

# Michael K Schwartz

## List of Publications by Year in descending order

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Version: 2024-02-01

184  
papers

13,844  
citations

50276

46  
h-index

24982

109  
g-index

188  
all docs

188  
docs citations

188  
times ranked

12329  
citing authors

#	ARTICLE	IF	CITATIONS
1	Landscape genetics: combining landscape ecology and population genetics. <i>Trends in Ecology and Evolution</i> , 2003, 18, 189-197.	8.7	1,907
2	Genetic monitoring as a promising tool for conservation and management. <i>Trends in Ecology and Evolution</i> , 2007, 22, 25-33.	8.7	934
3	Gene Flow in Complex Landscapes: Testing Multiple Hypotheses with Causal Modeling. <i>American Naturalist</i> , 2006, 168, 486-499.	2.1	571
4	Genomics and the challenging translation into conservation practice. <i>Trends in Ecology and Evolution</i> , 2015, 30, 78-87.	8.7	469
5	Compromising genetic diversity in the wild: unmonitored large-scale release of plants and animals. <i>Trends in Ecology and Evolution</i> , 2010, 25, 520-529.	8.7	454
6	Estimation of census and effective population sizes: the increasing usefulness of DNA-based approaches. <i>Conservation Genetics</i> , 2010, 11, 355-373.	1.5	444
7	Quantifying the lag time to detect barriers in landscape genetics. <i>Molecular Ecology</i> , 2010, 19, 4179-4191.	3.9	426
8	Robust Detection of Rare Species Using Environmental DNA: The Importance of Primer Specificity. <i>PLoS ONE</i> , 2013, 8, e59520.	2.5	405
9	Distance, flow and PCR inhibition: eDNA dynamics in two headwater streams. <i>Molecular Ecology Resources</i> , 2015, 15, 216-227.	4.8	391
10	Why sampling scheme matters: the effect of sampling scheme on landscape genetic results. <i>Conservation Genetics</i> , 2009, 10, 441-452.	1.5	334
11	ESTIMATING ANIMAL ABUNDANCE USING NONINVASIVE DNA SAMPLING: PROMISE AND PITFALLS. , 2000, 10, 283-294.		328
12	Understanding environmental DNA detection probabilities: A case study using a stream-dwelling char <i>Salvelinus fontinalis</i> . <i>Biological Conservation</i> , 2016, 194, 209-216.	4.1	307
13	Advancing ecological understandings through technological transformations in noninvasive genetics. <i>Molecular Ecology Resources</i> , 2009, 9, 1279-1301.	4.8	296
14	Understanding and Estimating Effective Population Size for Practical Application in Marine Species Management. <i>Conservation Biology</i> , 2011, 25, 438-449.	4.7	270
15	The climate velocity of the contiguous United States during the 20th century. <i>Global Change Biology</i> , 2013, 19, 241-251.	9.5	267
16	Use of Empirically Derived Source-Destination Models to Map Regional Conservation Corridors. <i>Conservation Biology</i> , 2009, 23, 368-376.	4.7	198
17	Neglect of Genetic Diversity in Implementation of the Convention on Biological Diversity. <i>Conservation Biology</i> , 2010, 24, 86-88.	4.7	182
18	Wolverine gene flow across a narrow climatic niche. <i>Ecology</i> , 2009, 90, 3222-3232.	3.2	166

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19	Why replication is important in landscape genetics: American black bear in the Rocky Mountains. <i>Molecular Ecology</i> , 2011, 20, 1092-1107.	3.9	165
20	Using Anecdotal Occurrence Data for Rare or Elusive Species: The Illusion of Reality and a Call for Evidentiary Standards. <i>BioScience</i> , 2008, 58, 549-555.	4.9	148
21	DNA reveals high dispersal synchronizing the population dynamics of Canada lynx. <i>Nature</i> , 2002, 415, 520-522.	27.8	144
22	Conservation genomics of natural and managed populations: building a conceptual and practical framework. <i>Molecular Ecology</i> , 2016, 25, 2967-2977.	3.9	141
23	GENETIC ERRORS ASSOCIATED WITH POPULATION ESTIMATION USING NON-INVASIVE MOLECULAR TAGGING: PROBLEMS AND NEW SOLUTIONS. <i>Journal of Wildlife Management</i> , 2004, 68, 439-448.	1.8	138
24	Spatial scaling and multi-model inference in landscape genetics: <i>Martes americana</i> in northern Idaho. <i>Landscape Ecology</i> , 2010, 25, 1601-1612.	4.2	138
25	Felid sex identification based on noninvasive genetic samples. <i>Molecular Ecology Notes</i> , 2005, 5, 60-61.	1.7	133
26	dropout: a program to identify problem loci and samples for noninvasive genetic samples in a capture-mark-recapture framework. <i>Molecular Ecology Notes</i> , 2005, 5, 716-718.	1.7	130
27	Forest structure and species traits mediate projected recruitment declines in western US tree species. <i>Global Ecology and Biogeography</i> , 2015, 24, 917-927.	5.8	129
28	Review of DNA-based census and effective population size estimators. <i>Animal Conservation</i> , 1998, 1, 293-299.	2.9	120
29	Landscape location affects genetic variation of Canada lynx ( <i>Lynx canadensis</i> ). <i>Molecular Ecology</i> , 2003, 12, 1807-1816.	3.9	116
30	Estimation of effective population size in continuously distributed populations: there goes the neighborhood. <i>Heredity</i> , 2013, 111, 189-199.	2.6	112
31	The bioclimatic envelope of the wolverine ( <i>Gulo gulo</i> ): do climatic constraints limit its geographic distribution?. <i>Canadian Journal of Zoology</i> , 2010, 88, 233-246.	1.0	99
32	Estimating abundance of mountain lions from unstructured spatial sampling. <i>Journal of Wildlife Management</i> , 2012, 76, 1551-1561.	1.8	96
33	Wolf survival and population trend using non-invasive capture-recapture techniques in the Western Alps. <i>Journal of Applied Ecology</i> , 2009, 46, 1003-1010.	4.0	93
34	Climate change predicted to shift wolverine distributions, connectivity, and dispersal corridors. , 2011, 21, 2882-2897.		92
35	Effects of time and rainfall on PCR success using DNA extracted from deer fecal pellets. <i>Conservation Genetics</i> , 2010, 11, 1547-1552.	1.5	88
36	Sampling large geographic areas for rare species using environmental DNA: a study of bull trout ( <i>Salvelinus confluentus</i> ) occupancy in western Montana. <i>Journal of Fish Biology</i> , 2016, 88, 1215-1222.	1.6	84

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37	When are genetic methods useful for estimating contemporary abundance and detecting population trends?. <i>Molecular Ecology Resources</i> , 2010, 10, 684-692.	4.8	82
38	Environmental DNA particle size distribution from Brook Trout ( <i>Salvelinus fontinalis</i> ). <i>Conservation Genetics Resources</i> , 2015, 7, 639-641.	0.8	79
39	Using environmental DNA methods to improve winter surveys for rare carnivores: DNA from snow and improved noninvasive techniques. <i>Biological Conservation</i> , 2019, 229, 50-58.	4.1	78
40	Candidate gene microsatellite variation is associated with parasitism in wild bighorn sheep. <i>Biology Letters</i> , 2008, 4, 228-231.	2.3	76
41	Identifying lynx and other North American felids based on MtDNA analysis. <i>Conservation Genetics</i> , 2000, 1, 285-288.	1.5	72
42	The Dual Challenges of Generality and Specificity When Developing Environmental DNA Markers for Species and Subspecies of <i>Oncorhynchus</i> . <i>PLoS ONE</i> , 2015, 10, e0142008.	2.5	72
43	Hybridization Between Canada Lynx and Bobcats: Genetic Results and Management Implications. <i>Conservation Genetics</i> , 2004, 5, 349-355.	1.5	71
44	POPULATION GROWTH OF ANTARCTIC FUR SEALS: LIMITATION BY A TOP PREDATOR, THE LEOPARD SEAL?. <i>Ecology</i> , 1998, 79, 2863-2877.	3.2	70
45	Mitochondrial genome sequences illuminate maternal lineages of conservation concern in a rare carnivore. <i>BMC Ecology</i> , 2011, 11, 10.	3.0	66
46	Tradeoffs and efficiencies in optimal budget-constrained multispecies corridor networks. <i>Conservation Biology</i> , 2017, 31, 192-202.	4.7	53
47	DNA Analysis of Hair and Scat Collected Along Snow Tracks to Document the Presence of Canada Lynx. <i>Wildlife Society Bulletin</i> , 2006, 34, 451-455.	1.6	52
48	Bridging the gaps between non-invasive genetic sampling and population parameter estimation. <i>European Journal of Wildlife Research</i> , 2011, 57, 1-13.	1.4	52
49	Temporal correlations in population trends: Conservation implications from time-series analysis of diverse animal taxa. <i>Biological Conservation</i> , 2015, 192, 247-257.	4.1	52
50	Integrating resource selection into spatial capture-recapture models for large carnivores. <i>Ecosphere</i> , 2015, 6, 1-15.	2.2	49
51	Spatially Explicit Power Analyses for Occupancy-Based Monitoring of Wolverine in the U.S. Rocky Mountains. <i>Conservation Biology</i> , 2014, 28, 52-62.	4.7	47
52	Female-solicited extrapair matings in Humboldt penguins fail to produce extrapair fertilizations. <i>Behavioral Ecology</i> , 1999, 10, 242-250.	2.2	46
53	Hunting and social behaviour of leopard seals ( <i>Hydrurga leptonyx</i> ) at Seal Island, South Shetland Islands, Antarctica. <i>Journal of Zoology</i> , 1999, 249, 97-109.	1.7	46
54	Meta-analyses of habitat selection by fishers at resting sites in the pacific coastal region. <i>Journal of Wildlife Management</i> , 2013, 77, 965-974.	1.8	45

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55	Effects of Weighting Schemes on the Identification of Wildlife Corridors Generated with Least-Cost Methods. <i>Conservation Biology</i> , 2013, 27, 145-154.	4.7	45
56	KINSHIP, SOCIAL RELATIONSHIPS, AND DEN SHARING IN KIT FOXES. <i>Journal of Mammalogy</i> , 2001, 82, 858.	1.3	44
57	Scale-dependent genetic structure of the Idaho giant salamander ( <i>Dicamptodon aterrimus</i> ) in stream networks. <i>Molecular Ecology</i> , 2010, 19, 898-909.	3.9	44
58	Detecting genotyping errors and describing American black bear movement in northern Idaho. <i>Ursus</i> , 2006, 17, 138-148.	0.5	42
59	Capture enrichment of aquatic environmental DNA: A first proof of concept. <i>Molecular Ecology Resources</i> , 2018, 18, 1392-1401.	4.8	42
60	Integrating motion-detection cameras and hair snags for wolverine identification. <i>Journal of Wildlife Management</i> , 2011, 75, 731-739.	1.8	41
61	Patterns of hybridization among cutthroat trout and rainbow trout in northern Rocky Mountain streams. <i>Ecology and Evolution</i> , 2016, 6, 688-706.	1.9	40
62	Genetic consequences of sex-biased dispersal in a solitary carnivore: Yellowstone cougars. <i>Biology Letters</i> , 2006, 2, 312-315.	2.3	39
63	Comment: The Importance of Sound Methodology in Environmental DNA Sampling. <i>North American Journal of Fisheries Management</i> , 2018, 38, 592-596.	1.0	38
64	Making environmental DNA (eDNA) biodiversity records globally accessible. <i>Environmental DNA</i> , 2021, 3, 699-705.	5.8	38
65	Inferring Geographic Isolation of Wolverines in California Using Historical DNA. <i>Journal of Wildlife Management</i> , 2007, 71, 2170-2179.	1.8	36
66	Identification of landscape features influencing gene flow: How useful are habitat selection models?. <i>Evolutionary Applications</i> , 2016, 9, 805-817.	3.1	36
67	DNA barcoding at riverscape scales: assessing biodiversity among fishes of the genus <i>Cottus</i> ( <i>T. eleostei</i> ) in northern Rocky Mountain streams. <i>Molecular Ecology Resources</i> , 2013, 13, 583-595.	4.8	35
68	Red flags: correlates of impaired species recovery. <i>Trends in Ecology and Evolution</i> , 2012, 27, 542-546.	8.7	34
69	Sampling affects the detection of genetic subdivision and conservation implications for fisher in the Sierra Nevada. <i>Conservation Genetics</i> , 2014, 15, 123-136.	1.5	33
70	The Efficacy of Wire and Glue Hair Snares in Identifying Mesocarnivores. <i>Wildlife Society Bulletin</i> , 2006, 34, 1152-1161.	1.6	32
71	Wolverine Confirmation in California after Nearly a Century: Native or Long-Distance Immigrant?. <i>Northwest Science</i> , 2009, 83, 154-162.	0.2	32
72	Evaluating sample allocation and effort in detecting population differentiation for discrete and continuously distributed individuals. <i>Conservation Genetics</i> , 2014, 15, 981-992.	1.5	32

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73	Using genetics to estimate the size of wild populations: many methods, much potential, uncertain utility. <i>Animal Conservation</i> , 1999, 2, 321-323.	2.9	30
74	Individual identification of Sitka black-tailed deer ( <i>Odocoileus hemionus sitkensis</i> ) using DNA from fecal pellets. <i>Conservation Genetics Resources</i> , 2010, 2, 115-118.	0.8	30
75	Pronounced differences in genetic structure despite overall ecological similarity for two <i>Ambystoma</i> salamanders in the same landscape. <i>Conservation Genetics</i> , 2014, 15, 573-591.	1.5	30
76	Long-distance dispersal of a subadult male cougar from South Dakota to Connecticut documented with DNA evidence. <i>Journal of Mammalogy</i> , 2016, 97, 1435-1440.	1.3	30
77	An environmental DNA assay for detecting Arctic grayling in the upper Missouri River basin, North America. <i>Conservation Genetics Resources</i> , 2016, 8, 197-199.	0.8	30
78	Repurposing environmental DNA samples to detect the western pearlshell ( <i>Margaritifera falcata</i> ) as a proof of concept. <i>Ecology and Evolution</i> , 2018, 8, 2659-2670.	1.9	30
79	Historical and Contemporary DNA Indicate Fisher Decline and Isolation Occurred Prior to the European Settlement of California. <i>PLoS ONE</i> , 2012, 7, e52803.	2.5	29
80	Spatial regression methods capture prediction uncertainty in species distribution model projections through time. <i>Global Ecology and Biogeography</i> , 2013, 22, 242-251.	5.8	29
81	Fine-scale environmental DNA sampling reveals climate-mediated interactions between native and invasive trout species. <i>Ecosphere</i> , 2018, 9, e02500.	2.2	29
82	Moa were many. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2004, 271, S430-2.	2.6	28
83	Sources and Patterns of Wolverine Mortality in Western Montana. <i>Journal of Wildlife Management</i> , 2007, 71, 2213.	1.8	28
84	Do male and female black-backed woodpeckers respond differently to gaps in habitat?. <i>Evolutionary Applications</i> , 2010, 3, 263-278.	3.1	28
85	An improved environmental DNA assay for bull trout ( <i>Salvelinus confluentus</i> ) based on the ribosomal internal transcribed spacer I. <i>PLoS ONE</i> , 2018, 13, e0206851.	2.5	28
86	Climate, Demography, and Zoogeography Predict Introgression Thresholds in Salmonid Hybrid Zones in Rocky Mountain Streams. <i>PLoS ONE</i> , 2016, 11, e0163563.	2.5	27
87	PROVIDING RELIABLE AND ACCURATE GENETIC CAPTURE-MARK-RECAPTURE ESTIMATES IN A COST-EFFECTIVE WAY. <i>Journal of Wildlife Management</i> , 2004, 68, 453-456.	1.8	26
88	Gene flow after inbreeding leads to higher survival in deer mice. <i>Biological Conservation</i> , 2005, 123, 413-420.	4.1	25
89	Evolutionary Community Ecology: Time to Think Outside the (Taxonomic) Box. <i>Trends in Ecology and Evolution</i> , 2018, 33, 240-250.	8.7	25
90	The Efficacy of Obtaining Genetic-Based Identifications from Putative Wolverine Snow Tracks. <i>Wildlife Society Bulletin</i> , 2006, 34, 1326-1332.	1.6	24

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91	Development of 22 new microsatellite loci for fishers ( <i>Martes pennanti</i> ) with variability results from across their range. <i>Molecular Ecology Notes</i> , 2007, 7, 797-801.	1.7	24
92	Reply to Garner et al.. <i>Trends in Ecology and Evolution</i> , 2016, 31, 83-84.	8.7	24
93	Dynamic occupancy modelling reveals a hierarchy of competition among fishers, grey foxes and ringtails. <i>Journal of Animal Ecology</i> , 2018, 87, 813-824.	2.8	24
94	Quantifying functional connectivity: The role of breeding habitat, abundance, and landscape features on range-wide gene flow in sage-grouse. <i>Evolutionary Applications</i> , 2018, 11, 1305-1321.	3.1	24
95	Landscape Genomics: A Brief Perspective. , 2010, , 165-174.		24
96	Demographic fragmentation of a protected wolverine population bisected by a major transportation corridor. <i>Biological Conservation</i> , 2019, 236, 616-625.	4.1	23
97	Parallel, targeted analysis of environmental samples via high-throughput quantitative PCR. <i>Environmental DNA</i> , 2020, 2, 544-553.	5.8	23
98	A blocking primer increases specificity in environmental DNA detection of bull trout ( <i>Salvelinus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 46	0.8	21
99	<sc>SNP</sc> discovery in candidate adaptive genes using exon capture in a free-ranging alpine ungulate. <i>Molecular Ecology Resources</i> , 2016, 16, 1147-1164.	4.8	21
100	Using environmental DNA sampling to monitor the invasion of nonnative <i>Esox lucius</i> (northern pike) in the Columbia River basin, USA. <i>Environmental DNA</i> , 2019, 1, 215-226.	5.8	21
101	WHEN REINTRODUCTIONS ARE AUGMENTATIONS: THE GENETIC LEGACY OF FISHERS ( <i>MARTES PENNANTI</i> ) IN MONTANA. <i>Journal of Mammalogy</i> , 2006, 87, 265-271.	1.3	20
102	Canada Lynx-bobcat ( <i>lynx canadensis</i> – <i>L. rufus</i> ) Hybrids at the Southern Periphery of Lynx range in Maine, Minnesota and New Brunswick. <i>American Midland Naturalist</i> , 2008, 159, 504-508.	0.4	20
103	Development and evaluation of 200 novel SNP assays for population genetic studies of westslope cutthroat trout and genetic identification of related taxa. <i>Molecular Ecology Resources</i> , 2012, 12, 942-949.	4.8	20
104	Stand- and landscape-scale selection of large trees by fishers in the Rocky Mountains of Montana and Idaho. <i>Forest Ecology and Management</i> , 2013, 305, 103-111.	3.2	20
105	Breed Locally, Disperse Globally: Fine-Scale Genetic Structure Despite Landscape-Scale Panmixia in a Fire-Specialist. <i>PLoS ONE</i> , 2013, 8, e67248.	2.5	20
106	Modeling the effects of dispersal and patch size on predicted fisher ( <i>Pekania</i> [ <i>Martes</i> ] <i>pennanti</i> ) distribution in the U.S. Rocky Mountains. <i>Biological Conservation</i> , 2014, 169, 89-98.	4.1	19
107	<sc>rSPACE</sc>: Spatially based power analysis for conservation and ecology. <i>Methods in Ecology and Evolution</i> , 2015, 6, 621-625.	5.2	19
108	An eDNA assay for river otter detection: a tool for surveying a semi-aquatic mammal. <i>Conservation Genetics Resources</i> , 2016, 8, 5-7.	0.8	19

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109	Gene flow among San Joaquin kit fox populations in a severely changed ecosystem. <i>Conservation Genetics</i> , 2005, 6, 25-37.	1.5	18
110	The genetic network of greater sage-grouse: Range-wide identification of keystone hubs of connectivity. <i>Ecology and Evolution</i> , 2018, 8, 5394-5412.	1.9	18
111	Environmental DNA Sampling Informs Fish Eradication Efforts: Case Studies and Lessons Learned. <i>North American Journal of Fisheries Management</i> , 2020, 40, 488-508.	1.0	18
112	Cross-species transmission and evolutionary dynamics of canine distemper virus during a spillover in African lions of Serengeti National Park. <i>Molecular Ecology</i> , 2020, 29, 4308-4321.	3.9	18
113	Environmental DNA Marker Development with Sparse Biological Information: A Case Study on Opossum Shrimp ( <i>Mysis diluviana</i> ). <i>PLoS ONE</i> , 2016, 11, e0161664.	2.5	17
114	Sex-biased dispersal and spatial heterogeneity affect landscape resistance to gene flow in fisher. <i>Ecosphere</i> , 2017, 8, e01839.	2.2	17
115	Estimating abundance of a cryptic social carnivore using spatially explicit capture-recapture. <i>Wildlife Society Bulletin</i> , 2019, 43, 31-41.	1.6	17
116	Wolverine Occupancy, Spatial Distribution, and Monitoring Design. <i>Journal of Wildlife Management</i> , 2020, 84, 841-851.	1.8	17
117	Lack of sex-biased dispersal promotes fine-scale genetic structure in alpine ungulates. <i>Conservation Genetics</i> , 2014, 15, 837-851.	1.5	16
118	Molecular genetic analysis of air, water, and soil to detect big brown bats in North America. <i>Biological Conservation</i> , 2021, 261, 109252.	4.1	16
119	Molecules and beyond: assessing the distinctness of the Great Lakes wolf. <i>Molecular Ecology</i> , 2009, 18, 2307-2309.	3.9	15
120	Recovery of wolverines in the Western United States: Recent extirpation and recolonization or range retraction and expansion?. <i>Journal of Wildlife Management</i> , 2014, 78, 325-334.	1.8	15
121	Genetic recapture identifies long-distance breeding dispersal in Greater Sage-Grouse ( <i>Centrocercus urophasianus</i> ). <i>Condor</i> , 2017, 119, 155-166.	1.6	15
122	A Non-Invasive Sampling Method for Detecting Non-Native Smallmouth Bass ( <i>Micropterus</i> ) Overlooked by 50% of Traps. <i>Conservation Genetics</i> , 2021, 22, 109-118.	0.2	15
123	Allometric scaling of eDNA production in stream-dwelling brook trout ( <i>Salvelinus fontinalis</i> ) inferred from population size structure. <i>Environmental DNA</i> , 2021, 3, 553-560.	5.8	15
124	Crowdsourced Databases as Essential Elements for Forest Service Partnerships and Aquatic Resource Conservation. <i>Fisheries</i> , 2018, 43, 423-430.	0.8	14
125	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
126	Ancient Dna Confirms Native Rocky Mountain Fisher ( <i>Martes pennanti</i> ) Avoided Early 20th Century Extinction. <i>Journal of Mammalogy</i> , 2007, 88, 921-925.	1.3	13

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127	Hierarchical population structure in greater sage-grouse provides insight into management boundary delineation. <i>Conservation Genetics</i> , 2016, 17, 1417-1433.	1.5	13
128	Immigration does not offset harvest mortality in groups of a cooperatively breeding carnivore. <i>Animal Conservation</i> , 2020, 23, 750-761.	2.9	13
129	Review of DNA-based census and effective population size estimators. <i>Animal Conservation</i> , 1998, 1, 293-299.	2.9	13
130	Combined use of mark-recapture and genetic analyses reveals response of a black bear population to changes in food productivity. <i>Journal of Wildlife Management</i> , 2013, 77, 1572-1582.	1.8	12
131	Ski areas affect Pacific marten movement, habitat use, and density. <i>Journal of Wildlife Management</i> , 2017, 81, 892-904.	1.8	12
132	Latent spatial models and sampling design for landscape genetics. <i>Annals of Applied Statistics</i> , 2016, 10, .	1.1	11
133	Phylogeography of moose in western North America. <i>Journal of Mammalogy</i> , 2020, 101, 10-23.	1.3	11
134	A Noninvasive Tool to Assess the Distribution of Pacific Lamprey ( <i>Entosphenus tridentatus</i> ) in the Columbia River Basin. <i>PLoS ONE</i> , 2017, 12, e0169334.	2.5	11
135	Measuring and interpreting connectivity for mammals in coniferous forests. , 2003, , 587-613.		10
136	Estimating Bighorn Sheep ( <i>Ovis canadensis</i> ) Abundance Using Noninvasive Sampling at a Mineral Lick within a National Park Wilderness Area. <i>Western North American Naturalist</i> , 2015, 75, 181-191.	0.4	10
137	Inferring presence of the western toad ( <i>Anaxyrus boreas</i> ) species complex using environmental DNA. <i>Global Ecology and Conservation</i> , 2018, 15, e00438.	2.1	10
138	Small geographic range but not panmictic: how forests structure the endangered Point Arena mountain beaver ( <i>Aplodontia rufa nigra</i> ). <i>Conservation Genetics</i> , 2013, 14, 369-383.	1.5	9
139	<i>Cottus schitsuumsh</i> , a new species of sculpin (Scorpaeniformes: Cottidae) in the Columbia River basin, Idaho-Montana, USA. <i>Zootaxa</i> , 2014, 3755, 241-58.	0.5	9
140	Discovery of 20,000 RADâ€“SNPs and development of a 52-SNP array for monitoring river otters. <i>Conservation Genetics Resources</i> , 2016, 8, 299-302.	0.8	9
141	Occupancy Patterns in a Reintroduced Fisher Population during Reestablishment. <i>Journal of Wildlife Management</i> , 2020, 84, 344-358.	1.8	9
142	Identifying Candidate Genetic Markers of CDV Cross-Species Pathogenicity in African Lions. <i>Pathogens</i> , 2020, 9, 872.	2.8	9
143	Wolf Dispersal Patterns in the Italian Alps and Implications for Wildlife Diseases Spreading. <i>Animals</i> , 2022, 12, 1260.	2.3	9
144	The Tyranny of Population Growth. <i>Conservation Biology</i> , 2000, 14, 1918-1919.	4.7	8

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145	Detecting population recovery using gametic disequilibrium-based effective population size estimates. <i>Conservation Genetics Resources</i> , 2012, 4, 987-989.	0.8	8
146	Kinship, Social Relationships, and Den Sharing in Kit Foxes. <i>Journal of Mammalogy</i> , 2001, 82, 858-866.	1.3	8
147	DNA Markers for Identifying Individual Snowshoe Hares Using Field-collected Pellets. <i>Northwest Science</i> , 2007, 81, 316-322.	0.2	7
148	An environmental DNA marker for detecting nonnative brown trout ( <i>Salmo trutta</i> ). <i>Conservation Genetics Resources</i> , 2016, 8, 259-261.	0.8	7
149	Ecological segregation moderates a climactic conclusion to trout hybridization. <i>Global Change Biology</i> , 2017, 23, 5021-5023.	9.5	7
150	Population Genomics for the Management of Wild Vertebrate Populations. <i>Population Genomics</i> , 2020, , 419-436.	0.5	7
151	The Tyranny of Population Growth. <i>Conservation Biology</i> , 2000, 14, 1918-1919.	4.7	7
152	Detection of 4 imperiled western North American freshwater mussel species from environmental DNA with multiplex qPCR assays. <i>Freshwater Science</i> , 2020, 39, 762-772.	1.8	7
153	<sc>eDNAAssay</sc>: A machine learning tool that accurately predicts <sc>qPCR</sc> cross&#amp;#228;amplification. <i>Molecular Ecology Resources</i> , 2022, 22, 2994-3005.	4.8	7
154	Integrative taxonomy refutes a species hypothesis: The asymmetric hybrid origin of <i>Arsapnia arapahoe</i> (Plecoptera, Capniidae). <i>Ecology and Evolution</i> , 2019, 9, 1364-1377.	1.9	6
155	Certain detection of uncertain taxa: eDNA detection of a cryptic mountain sucker ( <i>Pantosteus jordani</i> ) Tj ETQq1 1 0,784314,rgBT /Over 2.8	0.8	6
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