-421. | 1.6 | 6 |
| 82 | Balancing sample accumulation and <i>DNA</i> degradation rates to optimize noninvasive genetic sampling of sympatric carnivores. <i>Molecular Ecology Resources</i> , 2015, 15, 831-842. | 4.8 | 38 |
| 83 | Evaluating the reliability of field identification and morphometric classifications for carnivore scats confirmed with genetic analysis. <i>Wildlife Society Bulletin</i> , 2015, 39, 593-602. | 1.6 | 29 |
| 84 | Evaluating the interaction of faecal pellet deposition rates and <i>DNA</i> degradation rates to optimize sampling design for <i>DNA</i> -based mark-recapture analysis of Sonoran pronghorn. <i>Molecular Ecology Resources</i> , 2015, 15, 843-854. | 4.8 | 31 |
| 85 | Evaluation of Scat Deposition Transects versus Radio Telemetry for Developing a Species Distribution Model for a Rare Desert Carnivore, the Kit Fox. <i>PLoS ONE</i> , 2015, 10, e0138995. | 2.5 | 17 |
| 86 | Using Detection Dogs and Rspf Models to Assess Habitat Suitability for Bears in Greater Yellowstone. <i>Western North American Naturalist</i> , 2015, 75, 396-405. | 0.4 | 43 |
| 87 | ConGenR: rapid determination of consensus genotypes and estimates of genotyping errors from replicated genetic samples. <i>Conservation Genetics Resources</i> , 2015, 7, 841-843. | 0.8 | 20 |
| 88 | Factors influencing red wolf-coyote hybridization in eastern North Carolina, USA. <i>Biological Conservation</i> , 2015, 184, 108-116. | 4.1 | 60 |
| 89 | Using environmental DNA methods to improve detectability in a hellbender (<i>Cryptobranchus</i>) Tj ETQq1 1 0.784314, rgsBT /Overlock 10 4.1 212 | 4.1 | 212 |
| 90 | Recruitment in a social carnivore before and after harvest. <i>Animal Conservation</i> , 2015, 18, 415-423. | 2.9 | 36 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 91 | Evaluating noninvasive genetic sampling techniques to estimate large carnivore abundance. <i>Molecular Ecology Resources</i> , 2015, 15, 1133-1144. | 4.8 | 35 |
| 92 | Optimizing collection methods for noninvasive genetic sampling of neotropical felids. <i>Wildlife Society Bulletin</i> , 2015, 39, 403-412. | 1.6 | 23 |
| 93 | Coupled social and ecological outcomes of agricultural intensification in Costa Rica and the future of biodiversity conservation in tropical agricultural regions. <i>Global Environmental Change</i> , 2015, 32, 74-86. | 7.8 | 45 |
| 94 | Genetics as a Tool for Biodiversity Conservation: Examples from Central America. , 2015, , 573-602. | | 1 |
| 95 | Genetic Structure across Broad Spatial and Temporal Scales: Rocky Mountain Tailed Frogs (<i>Ascaphus</i>) Tj ETQq1 1 0.784314 rgBT /Over | 2.4 | 11 |
| 96 | The Challenges of Red Wolf Conservation and the Fate of an Endangered Species Recovery Program. <i>Conservation Letters</i> , 2015, 8, 338-344. | 5.7 | 15 |
| 97 | Rapid species identification of Sonoran pronghorn from fecal pellet DNA. <i>Wildlife Society Bulletin</i> , 2014, 38, 842-848. | 1.6 | 9 |
| 98 | Enhanced understanding of predator-prey relationships using molecular methods to identify predator species, individual and sex. <i>Molecular Ecology Resources</i> , 2014, 14, 100-108. | 4.8 | 41 |
| 99 | A long-term population monitoring approach for a wide-ranging carnivore: Noninvasive genetic sampling of gray wolf rendezvous sites in Idaho, USA. <i>Journal of Wildlife Management</i> , 2014, 78, 1040-1049. | 1.8 | 57 |
| 100 | A multi-method approach for analyzing hierarchical genetic structures: a case study with cougars (<i>Puma concolor</i>). <i>Ecography</i> , 2014, 37, 552-563. | 4.5 | 42 |
| 101 | Factors influencing detection of eDNA from a stream-dwelling amphibian. <i>Molecular Ecology Resources</i> , 2014, 14, 109-116. | 4.8 | 358 |
| 102 | Monitoring gray wolf populations using multiple survey methods. <i>Journal of Wildlife Management</i> , 2014, 78, 335-346. | 1.8 | 42 |
| 103 | Noninvasive individual and species identification of jaguars (<i>Panthera onca</i>), pumas (<i>Puma</i>) Tj ETQq1 1 0.784314 rgBT /Over microsatellites and faecal eDNA. <i>Molecular Ecology Resources</i> , 2014, 14, 1171-1182. | 4.8 | 48 |
| 104 | Molecular species identification for multiple carnivores. <i>Conservation Genetics Resources</i> , 2014, 6, 821-824. | 0.8 | 52 |
| 105 | Inbreeding and inbreeding depression in endangered red wolves (<i>Canis rufus</i>). <i>Molecular Ecology</i> , 2014, 23, 4241-4255. | 3.9 | 46 |
| 106 | Little fox on the prairie: genetic structure and diversity throughout the distribution of a grassland carnivore in the United States. <i>Conservation Genetics</i> , 2014, 15, 1503-1514. | 1.5 | 8 |
| 107 | Estimating cougar densities in northeast Oregon using conservation detection dogs. <i>Journal of Wildlife Management</i> , 2014, 78, 1104-1114. | 1.8 | 36 |
| 108 | Coyote (<i>Canis latrans</i>) mammalian prey diet shifts in response to seasonal vegetation change. <i>Isotopes in Environmental and Health Studies</i> , 2014, 50, 343-360. | 1.0 | 11 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 109 | Genetic Evidence Confirms the Presence of Pygmy Rabbits in Colorado. <i>Journal of Fish and Wildlife Management</i> , 2014, 5, 118-123. | 0.9 | 0 |
| 110 | Estimating occupancy and abundance of stream amphibians using environmental DNA from filtered water samples. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2013, 70, 1123-1130. | 1.4 | 444 |
| 111 | Diets of sympatric red wolves and coyotes in northeastern North Carolina. <i>Journal of Mammalogy</i> , 2013, 94, 1141-1148. | 1.3 | 34 |
| 112 | Social and genetic structure associated with migration in pronghorn. <i>Biological Conservation</i> , 2013, 168, 108-115. | 4.1 | 17 |
| 113 | Evaluating DNA degradation rates in faecal pellets of the endangered pygmy rabbit. <i>Molecular Ecology Resources</i> , 2013, 13, 654-662. | 4.8 | 37 |
| 114 | Environmental DNA as a new method for early detection of New Zealand mudsnails (<i>Potamopyrgus</i>) Tj ETQq0 0.0 rgBT /Overlock 10 | 1.8 | 320 |
| 115 | Genetic diversity in a reintroduced swift fox population. <i>Conservation Genetics</i> , 2013, 14, 93-102. | 1.5 | 22 |
| 116 | Capwire: a <sc>R</sc> package for estimating population census size from noninvasive genetic sampling. <i>Molecular Ecology Resources</i> , 2013, 13, 154-157. | 4.8 | 60 |
| 117 | Evaluating the ability of Bayesian clustering methods to detect hybridization and introgression using an empirical red wolf data set. <i>Molecular Ecology</i> , 2013, 22, 74-86. | 3.9 | 49 |
| 118 | A method for estimating population sex ratio for sagegrouse using noninvasive genetic samples. <i>Molecular Ecology Resources</i> , 2013, 13, 393-402. | 4.8 | 18 |
| 119 | A road map for molecular ecology. <i>Molecular Ecology</i> , 2013, 22, 2605-2626. | 3.9 | 100 |
| 120 | Detecting pygmy rabbits (<i>Brachylagus idahoensis</i>) using DNA extracted from fecal pellets of mixed-species groups. <i>Wildlife Society Bulletin</i> , 2013, 37, n/a-n/a. | 1.6 | 2 |
| 121 | Using a reference population yardstick to calibrate and compare genetic diversity reported in different studies: an example from the brown bear. <i>Heredity</i> , 2012, 109, 299-305. | 2.6 | 65 |
| 122 | Pack social dynamics and inbreeding avoidance in the cooperatively breeding red wolf. <i>Behavioral Ecology</i> , 2012, 23, 1186-1194. | 2.2 | 25 |
| 123 | Genetic versus Census Estimators of the Opportunity for Sexual Selection in the Wild. <i>American Naturalist</i> , 2012, 179, 451-462. | 2.1 | 6 |
| 124 | Genetic evidence of inbreeding avoidance in pronghorn. <i>Journal of Zoology</i> , 2012, 288, 119-126. | 1.7 | 5 |
| 125 | Developing an Interdisciplinary, Distributed Graduate Course for Twenty-First Century Scientists. <i>BioScience</i> , 2012, 62, 182-188. | 4.9 | 26 |
| 126 | Species limits and integrated taxonomy of the Idaho ground squirrel (<i>Urocitellus brunneus</i>): genetic and ecological differentiation. <i>Journal of Mammalogy</i> , 2012, 93, 589-604. | 1.3 | 13 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 127 | Species designation of the Bruneau Dune tiger beetle (<i>Cicindela waynei</i>) is supported by phylogenetic analysis of mitochondrial DNA sequence data. <i>Conservation Genetics</i> , 2012, 13, 373-380. | 1.5 | 3 |
| 128 | Evidence for a genetic basis for delayed dispersal in a cooperatively breeding canid. <i>Animal Behaviour</i> , 2012, 83, 1091-1098. | 1.9 | 14 |
| 129 | A simulation-based evaluation of methods for inferring linear barriers to gene flow. <i>Molecular Ecology Resources</i> , 2012, 12, 822-833. | 4.8 | 123 |
| 130 | Monitoring the effective population size of a brown bear (<i>Ursus arctos</i>) population using new single-sample approaches. <i>Molecular Ecology</i> , 2012, 21, 862-875. | 3.9 | 78 |
| 131 | The influence of landscape characteristics and home-range size on the quantification of landscape-genetics relationships. <i>Landscape Ecology</i> , 2012, 27, 253-266. | 4.2 | 30 |
| 132 | Estimating gray wolf pack size and family relationships using noninvasive genetic sampling at rendezvous sites. <i>Journal of Mammalogy</i> , 2011, 92, 784-795. | 1.3 | 73 |
| 133 | Food Habits of Red Wolves during Pup-Rearing Season. <i>Southeastern Naturalist</i> , 2011, 10, 731-740. | 0.4 | 15 |
| 134 | First Record of Multiple Paternity in the Pygmy Rabbit (<i>Brachylagus idahoensis</i>): Evidence from Analysis of 16 Microsatellite Loci. <i>Western North American Naturalist</i> , 2011, 71, 271-275. | 0.4 | 2 |
| 135 | Differentiating between Steller sea lion (<i>Eumetopias jubatus</i>) and northern fur seal (<i>Callorhinus ursinus</i>) scats through analysis of faecal DNA. <i>Molecular Ecology Resources</i> , 2011, 11, 166-170. | 4.8 | 3 |
| 136 | Rapid species identification of pygmy rabbits (<i>Brachylagus idahoensis</i>) from faecal pellet DNA. <i>Molecular Ecology Resources</i> , 2011, 11, 808-812. | 4.8 | 18 |
| 137 | Assessing the prevalence of hybridization between sympatric <i>Canis</i> species surrounding the red wolf (<i>Canis rufus</i>) recovery area in North Carolina. <i>Molecular Ecology</i> , 2011, 20, 2142-2156. | 3.9 | 54 |
| 138 | Inbreeding depression in pronghorn (<i>Antilocapra americana</i>) fawns. <i>Molecular Ecology</i> , 2011, 20, 4889-4898. | 3.9 | 24 |
| 139 | Genetic assessment of paternity and relatedness in a managed population of cougars. <i>Journal of Wildlife Management</i> , 2011, 75, 378-384. | 1.8 | 18 |
| 140 | Robust molecular sex identification of beaver (<i>Castor canadensis</i>) from non-destructive samples. <i>Conservation Genetics Resources</i> , 2011, 3, 729-731. | 0.8 | 3 |
| 141 | Hair of the dog: Obtaining samples from coyotes and wolves noninvasively. <i>Wildlife Society Bulletin</i> , 2011, 35, 105-111. | 1.6 | 14 |
| 142 | Helper effects on pup lifetime fitness in the cooperatively breeding red wolf (<i>Canis rufus</i>). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 1381-1389. | 2.6 | 54 |
| 143 | Predictions of ecological and social impacts of alternative residential development policies to inform decision making in a rural landscape. <i>Conservation Letters</i> , 2011, 4, 423-432. | 5.7 | 7 |
| 144 | Molecular Detection of Vertebrates in Stream Water: A Demonstration Using Rocky Mountain Tailed Frogs and Idaho Giant Salamanders. <i>PLoS ONE</i> , 2011, 6, e22746. | 2.5 | 397 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 145 | Direct fitness benefits of delayed dispersal in the cooperatively breeding red wolf (<i>Canis rufus</i>). <i>Behavioral Ecology</i> , 2011, 22, 199-205. | 2.2 | 39 |
| 146 | Social and Demographic Effects of Anthropogenic Mortality: A Test of the Compensatory Mortality Hypothesis in the Red Wolf. <i>PLoS ONE</i> , 2011, 6, e20868. | 2.5 | 26 |
| 147 | Multiplex pre-amplification for noninvasive genetic sampling: is the extra effort worth it?. <i>Molecular Ecology Resources</i> , 2010, 10, 659-665. | 4.8 | 7 |
| 148 | Ten polymorphic microsatellite markers for pronghorn (<i>Antilocapra americana</i>). <i>Conservation Genetics Resources</i> , 2010, 2, 81-84. | 0.8 | 12 |
| 149 | Applications of landscape genetics in conservation biology: concepts and challenges. <i>Conservation Genetics</i> , 2010, 11, 375-385. | 1.5 | 356 |
| 150 | Efficient, Noninvasive Genetic Sampling for Monitoring Reintroduced Wolves. <i>Journal of Wildlife Management</i> , 2010, 74, 1050-1058. | 1.8 | 96 |
| 151 | Comparative landscape genetics of two pond-breeding amphibian species in a highly modified agricultural landscape. <i>Molecular Ecology</i> , 2010, 19, 3650-3663. | 3.9 | 153 |
| 152 | Landscape genetics: where are we now?. <i>Molecular Ecology</i> , 2010, 19, 3496-3514. | 3.9 | 480 |
| 153 | Contributions of landscape genetics – approaches, insights, and future potential. <i>Molecular Ecology</i> , 2010, 19, 3489-3495. | 3.9 | 110 |
| 154 | The power of genetic monitoring for studying demography, ecology and genetics of a reintroduced brown bear population. <i>Molecular Ecology</i> , 2010, 19, 3938-3951. | 3.9 | 138 |
| 155 | Comparing opportunistic and systematic sampling methods for non-invasive genetic monitoring of a small translocated brown bear population. <i>Journal of Applied Ecology</i> , 2010, 47, 172-181. | 4.0 | 75 |
| 156 | Dispersal, gene flow, and population genetic structure in the pygmy rabbit (<i>Brachylagus</i>). <i>Journal of Wildlife Management</i> , 2010, 74, 1050-1058. | 1.3 | 33 |
| 157 | Predicted effects of residential development on a northern Idaho landscape under alternative growth management and land protection policies. <i>Landscape and Urban Planning</i> , 2010, 94, 255-263. | 7.5 | 26 |
| 158 | Impacts of sampling location within a faeces on DNA quality in two carnivore species. <i>Molecular Ecology Resources</i> , 2010, 10, 109-114. | 4.8 | 71 |
| 159 | Quantification and reduction of bias from sampling larvae to infer population and landscape genetic structure. <i>Molecular Ecology Resources</i> , 2010, 10, 304-313. | 4.8 | 74 |
| 160 | Highly efficient multiplex PCR of noninvasive DNA does not require pre-amplification. <i>Molecular Ecology Resources</i> , 2010, 10, 495-501. | 4.8 | 21 |
| 161 | <i>Batrachochytrium dendrobatidis</i> infection dynamics in the Columbia spotted frog <i>Rana luteiventris</i> in north Idaho, USA. <i>Diseases of Aquatic Organisms</i> , 2010, 92, 223-230. | 1.0 | 24 |
| 162 | Incorporating Genotyping Error Into Non-invasive DNA-Based Mark-recapture Population Estimates. <i>Journal of Wildlife Management</i> , 2009, 73, 598-604. | 1.8 | 33 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 163 | Identifying future research needs in landscape genetics: where to from here?. <i>Landscape Ecology</i> , 2009, 24, 455-463. | 4.2 | 167 |
| 164 | Molecular road ecology: exploring the potential of genetics for investigating transportation impacts on wildlife. <i>Molecular Ecology</i> , 2009, 18, 4151-4164. | 3.9 | 192 |
| 165 | Statistical approaches in landscape genetics: an evaluation of methods for linking landscape and genetic data. <i>Ecography</i> , 2009, 32, 818-830. | 4.5 | 273 |
| 166 | Molted feathers from clay licks in Peru provide DNA for three large macaws (<i>Ara</i>). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 627 Td (arara)</i> 183-192. | 0.5 | 23 |
| 167 | Identifying polymorphic microsatellite loci for Andean bear research. <i>Ursus</i> , 2009, 20, 102-108. | 0.5 | 47 |
| 168 | Estimating abundance of American black bears using DNA-based capture-mark-recapture models. <i>Ursus</i> , 2009, 20, 1-11. | 0.5 | 28 |
| 169 | Using habitat models to determine conservation priorities for pond-breeding amphibians in a privately-owned landscape of northern Idaho, USA. <i>Biological Conservation</i> , 2009, 142, 1096-1104. | 4.1 | 27 |
| 170 | Wolverine gene flow across a narrow climatic niche. <i>Ecology</i> , 2009, 90, 3222-3232. | 3.2 | 166 |
| 171 | Status of the Gobi bear in Mongolia as determined by noninvasive genetic methods. <i>Ursus</i> , 2009, 20, 30-38. | 0.5 | 24 |
| 172 | Predicting land use change: comparison of models based on landowner surveys and historical land cover trends. <i>Landscape Ecology</i> , 2008, 23, 195-210. | 4.2 | 62 |
| 173 | High error rates for avian molecular sex identification primer sets applied to molted feathers. <i>Journal of Field Ornithology</i> , 2008, 79, 286-292. | 0.5 | 15 |
| 174 | PERMANENT GENETIC RESOURCES: Ten polymorphic microsatellite markers for the pygmy rabbit (<i>Brachylagus idahoensis</i>). <i>Molecular Ecology Resources</i> , 2008, 8, 360-362. | 4.8 | 11 |
| 175 | PERMANENT GENETIC RESOURCES: Characterization of microsatellite markers for the almendro (<i>Dipteryx panamensis</i>), a tetraploid rainforest tree. <i>Molecular Ecology Resources</i> , 2008, 8, 425-427. | 4.8 | 5 |
| 176 | Pollen dispersal and genetic structure of the tropical tree <i>Dipteryx panamensis</i> in a fragmented Costa Rican landscape. <i>Molecular Ecology</i> , 2008, 17, 2060-2073. | 3.9 | 60 |
| 177 | To what extent do microsatellite markers reflect genome-wide genetic diversity in natural populations?. <i>Molecular Ecology</i> , 2008, 17, 3808-3817. | 3.9 | 230 |
| 178 | Grizzly Bear Density in Glacier National Park, Montana. <i>Journal of Wildlife Management</i> , 2008, 72, 1693-1705. | 1.8 | 154 |
| 179 | Assessing Estimators of Snow Leopard Abundance. <i>Journal of Wildlife Management</i> , 2008, 72, 1826-1833. | 1.8 | 74 |
| 180 | MULTIPLE DATA SOURCES IMPROVE DNA-BASED MARK-RECAPTURE POPULATION ESTIMATES OF GRIZZLY BEARS. , 2008, 18, 577-589. | | 115 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 181 | Cross-species amplification and optimization of microsatellite markers for use in six Neotropical parrots. <i>Molecular Ecology Resources</i> , 2008, 8, 835-839. | 4.8 | 20 |
| 182 | An apparent hybrid wild bear from Cambodia. <i>Ursus</i> , 2008, 19, 85-86. | 0.5 | 39 |
| 183 | Genetic resolution of composition and phylogenetic placement of the isabelline bear. <i>Ursus</i> , 2007, 18, 129-131. | 0.5 | 16 |
| 184 | Conventional and genetic measures of seed dispersal for <i>Dipteryx panamensis</i> (Fabaceae) in continuous and fragmented Costa Rican rain forest. <i>Journal of Tropical Ecology</i> , 2007, 23, 635-642. | 1.1 | 19 |
| 185 | Reintroduction and Genetic Structure: Rocky Mountain Elk in Yellowstone and the Western States. <i>Journal of Mammalogy</i> , 2007, 88, 129-138. | 1.3 | 46 |
| 186 | Evaluating Population Structure of Black Bears on the Kenai Peninsula using Mitochondrial and Nuclear DNA Analyses. <i>Journal of Mammalogy</i> , 2007, 88, 1288-1299. | 1.3 | 14 |
| 187 | Putting the "landscape"™ in landscape genetics. <i>Heredity</i> , 2007, 98, 128-142. | 2.6 | 732 |
| 188 | Locating hybrid individuals in the red wolf (<i>Canis rufus</i>) experimental population area using a spatially targeted sampling strategy and faecal DNA genotyping. <i>Molecular Ecology</i> , 2007, 16, 1823-1834. | 3.9 | 45 |
| 189 | A new individual-based spatial approach for identifying genetic discontinuities in natural populations. <i>Molecular Ecology</i> , 2007, 16, 2031-2043. | 3.9 | 72 |
| 190 | Ordered vs. unordered samples: response to Bromaghin. <i>Molecular Ecology</i> , 2007, 16, 4885-4885. | 3.9 | 2 |
| 191 | A select panel of polymorphic microsatellite loci for individual identification of snow leopards (<i>Panthera uncia</i>). <i>Molecular Ecology Notes</i> , 2007, 7, 311-314. | 1.7 | 16 |
| 192 | The impact of time and field conditions on brown bear (<i>Ursus arctos</i>) faecal DNA amplification. <i>Conservation Genetics</i> , 2007, 8, 1219-1224. | 1.5 | 128 |
| 193 | Taxonomic status and conservation strategy of the endangered red wolf: a response to Kyle et al. (2006). <i>Conservation Genetics</i> , 2007, 8, 1483-1485. | 1.5 | 17 |
| 194 | Detection of Predator Presence at Elk Mortality Sites Using mtDNA Analysis of Hair and Scat Samples. <i>Wildlife Society Bulletin</i> , 2006, 34, 815-820. | 1.6 | 50 |
| 195 | Phylogeography and mitochondrial diversity of extirpated brown bear (<i>Ursus arctos</i>) populations in the contiguous United States and Mexico. <i>Molecular Ecology</i> , 2006, 15, 4477-4485. | 3.9 | 81 |
| 196 | Genetic diversity and population structure of wolverine (<i>Gulo gulo</i>) populations at the southern edge of their current distribution in North America with implications for genetic viability. <i>Conservation Genetics</i> , 2006, 7, 197-211. | 1.5 | 48 |
| 197 | An efficient method for screening faecal DNA genotypes and detecting new individuals and hybrids in the red wolf (<i>Canis rufus</i>) experimental population area. <i>Conservation Genetics</i> , 2006, 8, 123-131. | 1.5 | 57 |
| 198 | Multiple breeding strategies in the swift fox, <i>Vulpes velox</i> . <i>Animal Behaviour</i> , 2006, 71, 1029-1038. | 1.9 | 53 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 199 | The dilemma of female mate selection in the brown bear, a species with sexually selected infanticide. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2006, 273, 283-291. | 2.6 | 95 |
| 200 | Good genes sexual selection in nature. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 16343-16345. | 7.1 | 107 |
| 201 | Implementing recovery of the red wolf-integrating research scientists and managers. <i>Wildlife Society Bulletin</i> , 2005, 33, 1145-1152. | 1.6 | 32 |
| 202 | NONINVASIVE GENETIC SAMPLING TOOLS FOR WILDLIFE BIOLOGISTS: A REVIEW OF APPLICATIONS AND RECOMMENDATIONS FOR ACCURATE DATA COLLECTION. <i>Journal of Wildlife Management</i> , 2005, 69, 1419-1433. | 1.8 | 540 |
| 203 | A new method for estimating the size of small populations from genetic mark-recapture data. <i>Molecular Ecology</i> , 2005, 14, 1991-2005. | 3.9 | 252 |
| 204 | Genetic and spatial structure within a swift fox population. <i>Journal of Animal Ecology</i> , 2005, 74, 1173-1181. | 2.8 | 45 |
| 205 | Genetic diversity and population divergence in fragmented habitats: Conservation of Idaho ground squirrels. <i>Conservation Genetics</i> , 2005, 6, 759-774. | 1.5 | 31 |
| 206 | A simulation test of the effectiveness of several methods for error-checking non-invasive genetic data. <i>Animal Conservation</i> , 2005, 8, 203-215. | 2.9 | 57 |
| 207 | Genetic variation and relatedness in grizzly bears in the Prudhoe Bay region and adjacent areas in northern Alaska. <i>Ursus</i> , 2005, 16, 70-84. | 0.5 | 10 |
| 208 | Changing numbers of spawning cutthroat trout in tributary streams of Yellowstone Lake and estimates of grizzly bears visiting streams from DNA. <i>Ursus</i> , 2005, 16, 167-180. | 0.5 | 28 |
| 209 | Evaluating mixed samples as a source of error in non-invasive genetic studies using microsatellites. <i>Molecular Ecology</i> , 2004, 14, 195-201. | 3.9 | 44 |
| 210 | Use of naturally occurring mercury to determine the importance of cutthroat trout to Yellowstone grizzly bears. <i>Canadian Journal of Zoology</i> , 2004, 82, 493-501. | 1.0 | 71 |
| 211 | Density and population size estimates for North Cascade grizzly bears using DNA hair-sampling techniques. <i>Biological Conservation</i> , 2004, 117, 417-428. | 4.1 | 27 |
| 212 | Widespread occurrence of a domestic dog mitochondrial DNA haplotype in southeastern US coyotes. <i>Molecular Ecology</i> , 2003, 12, 541-546. | 3.9 | 120 |
| 213 | The influence of diet on faecal DNA amplification and sex identification in brown bears (<i>Ursus arctos</i>) Tj ETQq1 1 0,784314 rgBT /Ove | 3.9 | 96 |
| 214 | Using faecal DNA sampling and GIS to monitor hybridization between red wolves (<i>Canis rufus</i>) and coyotes (<i>Canis latrans</i>). <i>Molecular Ecology</i> , 2003, 12, 2175-2186. | 3.9 | 110 |
| 215 | Assessing population structure and gene flow in Montana wolverines (<i>Gulo gulo</i>) using assignment-based approaches. <i>Molecular Ecology</i> , 2003, 12, 2907-2918. | 3.9 | 129 |
| 216 | Pedigree-based assignment tests for reversing coyote (<i>Canis latrans</i>) introgression into the wild red wolf (<i>Canis rufus</i>) population. <i>Molecular Ecology</i> , 2003, 12, 3287-3301. | 3.9 | 61 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 217 | A quantitative evaluation of two methods for preserving hair samples. <i>Molecular Ecology Notes</i> , 2003, 3, 163-166. | 1.7 | 51 |
| 218 | The history of effective population size and genetic diversity in the Yellowstone grizzly (Ursus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 70 United States of America, 2003, 100, 4334-4339. | 7.1 | 141 |
| 219 | Ancient DNA Analyses Reveal High Mitochondrial DNA Sequence Diversity and Parallel Morphological Evolution of Late Pleistocene Cave Bears. <i>Molecular Biology and Evolution</i> , 2002, 19, 1244-1250. | 8.9 | 94 |
| 220 | The Endangered Species Act: Dollars and Sense?. <i>BioScience</i> , 2002, 52, 163. | 4.9 | 56 |
| 221 | An evaluation of long-term preservation methods for brown bear (Ursus arctos) faecal DNA samples. <i>Conservation Genetics</i> , 2002, 3, 435-440. | 1.5 | 105 |
| 222 | Assessing Allelic Dropout and Genotype Reliability Using Maximum Likelihood. <i>Genetics</i> , 2002, 160, 357-366. | 2.9 | 285 |
| 223 | Estimating the probability of identity among genotypes in natural populations: cautions and guidelines. <i>Molecular Ecology</i> , 2001, 10, 249-256. | 3.9 | 1,101 |
| 224 | Microsatellite analysis of genetic variation among and within Alpine marmot populations in the French Alps. <i>Molecular Ecology</i> , 2001, 10, 41-52. | 3.9 | 48 |
| 225 | Nuclear DNA microsatellite analysis of genetic diversity and gene flow in the Scandinavian brown bear (Ursus arctos). <i>Molecular Ecology</i> , 2000, 9, 421-431. | 3.9 | 200 |
| 226 | Rapid Radiation Events in the Family Ursidae Indicated by Likelihood Phylogenetic Estimation from Multiple Fragments of mtDNA. <i>Molecular Phylogenetics and Evolution</i> , 1999, 13, 82-92. | 2.7 | 68 |
| 227 | Noninvasive genetic sampling: look before you leap. <i>Trends in Ecology and Evolution</i> , 1999, 14, 323-327. | 8.7 | 768 |
| 228 | Extra-pair paternity in the monogamous Alpine marmot revealed by nuclear DNA microsatellite analysis. <i>Behavioral Ecology and Sociobiology</i> , 1998, 43, 281-288. | 1.4 | 154 |
| 229 | Plucked hair samples as a source of DNA: reliability of dinucleotide microsatellite genotyping. <i>Molecular Ecology</i> , 1998, 7, 1237-1241. | 3.9 | 185 |
| 230 | Non-invasive genetic sampling. <i>Trends in Ecology and Evolution</i> , 1998, 13, 26-27. | 8.7 | 32 |
| 231 | Mitochondrial DNA Phylogeography of the North American Brown Bear and Implications for Conservation. <i>Conservation Biology</i> , 1998, 12, 408-417. | 4.7 | 17 |
| 232 | Variation in Genetic Diversity across the Range of North American Brown Bears. <i>Conservation Biology</i> , 1998, 12, 418-429. | 4.7 | 38 |
| 233 | Mitochondrial DNA Phylogeography of the North American Brown Bear and Implications for Conservation. <i>Conservation Biology</i> , 1998, 12, 408-417. | 4.7 | 147 |
| 234 | Variation in Genetic Diversity across the Range of North American Brown Bears. <i>Conservation Biology</i> , 1998, 12, 418-429. | 4.7 | 220 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 235 | Noninvasive genetic tracking of the endangered Pyrenean brown bear population. <i>Molecular Ecology</i> , 1997, 6, 869-876. | 3.9 | 333 |
| 236 | Noninvasive genetic tracking of the endangered Pyrenean brown bear population. <i>Molecular Ecology</i> , 1997, 6, 869-876. | 3.9 | 342 |
| 237 | An Empirical Evaluation of Genetic Distance Statistics Using Microsatellite Data From Bear (Ursidae) Populations. <i>Genetics</i> , 1997, 147, 1943-1957. | 2.9 | 330 |
| 238 | Noninvasive genetic tracking of the endangered Pyrenean brown bear population. <i>Molecular Ecology</i> , 1997, 6, 869-76. | 3.9 | 74 |
| 239 | Reliable genotyping of samples with very low DNA quantities using PCR. <i>Nucleic Acids Research</i> , 1996, 24, 3189-3194. | 14.5 | 1,193 |
| 240 | Cell-free transfer of sterols from dictyosome-like structures to plasma membrane vesicles of guinea pig testes. <i>Protoplasma</i> , 1990, 154, 8-15. | 2.1 | 4 |