

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	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
2	Environmental gradients of selection for an alpine-obligate bird, the white-tailed ptarmigan (<i>Lagopus lagopus lagopus</i>). <i>Evolution</i> , 2021, 75, 1070-1080.	2.5	1
3	Feral Horse Space Use and Genetic Characteristics from Fecal DNA. <i>Journal of Wildlife Management</i> , 2021, 85, 1074-1083.	1.8	7
4	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
5	Functional connectivity in a continuously distributed, migratory species as revealed by landscape genomics. <i>Ecography</i> , 2021, 44, 987.	4.5	7
6	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
7	The Transformative Impact of Genomics on Sage-Grouse Conservation and Management. <i>Population Genomics</i> , 2020, , 523-546.	0.5	4
8	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
9	Evaluation of genetic change from translocation among Gunnison Sage-Grouse (<i>Centrocercus urophasianus</i>). <i>Evolution</i> , 2020, 74, 1070-1080.	1.6	11
10	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
11	Signatures of adaptive divergence among populations of an avian species of conservation concern. <i>Evolutionary Applications</i> , 2019, 12, 1661-1677.	3.1	9
12	Evaluation of a Chicken 600K SNP genotyping array in non-model species of grouse. <i>Scientific Reports</i> , 2019, 9, 6407.	3.3	7
13	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
14	Development of microsatellite loci for two New World vultures (Cathartidae). <i>BMC Research Notes</i> , 2019, 12, 257.	1.4	4
15	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
16	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
17	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
18	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

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19	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
20	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
21	Genetic Mark-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
22	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
23	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
24	Polygamy slows down population divergence in shorebirds. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 1313-1326.	2.3	33
25	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
26	Critical considerations for the application of environmental <i>scp</i> <DNA> methods to detect aquatic species. <i>Methods in Ecology and Evolution</i> , 2016, 7, 1299-1307.	5.2	684
27	Latent spatial models and sampling design for landscape genetics. <i>Annals of Applied Statistics</i> , 2016, 10, .	1.1	11
28	A field ornithologist's guide to genomics: Practical considerations for ecology and conservation. <i>Auk</i> , 2016, 133, 626-648.	1.4	19
29	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
30	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
31	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
32	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
33	Environmental DNA (eDNA) Sampling Improves Occurrence and Detection Estimates of Invasive Burmese Pythons. <i>PLoS ONE</i> , 2015, 10, e0121655.	2.5	166
34	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</i>) <i>Tj ETQq0 0 0 rgBT /Overlock 10 1650 137 T</i>		
35	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
36	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

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37	Blood from a turnip: tissue origin of low-coverage shotgun sequencing libraries affects recovery of mitochondrial DNA, 2015, 26, 384-388.	0.6	9
38	Two Low Coverage Bird Genomes and a Comparison of Reference-Guided versus De Novo Genome Assemblies. PLoS ONE, 2014, 9, e106649.	2.5	30
39	The historical distribution of Gunnison Sage-Grouse in Colorado. Wilson Journal of Ornithology, 2014, 126, 207-217.	0.2	9
40	Hierarchical spatial genetic structure in a distinct population segment of greater sage-grouse. Conservation Genetics, 2014, 15, 1299-1311.	1.5	15
41	Development and characterization of thirteen microsatellite loci in Clark's nutcracker (<i>Nucifraga</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 222 Td (0.8	2
42	Genetic characterization of the Pacific sheath-tailed bat (<i>Emballonura semicaudata rotensis</i>) using mitochondrial DNA sequence data. Journal of Mammalogy, 2013, 94, 1030-1036.	1.3	2
43	Sample design effects in landscape genetics. Conservation Genetics, 2013, 14, 275-285.	1.5	79
44	The genetic structure of a relict population of wood frogs. Conservation Genetics, 2012, 13, 1521-1530.	1.5	2
45	Rapid Microsatellite Identification from Illumina Paired-End Genomic Sequencing in Two Birds and a Snake. PLoS ONE, 2012, 7, e30953.	2.5	208
46	Effects of sample size, number of markers, and allelic richness on the detection of spatial genetic pattern. Molecular Ecology Resources, 2012, 12, 276-284.	4.8	143
47	Genetic Applications in Avian Conservation. Auk, 2011, 128, 205-229.	1.4	68
48	Genetic consequences of trumpeter swan (<i>Cygnus buccinator</i>) reintroductions. Conservation Genetics, 2011, 12, 257-268.	1.5	7
49	Characterization of small microsatellite loci isolated in endangered Indiana bat (<i>Myotis sodalis</i>) for use in non-invasive sampling. Conservation Genetics Resources, 2011, 3, 243-245.	0.8	12
50	Characterization of ten microsatellite loci in the Broad-tailed Hummingbird (<i>Selasphorus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222 Td (0.8	10
51	Characterization of small microsatellite loci for use in non invasive sampling studies of Gunnison Sage-grouse (<i>Centrocercus minimus</i>). Conservation Genetics Resources, 2010, 2, 17-20.	0.8	12
52	Characterization of ten microsatellite loci in midget faded rattlesnake (<i>Crotalus oreganus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142 Td	0.8	2
53	A population genetic analysis of the midget faded rattlesnake in Wyoming. Conservation Genetics, 2010, 11, 1623-1629.	1.5	5
54	Regional Variation in mtDNA of the Lesser Prairie-Chicken. Condor, 2010, 112, 29-37.	1.6	8

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55	Chapter 10: Rapid Evolution in Lekking Grouse: Implications for Taxonomic Definitions. Ornithological Monographs, 2010, 67, 114-122.	1.3	22
56	POPULATION STRUCTURE OF MOUNTAIN PLOVER AS DETERMINED USING NUCLEAR MICROSATELLITES. Condor, 2008, 110, 493-499.	1.6	5
57	Characterization of microsatellite loci isolated in Mountain Plover (<i>Charadrius montanus</i>). Molecular Ecology Notes, 2007, 7, 802-804.	1.7	3
58	A rangewide population genetic study of trumpeter swans. Conservation Genetics, 2007, 8, 1339-1353.	1.5	11
59	Characterization of microsatellite loci isolated in trumpeter swan (<i>Cygnus buccinator</i>). Molecular Ecology Notes, 2006, 6, 1083-1085.	1.7	9
60	Characterization of microsatellite loci isolated in midget faded rattlesnake (<i>Crotalus viridis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 542 To	1.7	15
61	A multilocus population genetic survey of the greater sage-grouse across their range. Molecular Ecology, 2005, 14, 1293-1310.	3.9	75
62	POPULATION GENETICS OF GUNNISON SAGE-GROUSE: IMPLICATIONS FOR MANAGEMENT. Journal of Wildlife Management, 2005, 69, 630-637.	1.8	45
63	Population Genetic Analysis of Mountain Plover Using Mitochondrial DNA Sequence Data. Condor, 2005, 107, 353-362.	1.6	8
64	POPULATION GENETIC ANALYSIS OF MOUNTAIN PLOVER USING MITOCHONDRIAL DNA SEQUENCE DATA. Condor, 2005, 107, 353.	1.6	11
65	Title is missing!. Conservation Genetics, 2003, 4, 301-310.	1.5	34
66	Isolation and characterization of microsatellite loci in Greater Sage-Grouse (<i>Centrocercus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 302 Td	1.7	26
67	Occurrence of Greater Sage-Grouse $\tilde{\text{A}}$ — Sharp-Tailed Grouse Hybrids in Alberta. Condor, 2001, 103, 657-660.	1.6	6
68	OCCURRENCE OF GREATER SAGE-GROUSE $\tilde{\text{A}}$ — SHARP-TAILED GROUSE HYBRIDS IN ALBERTA. Condor, 2001, 103, 657.	1.6	5
69	Influence of Changes in Sagebrush on Gunnison Sage Grouse in Southwestern Colorado. Southwestern Naturalist, 2001, 46, 323.	0.1	29
70	A NEW SPECIES OF SAGE-GROUSE (PHASIANIDAE:CENTROCERCUS) FROM SOUTHWESTERN COLORADO. The Wilson Bulletin, 2000, 112, 445-453.	0.5	59
71	A population genetic comparison of large- and small-bodied sage grouse in Colorado using microsatellite and mitochondrial DNA markers. Molecular Ecology, 1999, 8, 1457-1465.	3.9	55
72	Population genetics reveals bidirectional fish movement across the Continental Divide via an interbasin water transfer. Conservation Genetics, 0, , .	1.5	0