

Sean M Hoban

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

3,846
citations

172207

29
h-index

149479

56
g-index

69
all docs

69
docs citations

69
times ranked

5015
citing authors

#	ARTICLE	IF	CITATIONS
1	Crop genetic erosion: understanding and responding to loss of crop diversity. <i>New Phytologist</i> , 2022, 233, 84-118.	3.5	137
2	The Coalition for Conservation Genetics: Working across organizations to build capacity and achieve change in policy and practice. <i>Conservation Science and Practice</i> , 2022, 4, .	0.9	17
3	Global genetic diversity status and trends: towards a suite of Essential Biodiversity Variables (<scp>EBVs</scp>) for genetic composition. <i>Biological Reviews</i> , 2022, 97, 1511-1538.	4.7	73
4	Assessing ex situ genetic and ecogeographic conservation in a threatened but widespread oak after range-wide collecting effort. <i>Evolutionary Applications</i> , 2022, 15, 1002-1017.	1.5	6
5	Bringing together approaches to reporting on within species genetic diversity. <i>Journal of Applied Ecology</i> , 2022, 59, 2227-2233.	1.9	24
6	Reduced representation sequencing to understand the evolutionary history of Torrey pine (<i>Pinus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 4622-4639.	2.0	5
7	Practical application of indicators for genetic diversity in CBD post-2020 global biodiversity framework implementation. <i>Ecological Indicators</i> , 2022, 142, 109167.	2.6	10
8	Effective population size remains a suitable, pragmatic indicator of genetic diversity for all species, including forest trees. <i>Biological Conservation</i> , 2021, 253, 108906.	1.9	32
9	Genetic Diversity Assessment of Ex Situ Collections of Endangered <i>Quercus hinckleyi</i>. <i>International Journal of Plant Sciences</i> , 2021, 182, 220-228.	0.6	4
10	Macrogenetic studies must not ignore limitations of genetic markers and scale. <i>Ecology Letters</i> , 2021, 24, 1282-1284.	3.0	27
11	Authorsâ€™ Reply to Letter to the Editor: Continued improvement to genetic diversity indicator for CBD. <i>Conservation Genetics</i> , 2021, 22, 533-536.	0.8	18
12	Genetic, Morphological, and Environmental Differentiation of an Arid-Adapted Oak with a Disjunct Distribution. <i>Forests</i> , 2021, 12, 465.	0.9	7
13	Comparing Genetic Diversity in Three Threatened Oaks. <i>Forests</i> , 2021, 12, 561.	0.9	10
14	Global Commitments to Conserving and Monitoring Genetic Diversity Are Now Necessary and Feasible. <i>BioScience</i> , 2021, 71, 964-976.	2.2	96
15	Ex Situ Conservation of Large and Small Plant Populations Illustrates Limitations of Common Conservation Metrics. <i>International Journal of Plant Sciences</i> , 2021, 182, 263-276.	0.6	10
16	Charting a course for genetic diversity in the UN Decade of Ocean Science. <i>Evolutionary Applications</i> , 2021, 14, 1497-1518.	1.5	19
17	Opportunities and challenges of macrogenetic studies. <i>Nature Reviews Genetics</i> , 2021, 22, 791-807.	7.7	55
18	Proportional sampling strategy often captures more genetic diversity when population sizes vary. <i>Biological Conservation</i> , 2021, 261, 109261.	1.9	8

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19	Genetic diversity is considered important but interpreted narrowly in country reports to the Convention on Biological Diversity: Current actions and indicators are insufficient. <i>Biological Conservation</i> , 2021, 261, 109233.	1.9	65
20	Save Our Species: A Blueprint for Restoring Butternut (<i>Juglans cinerea</i>) across Eastern North America. <i>Journal of Forestry</i> , 2021, 119, 196-206.	0.5	8
21	IUCN Red List and the value of integrating genetics. <i>Conservation Genetics</i> , 2020, 21, 795-801.	0.8	65
22	Hybrid Breeding for Restoration of Threatened Forest Trees: Evidence for Incorporating Disease Tolerance in <i>Juglans cinerea</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 580693.	1.7	9
23	Taxonomic similarity does not predict necessary sample size for <i>ex situ</i> conservation: a comparison among five genera. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20200102.	1.2	38
24	Can a Botanic Garden Metacollection Better Conserve Wild Plant Diversity? A Case Study Comparing Pooled Collections with an Ideal Sampling Model. <i>International Journal of Plant Sciences</i> , 2020, 181, 485-496.	0.6	26
25	Post-2020 goals overlook genetic diversity. <i>Science</i> , 2020, 367, 1083-1085.	6.0	132
26	Genetic diversity targets and indicators in the CBD post-2020 Global Biodiversity Framework must be improved. <i>Biological Conservation</i> , 2020, 248, 108654.	1.9	285
27	New guidance for <i>ex situ</i> gene conservation: Sampling realistic population systems and accounting for collection attrition. <i>Biological Conservation</i> , 2019, 235, 199-208.	1.9	51
28	Inference of biogeographic history by formally integrating distinct lines of evidence: genetic, environmental niche and fossil. <i>Ecography</i> , 2019, 42, 1991-2011.	2.1	19
29	“Intentional Genetic Manipulation” as a conservation threat. <i>Conservation Genetics Resources</i> , 2019, 11, 237-247.	0.4	16
30	Integrative conservation genetics: Prioritizing populations using climate predictions, adaptive potential and habitat connectivity. <i>Molecular Ecology Resources</i> , 2018, 18, 14-17.	2.2	17
31	Guidelines for planning genomic assessment and monitoring of locally adaptive variation to inform species conservation. <i>Evolutionary Applications</i> , 2018, 11, 1035-1052.	1.5	169
32	Implementing a new approach to effective conservation of genetic diversity, with ash (<i>Fraxinus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22	1.9	37
33	Optimizing Conservation Strategies for a Threatened Tree Species: In Situ Conservation of White Ash (<i>Fraxinus americana</i> L.) Genetic Diversity through Insecticide Treatment. <i>Forests</i> , 2018, 9, 202.	0.9	20
34	Quantitative evaluation of hybridization and the impact on biodiversity conservation. <i>Ecology and Evolution</i> , 2017, 7, 320-330.	0.8	39
35	Rangewide population differentiation and population substructure in <i>Quercus rubra</i> L.. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	12
36	Responsible <i>scp</i> >RAD</scp>: Striving for best practices in population genomic studies of adaptation. <i>Molecular Ecology Resources</i> , 2017, 17, 366-369.	2.2	58

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37	Ice ages leave genetic diversity "hotspots"™ in Europe but not in Eastern North America. <i>Ecology Letters</i> , 2017, 20, 1459-1468.	3.0	43
38	Breaking RAD: an evaluation of the utility of restriction site-associated DNA sequencing for genome scans of adaptation. <i>Molecular Ecology Resources</i> , 2017, 17, 142-152.	2.2	322
39	<scp>skelesim</scp>: an extensible, general framework for population genetic simulation in R. <i>Molecular Ecology Resources</i> , 2017, 17, 101-109.	2.2	9
40	Finding the Genomic Basis of Local Adaptation: Pitfalls, Practical Solutions, and Future Directions. <i>American Naturalist</i> , 2016, 188, 379-397.	1.0	663
41	Accounting for the nested nature of genetic variation across levels of organization improves our understanding of biodiversity and community ecology. <i>Oikos</i> , 2016, 125, 895-904.	1.2	9
42	Ecology, environment and evolutionary history influence genetic structure in five mammal species from the Italian Alps. <i>Biological Journal of the Linnean Society</i> , 2016, 117, 428-446.	0.7	10
43	The importance of effective sampling for exploring the population dynamics of haploid-diploid seaweeds. <i>Journal of Phycology</i> , 2016, 52, 1-9.	1.0	25
44	Ancient, but not recent, population declines have had a genetic impact on alpine yellow-bellied toad populations, suggesting potential for complete recovery. <i>Conservation Genetics</i> , 2016, 17, 727-743.	0.8	6
45	Chloroplast haplotypes suggest preglacial differentiation and separate postglacial migration paths for the threatened North American forest tree <i>Juglans cinerea</i> L.. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	38
46	Loci under selection during multiple range expansions of an invasive plant are mostly population specific, but patterns are associated with climate. <i>Molecular Ecology</i> , 2015, 24, 3360-3371.	2.0	10
47	Developing quantitative seed sampling protocols using simulations: A reply to comments from Guja et al. and Guerrant et al.. <i>Biological Conservation</i> , 2015, 184, 469-470.	1.9	5
48	Ex situ seed collections will benefit from considering spatial sampling design and species™ reproductive biology. <i>Biological Conservation</i> , 2015, 187, 182-191.	1.9	59
49	Comparative evaluation of potential indicators and temporal sampling protocols for monitoring genetic erosion. <i>Evolutionary Applications</i> , 2014, 7, 984-998.	1.5	102
50	An overview of the utility of population simulation software in molecular ecology. <i>Molecular Ecology</i> , 2014, 23, 2383-2401.	2.0	71
51	Optimal sampling of seeds from plant populations for ex-situ conservation of genetic biodiversity, considering realistic population structure. <i>Biological Conservation</i> , 2014, 177, 90-99.	1.9	115
52	Spatial genetic structure in 21 populations of butternut, a temperate forest tree (<i>Juglans cinerea</i> L.), is correlated to spatial arrangement, habitat, and land-use history. <i>Forest Ecology and Management</i> , 2014, 314, 50-58.	1.4	13
53	The number of markers and samples needed for detecting bottlenecks under realistic scenarios, with and without recovery: a simulation-based study. <i>Molecular Ecology</i> , 2013, 22, 3444-3450.	2.0	64
54	Conservation Genetic Resources for Effective Species Survival (ConGRESS): Bridging the divide between conservation research and practice. <i>Journal for Nature Conservation</i> , 2013, 21, 433-437.	0.8	32

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55	Bringing genetic diversity to the forefront of conservation policy and management. <i>Conservation Genetics Resources</i> , 2013, 5, 593-598.	0.4	145
56	Sample Planning Optimization Tool for conservation and population Genetics (<scp>SPOTG</scp>): a software for choosing the appropriate number of markers and samples. <i>Methods in Ecology and Evolution</i> , 2013, 4, 299-303.	2.2	66
57	Challenges in global biodiversity conservation and solutions that cross sociology, politics, economics and ecology. <i>Biology Letters</i> , 2012, 8, 897-899.	1.0	7
58	A rare case of natural regeneration in butternut, a threatened forest tree, is parent and space limited. <i>Conservation Genetics</i> , 2012, 13, 1447-1457.	0.8	13
59	Homonymy, synonymy and hybrid misassignments in butternut (<i>Juglans cinerea</i>) and Japanese walnut (<i>Juglans ailantifolia</i>) nut cultivars. <i>Genetic Resources and Crop Evolution</i> , 2012, 59, 1397-1405.	0.8	8
60	Computer simulations: tools for population and evolutionary genetics. <i>Nature Reviews Genetics</i> , 2012, 13, 110-122.	7.7	221
61	Challenging a "Why Should I Care" Attitude by Incorporating Societal Issues in the Classroom. <i>American Biology Teacher</i> , 2011, 73, 39-41.	0.1	0
62	Range-wide distribution of genetic diversity in the North American tree <i>Juglans cinerea</i> : a product of range shifts, not ecological marginality or recent population decline. <i>Molecular Ecology</i> , 2010, 19, 4876-4891.	2.0	78
63	Geographically extensive hybridization between the forest trees American butternut and Japanese walnut. <i>Biology Letters</i> , 2009, 5, 324-327.	1.0	46
64	Thirteen nuclear microsatellite loci for butternut (<i>Juglans cinerea</i> L.). <i>Molecular Ecology Resources</i> , 2008, 8, 643-646.	2.2	31
65	Range shifts in butternut, a rare, endangered tree, in response to past climate and modern conditions. <i>Journal of Biogeography</i> , 0, , .	1.4	1