Lisette P Waits

List of Publications by Year
in descending order

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	Reliable genotyping of samples with very low DNA quantities using PCR. Nucleic Acids Research, 1996, 24, 3189-3194.	14.5	1,193
2	Estimating the probability of identity among genotypes in natural populations: cautions and guidelines. Molecular Ecology, 2001, 10, 249-256.	3.9	1,101
3	Noninvasive genetic sampling: look before you leap. Trends in Ecology and Evolution, 1999, 14, 323-327.	8.7	768
4	Putting the â€˜landscapeâ€™ in landscape genetics. Heredity, 2007, 98, 128-142.	2.6	732
5	Critical considerations for the application of environmental <scp>DNA</scp> methods to detect aquatic species. Methods in Ecology and Evolution, 2016, 7, 1299-1307.	5.2	684
6	NONINVASIVE GENETIC SAMPLING TOOLS FOR WILDLIFE BIOLOGISTS: A REVIEW OF APPLICATIONS AND RECOMMENDATIONS FOR ACCURATE DATA COLLECTION. Journal of Wildlife Management, 2005, 69, 1419-1433.	1.8	540
7	Landscape genetics: where are we now?. Molecular Ecology, 2010, 19, 3496-3514.	3.9	480
8	Estimating occupancy and abundance of stream amphibians using environmental DNA from filtered water samples. Canadian Journal of Fisheries and Aquatic Sciences, 2013, 70, 1123-1130.	1.4	444
9	Molecular Detection of Vertebrates in Stream Water: A Demonstration Using Rocky Mountain Tailed Frogs and Idaho Giant Salamanders. PLoS ONE, 2011, 6, e22746.	2.5	397
10	Factors influencing detection of <scp>eDNA</scp> from a streamâ€dwelling amphibian. Molecular Ecology Resources, 2014, 14, 109-116.	4.8	358
11	Applications of landscape genetics in conservation biology: concepts and challenges. Conservation Genetics, 2010, 11, 375-385.	1.5	356
12	Noninvasive genetic tracking of the endangered Pyrenean brown bear population. Molecular Ecology, 1997, 6, 869-876.	3.9	342
13	Noninvasive genetic tracking of the endangered Pyrenean brown bear population. Molecular Ecology, 1997, 6, 869-876.	3.9	333
14	An Empirical Evaluation of Genetic Distance Statistics Using Microsatellite Data From Bear (Ursidae) Populations. Genetics, 1997, 147, 1943-1957.	2.9	330
15	Environmental DNA as a new method for early detection of New Zealand mudsnails (<i>Potamopyrgus) Tj ETQq1 1 0.784314 rgBT /Ov	1.8	320
16	Genetic diversity targets and indicators in the CBD post-2020 Global Biodiversity Framework must be improved. Biological Conservation, 2020, 248, 108654.	4.1	285
17	Assessing Allelic Dropout and Genotype Reliability Using Maximum Likelihood. Genetics, 2002, 160, 357-366.	2.9	285
18	Statistical approaches in landscape genetics: an evaluation of methods for linking landscape and genetic data. Ecography, 2009, 32, 818-830.	4.5	273

#	ARTICLE	IF	CITATIONS
19	A new method for estimating the size of small populations from genetic mark-recapture data. Molecular Ecology, 2005, 14, 1991-2005.	3.9	252
20	To what extent do microsatellite markers reflect genome–wide genetic diversity in natural populations?. Molecular Ecology, 2008, 17, 3808-3817.	3.9	230
21	Variation in Genetic Diversity across the Range of North American Brown Bears. Conservation Biology, 1998, 12, 418-429.	4.7	220
22	Using environmental DNA methods to improve detectability in a hellbender (Cryptobranchus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622	4.1	212
23	Nuclear DNA microsatellite analysis of genetic diversity and gene flow in the Scandinavian brown bear (Ursus arctos). Molecular Ecology, 2000, 9, 421-431.	3.9	200
24	Molecular road ecology: exploring the potential of genetics for investigating transportation impacts on wildlife. Molecular Ecology, 2009, 18, 4151-4164.	3.9	192
25	Plucked hair samples as a source of DNA: reliability of dinucleotide microsatellite genotyping. Molecular Ecology, 1998, 7, 1237-1241.	3.9	185
26	Identifying future research needs in landscape genetics: where to from here?. Landscape Ecology, 2009, 24, 455-463.	4.2	167
27	Wolverine gene flow across a narrow climatic niche. Ecology, 2009, 90, 3222-3232.	3.2	166
28	Extra-pair paternity in the monogamous Alpine marmot revealed by nuclear DNA microsatellite analysis. Behavioral Ecology and Sociobiology, 1998, 43, 281-288.	1.4	154
29	Grizzly Bear Density in Glacier National Park, Montana. Journal of Wildlife Management, 2008, 72, 1693-1705.	1.8	154
30	Comparative landscape genetics of two pond–breeding amphibian species in a highly modified agricultural landscape. Molecular Ecology, 2010, 19, 3650-3663.	3.9	153
31	Mitochondrial DNA Phylogeography of the North American Brown Bear and Implications for Conservation. Conservation Biology, 1998, 12, 408-417.	4.7	147
32	The history of effective population size and genetic diversity in the Yellowstone grizzly (Ursus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 227 United States of America, 2003, 100, 4334-4339.	7.1	141
33	The power of genetic monitoring for studying demography, ecology and genetics of a reintroduced brown bear population. Molecular Ecology, 2010, 19, 3938-3951.	3.9	138
34	Assessing population structure and gene flow in Montana wolverines (Gulo gulo) using assignment–based approaches. Molecular Ecology, 2003, 12, 2907-2918.	3.9	129
35	The impact of time and field conditions on brown bear (Ursus arctos) faecal DNA amplification. Conservation Genetics, 2007, 8, 1219-1224.	1.5	128
36	Genetic and genomic monitoring with minimally invasive sampling methods. Evolutionary Applications, 2018, 11, 1094-1119.	3.1	126

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37	A simulation€based evaluation of methods for inferring linear barriers to gene flow. Molecular Ecology Resources, 2012, 12, 822-833.	4.8	123
38	Widespread occurrence of a domestic dog mitochondrial DNA haplotype in southeastern US coyotes. Molecular Ecology, 2003, 12, 541-546.	3.9	120
39	MULTIPLE DATA SOURCES IMPROVE DNA-BASED MARK€"RECAPTURE POPULATION ESTIMATES OF GRIZZLY BEARS. , 2008, 18, 577-589.		115
40	Using faecal DNA sampling and GIS to monitor hybridization between red wolves (Canis rufus) and coyotes (Canis latrans). Molecular Ecology, 2003, 12, 2175-2186.	3.9	110
41	Contributions of landscape genetics €" approaches, insights, and future potential. Molecular Ecology, 2010, 19, 3489-3495.	3.9	110
42	Good genes sexual selection in nature. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 16343-16345.	7.1	107
43	An evaluation of long-term preservation methods for brown bear (Ursus arctos) faecal DNA samples. Conservation Genetics, 2002, 3, 435-440.	1.5	105
44	A road map for molecular ecology. Molecular Ecology, 2013, 22, 2605-2626.	3.9	100
45	The influence of diet on faecal DNA amplification and sex identification in brown bears (Ursus arctos) Tj ETQq1 1 0.784314 rgBT /Overl	3.9	96
46	Efficient, Noninvasive Genetic Sampling for Monitoring Reintroduced Wolves. Journal of Wildlife Management, 2010, 74, 1050-1058.	1.8	96
47	The dilemma of female mate selection in the brown bear, a species with sexually selected infanticide. Proceedings of the Royal Society B: Biological Sciences, 2006, 273, 283-291.	2.6	95
48	Ancient DNA Analyses Reveal High Mitochondrial DNA Sequence Diversity and Parallel Morphological Evolution of Late Pleistocene Cave Bears. Molecular Biology and Evolution, 2002, 19, 1244-1250.	8.9	94
49	Next€generation metrics for monitoring genetic erosion within populations of conservation concern. Evolutionary Applications, 2018, 11, 1066-1083.	3.1	93
50	Phylogeography and mitochondrial diversity of extirpated brown bear (Ursus arctos) populations in the contiguous United States and Mexico. Molecular Ecology, 2006, 15, 4477-4485.	3.9	81
51	Monitoring the effective population size of a brown bear (<i>Ursus arctos</i>) population using new single€sample approaches. Molecular Ecology, 2012, 21, 862-875.	3.9	78
52	Comparing opportunistic and systematic sampling methods for non€invasive genetic monitoring of a small translocated brown bear population. Journal of Applied Ecology, 2010, 47, 172-181.	4.0	75
53	Assessing Estimators of Snow Leopard Abundance. Journal of Wildlife Management, 2008, 72, 1826-1833.	1.8	74
54	Quantification and reduction of bias from sampling larvae to infer population and landscape genetic structure. Molecular Ecology Resources, 2010, 10, 304-313.	4.8	74

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55	Noninvasive genetic tracking of the endangered Pyrenean brown bear population. Molecular Ecology, 1997, 6, 869-76.	3.9	74
56	Estimating gray wolf pack size and family relationships using noninvasive genetic sampling at rendezvous sites. Journal of Mammalogy, 2011, 92, 784-795.	1.3	73
57	A new individual-based spatial approach for identifying genetic discontinuities in natural populations. Molecular Ecology, 2007, 16, 2031-2043.	3.9	72
58	Use of naturally occurring mercury to determine the importance of cutthroat trout to Yellowstone grizzly bears. Canadian Journal of Zoology, 2004, 82, 493-501.	1.0	71
59	Impacts of sampling location within a faeces on DNA quality in two carnivore species. Molecular Ecology Resources, 2010, 10, 109-114.	4.8	71
60	Rapid Radiation Events in the Family Ursidae Indicated by Likelihood Phylogenetic Estimation from Multiple Fragments of mtDNA. Molecular Phylogenetics and Evolution, 1999, 13, 82-92.	2.7	68
61	Using a reference population yardstick to calibrate and compare genetic diversity reported in different studies: an example from the brown bear. Heredity, 2012, 109, 299-305.	2.6	65
62	Managing hybridization of a recovering endangered species: The red wolf Canis rufus as a case study. Environmental Epigenetics, 2015, 61, 191-205.	1.8	63
63	Predicting land use change: comparison of models based on landowner surveys and historical land cover trends. Landscape Ecology, 2008, 23, 195-210.	4.2	62
64	Pedigree‐based assignment tests for reversing coyote (Canis latrans) introgression into the wild red wolf (Canis rufus) population. Molecular Ecology, 2003, 12, 3287-3301.	3.9	61
65	Pollen dispersal and genetic structure of the tropical tree *Dipteryx panamensis* in a fragmented Costa Rican landscape. Molecular Ecology, 2008, 17, 2060-2073.	3.9	60
66	Capwire: a R package for estimating population census size from non‐invasive genetic sampling. Molecular Ecology Resources, 2013, 13, 154-157.	4.8	60
67	Factors influencing red wolf‐coyote hybridization in eastern North Carolina, USA. Biological Conservation, 2015, 184, 108-116.	4.1	60
68	Feeding ecological knowledge: the underutilised power of faecal DNA approaches for carnivore diet analysis. Mammal Review, 2019, 49, 97-112.	4.8	60
69	A simulation test of the effectiveness of several methods for error-checking non-invasive genetic data. Animal Conservation, 2005, 8, 203-215.	2.9	57
70	An efficient method for screening faecal DNA genotypes and detecting new individuals and hybrids in the red wolf (Canis rufus) experimental population area. Conservation Genetics, 2006, 8, 123-131.	1.5	57
71	A long-term population monitoring approach for a wide-ranging carnivore: Noninvasive genetic sampling of gray wolf rendezvous sites in Idaho, USA. Journal of Wildlife Management, 2014, 78, 1040-1049.	1.8	57
72	The Endangered Species Act: Dollars and Sense?. BioScience, 2002, 52, 163.	4.9	56

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73	Bias in carnivore diet analysis resulting from misclassification of predator scats based on field identification. Wildlife Society Bulletin, 2016, 40, 669-677.	1.6	56
74	Assessing the prevalence of hybridization between sympatric Canis species surrounding the red wolf (Canis rufus) recovery area in North Carolina. Molecular Ecology, 2011, 20, 2142-2156.	3.9	54
75	Helper effects on pup lifetime fitness in the cooperatively breeding red wolf (*Canis rufus*). Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 1381-1389.	2.6	54
76	Multiple breeding strategies in the swift fox, Vulpes velox. Animal Behaviour, 2006, 71, 1029-1038.	1.9	53
77	Molecular species identification for multiple carnivores. Conservation Genetics Resources, 2014, 6, 821-824.	0.8	52
78	A quantitative evaluation of two methods for preserving hair samples. Molecular Ecology Notes, 2003, 3, 163-166.	1.7	51
79	Detection of Predator Presence at Elk Mortality Sites Using mtDNA Analysis of Hair and Scat Samples. Wildlife Society Bulletin, 2006, 34, 815-820.	1.6	50
80	Spatiotemporal heterogeneity in prey abundance and vulnerability shapes the foraging tactics of an omnivore. Journal of Animal Ecology, 2018, 87, 874-887.	2.8	50
81	Evaluating the ability of Bayesian clustering methods to detect hybridization and introgression using an empirical red wolf data set. Molecular Ecology, 2013, 22, 74-86.	3.9	49
82	Microsatellite analysis of genetic variation among and within Alpine marmot populations in the French Alps. Molecular Ecology, 2001, 10, 41-52.	3.9	48
83	Genetic diversity and population structure of wolverine (Gulo gulo) populations at the southern edge of their current distribution in North America with implications for genetic viability. Conservation Genetics, 2006, 7, 197-211.	1.5	48
84	Noninvasive individual and species identification of jaguars (*Panthera onca*), pumas (*Puma) Tj ETQq0 0 0 rgBT /Overlock 10 Tf microsatellites and faecal <scp>DNA</scp>. Molecular Ecology Resources, 2014, 14, 1171-1182.	4.8	48
85	Alaskan brown bears (*Ursus arctos*) aggregate and display fidelity to foraging neighborhoods while preying on Pacific salmon along small streams. Ecology and Evolution, 2018, 8, 9048-9061.	1.9	48
86	Identifying polymorphic microsatellite loci for Andean bear research. Ursus, 2009, 20, 102-108.	0.5	47
87	Reintroduction and Genetic Structure: Rocky Mountain Elk in Yellowstone and the Western States. Journal of Mammalogy, 2007, 88, 129-138.	1.3	46
88	Inbreeding and inbreeding depression in endangered red wolves (*Canis rufus*). Molecular Ecology, 2014, 23, 4241-4255.	3.9	46
89	Sampling technique affects detection of habitat factors influencing wild bee communities. Journal of Insect Conservation, 2017, 21, 703-714.	1.4	46
90	Genetic and spatial structure within a swift fox population. Journal of Animal Ecology, 2005, 74, 1173-1181.	2.8	45

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91	Locating hybrid individuals in the red wolf (Canis rufus) experimental population area using a spatially targeted sampling strategy and faecal DNA genotyping. Molecular Ecology, 2007, 16, 1823-1834.	3.9	45
92	Coupled social and ecological outcomes of agricultural intensification in Costa Rica and the future of biodiversity conservation in tropical agricultural regions. Global Environmental Change, 2015, 32, 74-86.	7.8	45
93	A bioinformatic pipeline for identifying informative SNP panels for parentage assignment from <scp>RAD</scp>seq data. Molecular Ecology Resources, 2018, 18, 1263-1281.	4.8	45
94	Evaluating mixed samples as a source of error in non-invasive genetic studies using microsatellites. Molecular Ecology, 2004, 14, 195-201.	3.9	44
95	Using Detection Dogs and Rspf Models to Assess Habitat Suitability for Bears in Greater Yellowstone. Western North American Naturalist, 2015, 75, 396-405.	0.4	43
96	Monitoring coyote population dynamics with fecal DNA and spatial capture-recapture. Journal of Wildlife Management, 2016, 80, 824-836.	1.8	43
97	A multi€method approach for analyzing hierarchical genetic structures: a case study with cougars <i>Puma concolor</i>. Ecography, 2014, 37, 552-563.	4.5	42
98	Monitoring gray wolf populations using multiple survey methods. Journal of Wildlife Management, 2014, 78, 335-346.	1.8	42
99	Enhanced understanding of predator–prey relationships using molecular methods to identify predator species, individual and sex. Molecular Ecology Resources, 2014, 14, 100-108.	4.8	41
100	A Comparative Analysis of Genetic Diversity and Structure in Jaguars (Panthera onca), Pumas (Puma) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Linkage Zone. PLoS ONE, 2016, 11, e0151043.	2.5	41
101	A Pedagogical Model for Team-Based, Problem-Focused Interdisciplinary Doctoral Education. BioScience, 2016, 66, 477-488.	4.9	41
102	An apparent hybrid wild bear from Cambodia. Ursus, 2008, 19, 85-86.	0.5	39
103	Direct fitness benefits of delayed dispersal in the cooperatively breeding red wolf (Canis rufus). Behavioral Ecology, 2011, 22, 199-205.	2.2	39
104	Age€specific infectious period shapes dynamics of pneumonia in bighorn sheep. Ecology Letters, 2017, 20, 1325-1336.	6.4	39
105	Variation in Genetic Diversity across the Range of North American Brown Bears. Conservation Biology, 1998, 12, 418-429.	4.7	38
106	Balancing sample accumulation and <scp>DNA</scp> degradation rates to optimize noninvasive genetic sampling of sympatric carnivores. Molecular Ecology Resources, 2015, 15, 831-842.	4.8	38
107	A comparison of morphological and molecular diet analyses of predator scats. Journal of Mammalogy, 2016, 97, 112-120.	1.3	38
108	Evaluating DNA degradation rates in faecal pellets of the endangered pygmy rabbit. Molecular Ecology Resources, 2013, 13, 654-662.	4.8	37

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109	Estimating cougar densities in northeast Oregon using conservation detection dogs. Journal of Wildlife Management, 2014, 78, 1104-1114.	1.8	36
110	Recruitment in a social carnivore before and after harvest. Animal Conservation, 2015, 18, 415-423.	2.9	36
111	Evaluating noninvasive genetic sampling techniques to estimate large carnivore abundance. Molecular Ecology Resources, 2015, 15, 1133-1144.	4.8	35
112	Diets of sympatric red wolves and coyotes in northeastern North Carolina. Journal of Mammalogy, 2013, 94, 1141-1148.	1.3	34
113	Incorporating Genotyping Error Into Non‐Invasive DNA‐Based Mark—Recapture Population Estimates. Journal of Wildlife Management, 2009, 73, 598-604.	1.8	33
114	Dispersal, gene flow, and population genetic structure in the pygmy rabbit (<i>Brachylagus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 542 T	1.3	33
115	Efficient single‐survey estimation of carnivore density using fecal DNA and spatial capture‐recapture: a bobcat case study. Population Ecology, 2018, 60, 197-209.	1.2	33
116	Non-invasive genetic sampling. Trends in Ecology and Evolution, 1998, 13, 26-27.	8.7	32
117	Implementing recovery of the red wolf-integrating research scientists and managers. Wildlife Society Bulletin, 2005, 33, 1145-1152.	1.6	32
118	Genetic diversity and population divergence in fragmented habitats: Conservation of Idaho ground squirrels. Conservation Genetics, 2005, 6, 759-774.	1.5	31
119	Evaluating the interaction of faecal pellet deposition rates and <scp>DNA</scp> degradation rates to optimize sampling design for <scp>DNA</scp>‐based mark—recapture analysis of Sonoran pronghorn. Molecular Ecology Resources, 2015, 15, 843-854.	4.8	31
120	The roles of habitat and intraguild predation by coyotes on the spatial dynamics of kit foxes. Ecosphere, 2017, 8, e01749.	2.2	31
121	The influence of landscape characteristics and home-range size on the quantification of landscape-genetics relationships. Landscape Ecology, 2012, 27, 253-266.	4.2	30
122	Evaluating the reliability of field identification and morphometric classifications for carnivore scats confirmed with genetic analysis. Wildlife Society Bulletin, 2015, 39, 593-602.	1.6	29
123	Describing a developing hybrid zone between red wolves and coyotes in eastern North Carolina, <scp>USA</scp>. Evolutionary Applications, 2016, 9, 791-804.	3.1	29
124	Changing numbers of spawning cutthroat trout in tributary streams of Yellowstone Lake and estimates of grizzly bears visiting streams from DNA. Ursus, 2005, 16, 167-180.	0.5	28
125	Estimating abundance of American black bears using DNA-based capture‐mark‐recapture models. Ursus, 2009, 20, 1-11.	0.5	28
126	Comparing morphological and molecular diet analyses and fecal DNA sampling protocols for a terrestrial carnivore. Wildlife Society Bulletin, 2017, 41, 362-369.	1.6	28

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127	Density and population size estimates for North Cascade grizzly bears using DNA hair-sampling techniques. Biological Conservation, 2004, 117, 417-428.	4.1	27
128	Using habitat models to determine conservation priorities for pond-breeding amphibians in a privately-owned landscape of northern Idaho, USA. Biological Conservation, 2009, 142, 1096-1104.	4.1	27
129	Predicted effects of residential development on a northern Idaho landscape under alternative growth management and land protection policies. Landscape and Urban Planning, 2010, 94, 255-263.	7.5	26
130	Developing an Interdisciplinary, Distributed Graduate Course for Twenty-First Century Scientists. BioScience, 2012, 62, 182-188.	4.9	26
131	Social and Demographic Effects of Anthropogenic Mortality: A Test of the Compensatory Mortality Hypothesis in the Red Wolf. PLoS ONE, 2011, 6, e20868.	2.5	26
132	Pack social dynamics and inbreeding avoidance in the cooperatively breeding red wolf. Behavioral Ecology, 2012, 23, 1186-1194.	2.2	25
133	Assessment of genetic diversity, population structure, and gene flow of tigers (Panthera tigris tigris) across Nepal's Terai Arc Landscape. PLoS ONE, 2018, 13, e0193495.	2.5	25
134	Status of the Gobi bear in Mongolia as determined by noninvasive genetic methods. Ursus, 2009, 20, 30-38.	0.5	24
135	Inbreeding depression in pronghorn (Antilocapra americana) fawns. Molecular Ecology, 2011, 20, 4889-4898.	3.9	24
136	Agricultural intensification alters bat assemblage composition and abundance in a dynamic Neotropical landscape. Biotropica, 2016, 48, 667-676.	1.6	24
137	Advances in Using Non-invasive, Archival, and Environmental Samples for Population Genomic Studies. Population Genomics, 2018, , 63-99.	0.5	24
138	Batrachochytrium dendrobatidis infection dynamics in the Columbia spotted frog Rana luteiventris in north Idaho, USA. Diseases of Aquatic Organisms, 2010, 92, 223-230.	1.0	24
139	Molted feathers from clay licks in Peru provide DNA for three large macaws (<i>Ara) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 26?? 183-192.	0.5	23
140	Optimizing collection methods for noninvasive genetic sampling of neotropical felids. Wildlife Society Bulletin, 2015, 39, 403-412.	1.6	23
141	Applying genomics in assisted migration under climate change: Framework, empirical applications, and case studies. Evolutionary Applications, 2022, 15, 3-21.	3.1	23
142	Genetic diversity in a reintroduced swift fox population. Conservation Genetics, 2013, 14, 93-102.	1.5	22
143	Estimating Sonoran pronghorn abundance and survival with fecal DNA and capture–recapture methods. Conservation Biology, 2016, 30, 1102-1111.	4.7	22
144	Comment on â€œWhole-genome sequence analysis shows two endemic species of North American wolf are admixtures of the coyote and gray wolfâ€. Science Advances, 2017, 3, e1602250.	10.3	22

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145	Highly efficient multiplex PCR of noninvasive DNA does not require preâ€amplification. Molecular Ecology Resources, 2010, 10, 495-501.	4.8	21
146	Crossâ€species amplification and optimization of microsatellite markers for use in six Neotropical parrots. Molecular Ecology Resources, 2008, 8, 835-839.	4.8	20
147	ConGenR: rapid determination of consensus genotypes and estimates of genotyping errors from replicated genetic samples. Conservation Genetics Resources, 2015, 7, 841-843.	0.8	20
148	Conventional and genetic measures of seed dispersal for Dipteryx panamensis (Fabaceae) in continuous and fragmented Costa Rican rain forest. Journal of Tropical Ecology, 2007, 23, 635-642.	1.1	19
149	Comparative landscape genetics of two frugivorous bats in a biological corridor undergoing agricultural intensification. Molecular Ecology, 2017, 26, 4603-4617.	3.9	19
150	Genetic monitoring of an endangered species recovery: demographic and genetic trends for reintroduced pygmy rabbits (Brachylagus idahoensis). Journal of Mammalogy, 2017, 98, 350-364.	1.3	19
151	Rapid species identification of pygmy rabbits *(Brachylagus idahoensis)* from faecal pellet DNA. Molecular Ecology Resources, 2011, 11, 808-812.	4.8	18
152	Genetic assessment of paternity and relatedness in a managed population of cougars. Journal of Wildlife Management, 2011, 75, 378-384.	1.8	18
153	A method for estimating population sex ratio for sageâ€grouse using noninvasive genetic samples. Molecular Ecology Resources, 2013, 13, 393-402.	4.8	18
154	Harvest and group effects on pup survival in a cooperative breeder. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20170580.	2.6	18
155	Substantial red wolf genetic ancestry persists in wild canids of southwestern Louisiana. Conservation Letters, 2019, 12, e12621.	5.7	18
156	Taxonomic status and conservation strategy of the endangered red wolf: a response to Kyle etÂal. (2006). Conservation Genetics, 2007, 8, 1483-1485.	1.5	17
157	Mitochondrial DNA Phylogeography of the North American Brown Bear and Implications for Conservation. Conservation Biology, 1998, 12, 408-417.	4.7	17
158	Social and genetic structure associated with migration in pronghorn. Biological Conservation, 2013, 168, 108-115.	4.1	17
159	Evaluation of Scat Deposition Transects versus Radio Telemetry for Developing a Species Distribution Model for a Rare Desert Carnivore, the Kit Fox. PLoS ONE, 2015, 10, e0138995.	2.5	17
160	Identifying gray wolf packs and dispersers using noninvasive genetic samples. Journal of Wildlife Management, 2016, 80, 1408-1419.	1.8	17
161	Genetic resolution of composition and phylogenetic placement of the isabelline bear. Ursus, 2007, 18, 129-131.	0.5	16
162	A select panel of polymorphic microsatellite loci for individual identification of snow leopards (Panthera uncia). Molecular Ecology Notes, 2007, 7, 311-314.	1.7	16

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163	Behavioral connectivity among bighorn sheep suggests potential for disease spread. Journal of Wildlife Management, 2017, 81, 38-45.	1.8	16
164	Evaluating effective population size and genetic diversity of a declining kit fox population using contemporary and historical specimens. Ecology and Evolution, 2018, 8, 12011-12021.	1.9	16
165	High error rates for avian molecular sex identification primer sets applied to molted feathers. Journal of Field Ornithology, 2008, 79, 286-292.	0.5	15
166	Food Habits of Red Wolves during Pup-Rearing Season. Southeastern Naturalist, 2011, 10, 731-740.	0.4	15
167	The Challenges of Red Wolf Conservation and the Fate of an Endangered Species Recovery Program. Conservation Letters, 2015, 8, 338-344.	5.7	15
168	Effects of breeder turnover and harvest on group composition and recruitment in a social carnivore. Journal of Animal Ecology, 2017, 86, 1094-1101.	2.8	15
169	Species, sex and geo-location identification of seized tiger (Panthera tigris tigris) parts in Nepalâ€"A molecular forensic approach. PLoS ONE, 2018, 13, e0201639.	2.5	15
170	Evaluating Population Structure of Black Bears on the Kenai Peninsula using Mitochondrial and Nuclear DNA Analyses. Journal of Mammalogy, 2007, 88, 1288-1299.	1.3	14
171	Hair of the dog: Obtaining samples from coyotes and wolves noninvasively. Wildlife Society Bulletin, 2011, 35, 105-111.	1.6	14
172	Evidence for a genetic basis for delayed dispersal in a cooperatively breeding canid. Animal Behaviour, 2012, 83, 1091-1098.	1.9	14
173	Examining the use of fecal pellet morphometry to differentiate age classes in Sonoran pronghorn. Wildlife Biology, 2016, 22, 217-227.	1.4	14
174	Quantifying and correcting for scat removal in noninvasive carnivore scat surveys. Wildlife Biology, 2016, 22, 45-54.	1.4	14
175	Phylogeography, genetic diversity, and connectivity of brown bear populations in Central Asia. PLoS ONE, 2019, 14, e0220746.	2.5	14
176	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
177	Species limits and integrated taxonomy of the Idaho ground squirrel (<i>Urocitellus brunneus</i>): genetic and ecological differentiation. Journal of Mammalogy, 2012, 93, 589-604.	1.3	13
178	Integrating multiple genetic detection methods to estimate population density of social and territorial carnivores. Ecosphere, 2018, 9, e02479.	2.2	13
179	Natural re-colonization and admixture of wolves (Canis lupus) in the US Pacific Northwest: challenges for the protection and management of rare and endangered taxa. Heredity, 2019, 122, 133-149.	2.6	13
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