

# Joshua Moses Miller

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4320342/publications.pdf>

Version: 2024-02-01

45  
papers

2,195  
citations

304368

22  
h-index

253896

43  
g-index

47  
all docs

47  
docs citations

47  
times ranked

3552  
citing authors

#	ARTICLE	IF	CITATIONS
1	The $K = 2$ conundrum. <i>Molecular Ecology</i> , 2017, 26, 3594-3602.	2.0	454
2	Adaptive introgression as a resource for management and genetic conservation in a changing climate. <i>Conservation Biology</i> , 2016, 30, 33-41.	2.4	257
3	The crucial role of genome-wide genetic variation in conservation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	196
4	Estimating genome-wide heterozygosity: effects of demographic history and marker type. <i>Heredity</i> , 2014, 112, 240-247.	1.2	84
5	A genome-wide set of SNPs detects population substructure and long range linkage disequilibrium in wild sheep. <i>Molecular Ecology Resources</i> , 2011, 11, 314-322.	2.2	80
6	Genomic consequences of genetic rescue in an insular population of bighorn sheep ( <i>Ovis montanus</i> ). <i>Evolution</i> , 2010, 64, 50-54.	2.0	80
7	Giant tortoise genomes provide insights into longevity and age-related disease. <i>Nature Ecology and Evolution</i> , 2019, 3, 87-95.	3.4	79
8	The influence of a priori grouping on inference of genetic clusters: simulation study and literature review of the DAPC method. <i>Heredity</i> , 2020, 125, 269-280.	1.2	77
9	Global genetic diversity status and trends: towards a suite of Essential Biodiversity Variables (EBVs) for genetic composition. <i>Biological Reviews</i> , 2022, 97, 1511-1538.	4.7	73
10	Assessment of identity disequilibrium and its relation to empirical heterozygosity fitness correlations: a meta-analysis. <i>Molecular Ecology</i> , 2014, 23, 1899-1909.	2.0	71
11	Confidently identifying the correct $K$ value using the $\hat{K}$ method: When does $\hat{K} = K$ ? <i>Molecular Ecology</i> , 2020, 29, 862-869.	2.0	67
12	Consistent divergence times and allele sharing measured from cross-species application of SNP chips developed for three domestic species. <i>Molecular Ecology Resources</i> , 2012, 12, 1145-1150.	2.2	56
13	Assessing polar bear ( <i>Ursus maritimus</i> ) population structure in the Hudson Bay region using SNPs. <i>Ecology and Evolution</i> , 2016, 6, 8474-8484.	0.8	56
14	Opportunities and challenges of macrogenetic studies. <i>Nature Reviews Genetics</i> , 2021, 22, 791-807.	7.7	55
15	Historical Introgression from Wild Relatives Enhanced Climatic Adaptation and Resistance to Pneumonia in Sheep. <i>Molecular Biology and Evolution</i> , 2021, 38, 838-855.	3.5	44
16	Genetic linkage map of a wild genome: genomic structure, recombination and sexual dimorphism in bighorn sheep. <i>BMC Genomics</i> , 2010, 11, 524.	1.2	38
17	Long-term isolation of a highly mobile seabird on the Galapagos. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 817-825.	1.2	34
18	Research management partnerships: An opportunity to integrate genetics in conservation actions. <i>Conservation Science and Practice</i> , 2020, 2, e218.	0.9	31

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19	Phylogeographic analysis of nuclear and mtDNA supports subspecies designations in the ostrich ( <i>Struthio camelus</i> ). <i>Conservation Genetics</i> , 2011, 12, 423-431.	0.8	29
20	Population genomics through time provides insights into the consequences of decline and rapid demographic recovery through head-starting in a Galapagos giant tortoise. <i>Evolutionary Applications</i> , 2018, 11, 1811-1821.	1.5	29
21	Theory, practice, and conservation in the age of genomics: The Galapagos giant tortoise as a case study. <i>Evolutionary Applications</i> , 2018, 11, 1084-1093.	1.5	28
22	Identification of Genetically Important Individuals of the Rediscovered Floreana Galapagos Giant Tortoise ( <i>Chelonoidis elephantopus</i> ) Provides Founders for Species Restoration Program. <i>Scientific Reports</i> , 2017, 7, 11471.	1.6	27
23	Macrogenetic studies must not ignore limitations of genetic markers and scale. <i>Ecology Letters</i> , 2021, 24, 1282-1284.	3.0	27
24	Short Reads, Circular Genome: Skimming SOLiD Sequence to Construct the Bighorn Sheep Mitochondrial Genome. <i>Journal of Heredity</i> , 2012, 103, 140-146.	1.0	26
25	Genome-Wide Assessment of Diversity and Divergence Among Extant Galapagos Giant Tortoise Species. <i>Journal of Heredity</i> , 2018, 109, 611-619.	1.0	22
26	Harnessing cross-species alignment to discover SNPs and generate a draft genome sequence of a bighorn sheep ( <i>Ovis canadensis</i> ). <i>BMC Genomics</i> , 2015, 16, 397.	1.2	19
27	Genetically informed captive breeding of hybrids of an extinct species of Galapagos tortoise. <i>Conservation Biology</i> , 2019, 33, 1404-1414.	2.4	18
28	The genetic basis of animal behavioural diversity in natural populations. <i>Molecular Ecology</i> , 2020, 29, 1957-1971.	2.0	18
29	Genomic analysis of morphometric traits in bighorn sheep using the Ovine Infinium SNP BeadChip. <i>PeerJ</i> , 2018, 6, e4364.	0.9	18
30	Population structure and dispersal of wolves in the Canadian Rocky Mountains. <i>Journal of Mammalogy</i> , 2016, 97, 839-851.	0.6	15
31	Colonization history of Galapagos giant tortoises: Insights from mitogenomes support the progression rule. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 1262-1275.	0.6	14
32	Temporal Mitogenomics of the Galapagos Giant Tortoise from Pinzón Reveals Potential Biases in Population Genetic Inference. <i>Journal of Heredity</i> , 2018, 109, 631-640.	1.0	12
33	Cross-Species Application of SNP Chips is Not Suitable for Identifying Runs of Homozygosity. <i>Journal of Heredity</i> , 2016, 107, 193-195.	1.0	11
34	Genetic Pedigree Analysis of the Pilot Breeding Program for the Rediscovered Galapagos Giant Tortoise from Floreana Island. <i>Journal of Heredity</i> , 2018, 109, 620-630.	1.0	11
35	Temporal dynamics of linkage disequilibrium in two populations of bighorn sheep. <i>Ecology and Evolution</i> , 2015, 5, 3401-3412.	0.8	10
36	Interspecies hybridization in the conservation toolbox: response to Kovach et al. (2016). <i>Conservation Biology</i> , 2016, 30, 431-433.	2.4	8

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37	Ancient hybridization patterns between bighorn and thornhorn sheep. <i>Molecular Ecology</i> , 2021, 30, 6273-6288.	2.0	4
38	Genomic Resources Notes accepted 1 April 2013–31 May 2013. <i>Molecular Ecology Resources</i> , 2013, 13, 965-965.	2.2	3
39	Seeking compromise across competing goals in conservation translocations: The case of the “extinct”™ Floreana Island Galapagos giant tortoise. <i>Journal of Applied Ecology</i> , 2020, 57, 136-148.	1.9	3
40	A new lineage of Galapagos giant tortoises identified from museum samples. <i>Heredity</i> , 2022, 128, 261-270.	1.2	3
41	From transects to transcripts: Teasing apart the architecture of reproductive isolation. <i>Molecular Ecology</i> , 2018, 27, 1339-1341.	2.0	2
42	Ewe are what we wear: bigger horns, better ewes and the potential consequence of trophy hunting on female fitness in bighorn sheep. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, 20212534.	1.2	2
43	Linking genetic, morphological, and behavioural divergence between inland island and mainland deer mice. <i>Heredity</i> , 2022, 128, 97-106.	1.2	2
44	Evaluation of novel genomic markers for pedigree construction in an isolated population of Weddell Seals ( <i>Leptonychotes weddellii</i> ) at White Island, Antarctica. <i>Conservation Genetics Resources</i> , 0, , 1.	0.4	0
45	A Phylogeographic Contact Zone for Arctic Grayling in Alberta, Canada. <i>North American Journal of Fisheries Management</i> , 2021, 41, 1619-1630.	0.5	0