

Sara J Oyler-McCance

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

2,484
citations

331670

21
h-index

214800

47
g-index

78
all docs

78
docs citations

78
times ranked

3240
citing authors

#	ARTICLE	IF	CITATIONS
1	Critical considerations for the application of environmental <scp>DNA</scp> methods to detect aquatic species. <i>Methods in Ecology and Evolution</i> , 2016, 7, 1299-1307.	5.2	684
2	Rapid Microsatellite Identification from Illumina Paired-End Genomic Sequencing in Two Birds and a Snake. <i>PLoS ONE</i> , 2012, 7, e30953.	2.5	208
3	Environmental DNA (eDNA) Sampling Improves Occurrence and Detection Estimates of Invasive Burmese Pythons. <i>PLoS ONE</i> , 2015, 10, e0121655.	2.5	166
4	Effects of sample size, number of markers, and allelic richness on the detection of spatial genetic pattern. <i>Molecular Ecology Resources</i> , 2012, 12, 276-284.	4.8	143
5	An empirical comparison of population genetic analyses using microsatellite and SNP data for a species of conservation concern. <i>BMC Genomics</i> , 2020, 21, 382.	2.8	86
6	Sample design effects in landscape genetics. <i>Conservation Genetics</i> , 2013, 14, 275-285.	1.5	79
7	A multilocus population genetic survey of the greater sage-grouse across their range. <i>Molecular Ecology</i> , 2005, 14, 1293-1310.	3.9	75
8	Genetic Applications in Avian Conservation. <i>Auk</i> , 2011, 128, 205-229.	1.4	68
9	Developing approaches for linear mixed modeling in landscape genetics through landscape-directed dispersal simulations. <i>Ecology and Evolution</i> , 2017, 7, 3751-3761.	1.9	62
10	A NEW SPECIES OF SAGE-GROUSE (PHASIANIDAE:CENTROCERCUS) FROM SOUTHWESTERN COLORADO. <i>The Wilson Bulletin</i> , 2000, 112, 445-453.	0.5	59
11	A population genetic comparison of large- and small-bodied sage grouse in Colorado using microsatellite and mitochondrial DNA markers. <i>Molecular Ecology</i> , 1999, 8, 1457-1465.	3.9	55
12	POPULATION GENETICS OF GUNNISON SAGE-GROUSE: IMPLICATIONS FOR MANAGEMENT. <i>Journal of Wildlife Management</i> , 2005, 69, 630-637.	1.8	45
13	Conservation Genomics in the Sagebrush Sea: Population Divergence, Demographic History, and Local Adaptation in Sage-Grouse (<i>Centrocercus</i> spp.). <i>Genome Biology and Evolution</i> , 2019, 11, 2023-2034.	2.5	35
14	Title is missing!. <i>Conservation Genetics</i> , 2003, 4, 301-310.	1.5	34
15	Polygamy slows down population divergence in shorebirds. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 1313-1326.	2.3	33
16	Two Low Coverage Bird Genomes and a Comparison of Reference-Guided versus De Novo Genome Assemblies. <i>PLoS ONE</i> , 2014, 9, e106649.	2.5	30
17	Influence of Changes in Sagebrush on Gunnison Sage Grouse in Southwestern Colorado. <i>Southwestern Naturalist</i> , 2001, 46, 323.	0.1	29
18	Z chromosome divergence, polymorphism and relative effective population size in a genus of lekking birds. <i>Heredity</i> , 2015, 115, 452-459.	2.6	28

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19	Isolation and characterization of microsatellite loci in Greater Sage-Grouse (<i>Centrocercus urophasianus</i>) Tj ETQq1 1 0.784314 rgBT /Overlap 10 Tf 50 302 To	1.7	26
20	Contrasting evolutionary histories of MHC class I and class II loci in grouse—effects of selection and gene conversion. <i>Heredity</i> , 2016, 116, 466-476.	2.6	26
21	Landscape characteristics influencing the genetic structure of greater sage-grouse within the stronghold of their range: a holistic modeling approach. <i>Ecology and Evolution</i> , 2015, 5, 1955-1969.	1.9	25
22	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
23	Chapter 10: Rapid Evolution in Lekking Grouse: Implications for Taxonomic Definitions. <i>Ornithological Monographs</i> , 2010, 67, 114-122.	1.3	22
24	Genomic single-nucleotide polymorphisms confirm that Gunnison and Greater sage-grouse are genetically well differentiated and that the Bi-State population is distinct. <i>Condor</i> , 2015, 117, 217-227.	1.6	20
25	Rangewide genetic analysis of Lesser Prairie-Chicken reveals population structure, range expansion, and possible introgression. <i>Conservation Genetics</i> , 2016, 17, 643-660.	1.5	20
26	A field ornithologist's guide to genomics: Practical considerations for ecology and conservation. <i>Auk</i> , 2016, 133, 626-648.	1.4	19
27	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
28	An experimental comparison of composite and grab sampling of stream water for metagenetic analysis of environmental DNA. <i>PeerJ</i> , 2018, 6, e5871.	2.0	18
29	Mismatches between breeding phenology and resource abundance of resident alpine ptarmigan negatively affect chick survival. <i>Ecology and Evolution</i> , 2019, 9, 7200-7212.	1.9	16
30	Characterization of microsatellite loci isolated in midget faded rattlesnake (<i>Crotalus viridis</i>) Tj ETQq0 0 0 rgBT /Overlap 10 Tf 50 302 To	1.7	15
31	Hierarchical spatial genetic structure in a distinct population segment of greater sage-grouse. <i>Conservation Genetics</i> , 2014, 15, 1299-1311.	1.5	15
32	Long-term persistence of horse fecal DNA in the environment makes equids particularly good candidates for noninvasive sampling. <i>Ecology and Evolution</i> , 2018, 8, 4053-4064.	1.9	14
33	Genetic Markers—Recapture Improves Estimates of Maternity Colony Size for Indiana Bats. <i>Journal of Fish and Wildlife Management</i> , 2018, 9, 25-35.	0.9	14
34	Characterization of small microsatellite loci for use in non invasive sampling studies of Gunnison Sage-grouse (<i>Centrocercus minimus</i>). <i>Conservation Genetics Resources</i> , 2010, 2, 17-20.	0.8	12
35	Characterization of small microsatellite loci isolated in endangered Indiana bat (<i>Myotis sodalis</i>) for use in non-invasive sampling. <i>Conservation Genetics Resources</i> , 2011, 3, 243-245.	0.8	12
36	POPULATION GENETIC ANALYSIS OF MOUNTAIN PLOVER USING MITOCHONDRIAL DNA SEQUENCE DATA. <i>Condor</i> , 2005, 107, 353.	1.6	11

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37	A rangewide population genetic study of trumpeter swans. <i>Conservation Genetics</i> , 2007, 8, 1339-1353.	1.5	11
38	Latent spatial models and sampling design for landscape genetics. <i>Annals of Applied Statistics</i> , 2016, 10, .	1.1	11
39	Characterizing range-wide divergence in an alpine-endemic bird: a comparison of genetic and genomic approaches. <i>Conservation Genetics</i> , 2018, 19, 1471-1485.	1.5	11
40	Evaluation of genetic change from translocation among Gunnison Sage-Grouse (<i>Centrocercus urophasianus</i>) using microsatellite markers. <i>Conservation Genetics</i> , 2010, 11, 50-52.	1.6	11
41	Characterization of ten microsatellite loci in the Broad-tailed Hummingbird (<i>Selasphorus selenis</i>) using microsatellite markers. <i>Conservation Genetics</i> , 2010, 11, 53-57.	0.8	10
42	Development of 13 microsatellites for Gunnison Sage-grouse (<i>Centrocercus minimus</i>) using next-generation shotgun sequencing and their utility in Greater Sage-grouse (<i>Centrocercus urophasianus</i>) using microsatellite markers. <i>Conservation Genetics</i> , 2010, 11, 53-57.	1.6	10
43	Integration of genetic and demographic data to assess population risk in a continuously distributed species. <i>Conservation Genetics</i> , 2017, 18, 89-104.	1.5	10
44	Characterization of microsatellite loci isolated in trumpeter swan (<i>Cygnus buccinator</i>). <i>Molecular Ecology Notes</i> , 2006, 6, 1083-1085.	1.7	9
45	The historical distribution of Gunnison Sage-Grouse in Colorado. <i>Wilson Journal of Ornithology</i> , 2014, 126, 207-217.	0.2	9
46	Blood from a turnip: tissue origin of low-coverage shotgun sequencing libraries affects recovery of mitochondrial DNA. <i>Mitochondrial DNA</i> , 2015, 26, 384-388.	0.6	9
47	Signatures of adaptive divergence among populations of an avian species of conservation concern. <i>Evolutionary Applications</i> , 2019, 12, 1661-1677.	3.1	9
48	Genetic mark-recapture analysis of winter faecal pellets allows estimation of population size in Sage Grouse (<i>Centrocercus urophasianus</i>). <i>Ibis</i> , 2020, 162, 749-765.	1.9	9
49	Population Genetic Analysis of Mountain Plover Using Mitochondrial DNA Sequence Data. <i>Condor</i> , 2005, 107, 353-362.	1.6	8
50	Regional Variation in mtDNA of the Lesser Prairie-Chicken. <i>Condor</i> , 2010, 112, 29-37.	1.6	8
51	Using Fecal DNA and Closed-Capture Models to Estimate Feral Horse Population Size. <i>Journal of Wildlife Management</i> , 2021, 85, 1150-1161.	1.8	8
52	Genetic consequences of trumpeter swan (<i>Cygnus buccinator</i>) reintroductions. <i>Conservation Genetics</i> , 2011, 12, 257-268.	1.5	7
53	Evaluation of a Chicken 600K SNP genotyping array in non-model species of grouse. <i>Scientific Reports</i> , 2019, 9, 6407.	3.3	7
54	Feral Horse Space Use and Genetic Characteristics from Fecal DNA. <i>Journal of Wildlife Management</i> , 2021, 85, 1074-1083.	1.8	7

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55	Functional connectivity in a continuously distributed, migratory species as revealed by landscape genomics. <i>Ecography</i> , 2021, 44, 987.	4.5	7
56	Occurrence of Greater Sage-Grouse – Sharp-Tailed Grouse Hybrids in Alberta. <i>Condor</i> , 2001, 103, 657-660.	1.6	6
57	Differential influences of local subpopulations on regional diversity and differentiation for greater sage-grouse (<i>Centrocercus urophasianus</i>). <i>Molecular Ecology</i> , 2016, 25, 4424-4437.	3.9	6
58	OCCURRENCE OF GREATER SAGE-GROUSE – SHARP-TAILED GROUSE HYBRIDS IN ALBERTA. <i>Condor</i> , 2001, 103, 657.	1.6	5
59	POPULATION STRUCTURE OF MOUNTAIN PLOVER AS DETERMINED USING NUCLEAR MICROSATELLITES. <i>Condor</i> , 2008, 110, 493-499.	1.6	5
60	A population genetic analysis of the midget faded rattlesnake in Wyoming. <i>Conservation Genetics</i> , 2010, 11, 1623-1629.	1.5	5
61	Extensive shared polymorphism at non-MHC immune genes in recently diverged North American prairie grouse. <i>Immunogenetics</i> , 2018, 70, 195-204.	2.4	4
62	Development of microsatellite loci for two New World vultures (Cathartidae). <i>BMC Research Notes</i> , 2019, 12, 257.	1.4	4
63	The Transformative Impact of Genomics on Sage-Grouse Conservation and Management. <i>Population Genomics</i> , 2020, , 523-546.	0.5	4
64	Scale-dependent influence of the sagebrush community on genetic connectivity of the sagebrush obligate Gunnison sage-grouse. <i>Molecular Ecology</i> , 2022, 31, 3267-3285.	3.9	4
65	Characterization of microsatellite loci isolated in Mountain Plover (<i>Charadrius montanus</i>). <i>Molecular Ecology Notes</i> , 2007, 7, 802-804.	1.7	3
66	Characterization of ten microsatellite loci in midget faded rattlesnake (<i>Crotalus oreganus</i>)	0.8	2
67	The genetic structure of a relict population of wood frogs. <i>Conservation Genetics</i> , 2012, 13, 1521-1530.	1.5	2
68	Development and characterization of thirteen microsatellite loci in Clark's nutcracker (<i>Nucifraga</i>)	0.8	2
69	Genetic characterization of the Pacific sheath-tailed bat (<i>Emballonura semicaudata rotensis</i>) using mitochondrial DNA sequence data. <i>Journal of Mammalogy</i> , 2013, 94, 1030-1036.	1.3	2
70	Post-release breeding of translocated sharp-tailed grouse and an absence of artificial insemination effects. <i>Wildlife Research</i> , 2019, 46, 12.	1.4	2
71	Environmental gradients of selection for an alpine-obligate bird, the white-tailed ptarmigan (<i>Lagopus</i>)	2.6	1
72	Population genetics reveals bidirectional fish movement across the Continental Divide via an interbasin water transfer. <i>Conservation Genetics</i> , 0, , .	1.5	0