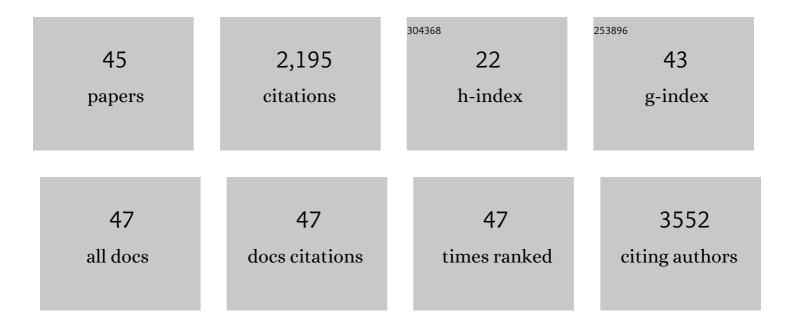
Joshua Moses Miller

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4320342/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	A new lineage of Galapagos giant tortoises identified from museum samples. Heredity, 2022, 128, 261-270.	1.2	3
2	Ewe are what ewe wear: bigger horns, better ewes and the potential consequence of trophy hunting on female fitness in bighorn sheep. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, 20212534.	1.2	2
3	Linking genetic, morphological, and behavioural divergence between inland island and mainland deer mice. Heredity, 2022, 128, 97-106.	1.2	2
4	Global genetic diversity status and trends: towards a suite of Essential Biodiversity Variables (<scp>EBVs</scp>) for genetic composition. Biological Reviews, 2022, 97, 1511-1538.	4.7	73
5	Historical Introgression from Wild Relatives Enhanced Climatic Adaptation and Resistance to Pneumonia in Sheep. Molecular Biology and Evolution, 2021, 38, 838-855.	3.5	44
6	Macrogenetic studies must not ignore limitations of genetic markers and scale. Ecology Letters, 2021, 24, 1282-1284.	3.0	27
7	Opportunities and challenges of macrogenetic studies. Nature Reviews Genetics, 2021, 22, 791-807.	7.7	55
8	A Phylogeographic Contact Zone for Arctic Grayling in Alberta, Canada. North American Journal of Fisheries Management, 2021, 41, 1619-1630.	0.5	0
9	The crucial role of genome-wide genetic variation in conservation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	196
10	Ancient hybridization patterns between bighorn and thinhorn sheep. Molecular Ecology, 2021, 30, 6273-6288.	2.0	4
11	Seeking compromise across competing goals in conservation translocations: The case of the †extinct' Floreana Island Galapagos giant tortoise. Journal of Applied Ecology, 2020, 57, 136-148.	1.9	3
12	The influence of a priori grouping on inference of genetic clusters: simulation study and literature review of the DAPC method. Heredity, 2020, 125, 269-280.	1.2	77
13	Research–management partnerships: An opportunity to integrate genetics in conservation actions. Conservation Science and Practice, 2020, 2, e218.	0.9	31
14	Colonization history of Galapagos giant tortoises: Insights from mitogenomes support the progression rule. Journal of Zoological Systematics and Evolutionary Research, 2020, 58, 1262-1275.	0.6	14
15	The genetic basis of animal behavioural diversity in natural populations. Molecular Ecology, 2020, 29, 1957-1971.	2.0	18
16	Confidently identifying the correct <i>K</i> value using the Δ <i>K</i> method: When does <i>K</i> Â=Â2?. Molecular Ecology, 2020, 29, 862-869.	2.0	67
17	Genetically informed captive breeding of hybrids of an extinct species of Galapagos tortoise. Conservation Biology, 2019, 33, 1404-1414.	2.4	18
18	Giant tortoise genomes provide insights into longevity and age-related disease. Nature Ecology and Evolution, 2019, 3, 87-95.	3.4	79

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#	Article	IF	CITATIONS
19	Genetic Pedigree Analysis of the Pilot Breeding Program for the Rediscovered Galapagos Giant Tortoise from Floreana Island. Journal of Heredity, 2018, 109, 620-630.	1.0	11
20	From transects to transcripts: Teasing apart the architecture of reproductive isolation. Molecular Ecology, 2018, 27, 1339-1341.	2.0	2
21	Temporal Mitogenomics of the Galapagos Giant Tortoise from PinzÃ ³ n Reveals Potential Biases in Population Genetic Inference. Journal of Heredity, 2018, 109, 631-640.	1.0	12
22	Theory, practice, and conservation in the age of genomics: The Galápagos giant tortoise as a case study. Evolutionary Applications, 2018, 11, 1084-1093.	1.5	28
23	Population genomics through time provides insights into the consequences of decline and rapid demographic recovery through headâ€starting in a Galapagos giant tortoise. Evolutionary Applications, 2018, 11, 1811-1821.	1.5	29
24	Genome-Wide Assessment of Diversity and Divergence Among Extant Galapagos Giant Tortoise Species. Journal of Heredity, 2018, 109, 611-619.	1.0	22
25	Genomic analysis of morphometric traits in bighorn sheep using the Ovine Infinium [®] ÂHD SNP BeadChip. PeerJ, 2018, 6, e4364.	0.9	18
26	The <i>K</i> = 2 conundrum. Molecular Ecology, 2017, 26, 3594-3602.	2.0	454
27	Identification of Genetically Important Individuals of the Rediscovered Floreana Galápagos Giant Tortoise (Chelonoidis elephantopus) Provides Founders for Species Restoration Program. Scientific Reports, 2017, 7, 11471.	1.6	27
28	Interspecies hybridization in the conservation toolbox: response to Kovach etÂal. (2016). Conservation Biology, 2016, 30, 431-433.	2.4	8
29	Assessing polar bear (<i>Ursus maritimus</i>) population structure in the Hudson Bay region using <scp>SNP</scp> s. Ecology and Evolution, 2016, 6, 8474-8484.	0.8	56
30	Cross-Species Application of SNP Chips is Not Suitable for Identifying Runs of Homozygosity. Journal of Heredity, 2016, 107, 193-195.	1.0	11
31	Adaptive introgression as a resource for management and genetic conservation in a changing climate. Conservation Biology, 2016, 30, 33-41.	2.4	257
32	Population structure and dispersal of wolves in the Canadian Rocky Mountains. Journal of Mammalogy, 2016, 97, 839-851.	0.6	15
33	Temporal dynamics of linkage disequilibrium in two populations of bighorn sheep. Ecology and Evolution, 2015, 5, 3401-3412.	0.8	10
34	Harnessing cross-species alignment to discover SNPs and generate a draft genome sequence of a bighorn sheep (Ovis canadensis). BMC Genomics, 2015, 16, 397.	1.2	19
35	Assessment of identity disequilibrium and its relation to empirical heterozygosity fitness correlations: a metaâ€analysis. Molecular Ecology, 2014, 23, 1899-1909.	2.0	71
36	Estimating genome-wide heterozygosity: effects of demographic history and marker type. Heredity, 2014, 112, 240-247.	1.2	84

#	Article	IF	CITATIONS
37	Genomic Resources Notes accepted 1 April 2013–31 May 2013. Molecular Ecology Resources, 2013, 13, 965-965.	2.2	3
38	Short Reads, Circular Genome: Skimming SOLiD Sequence to Construct the Bighorn Sheep Mitochondrial Genome. Journal of Heredity, 2012, 103, 140-146.	1.0	26
39	Consistent divergence times and allele sharing measured from crossâ€species application of <scp>SNP</scp> chips developed for three domestic species. Molecular Ecology Resources, 2012, 12, 1145-1150.	2.2	56
40	Genomic consequences of genetic rescue in an insular population of bighorn sheep (<i>Ovis) Tj ETQq0 0 0 rgBT /</i>	Overlock 1 2.0	.0 Tf 50 622
41	A genomeâ€wide set of SNPs detects population substructure and long range linkage disequilibrium in wild sheep. Molecular Ecology Resources, 2011, 11, 314-322.	2.2	80
42	Phylogeographic analysis of nuclear and mtDNA supports subspecies designations in the ostrich (Struthio camelus). Conservation Genetics, 2011, 12, 423-431.	0.8	29

43	Long-term isolation of a highly mobile seabird on the Galapagos. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 817-825.	1.2	34
44	Genetic linkage map of a wild genome: genomic structure, recombination and sexual dimorphism in bighorn sheep. BMC Genomics, 2010, 11, 524.	1.2	38
45	Evaluation of novel genomic markers for pedigree construction in an isolated population of Weddell Seals (Leptonychotes weddellii) at White Island, Antarctica. Conservation Genetics Resources, 0, , 1.	0.4	0