

Kimberly R Andrews

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

2,645
citations

331670

21
h-index

377865

34
g-index

34
all docs

34
docs citations

34
times ranked

4487
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic association with pathogen carriage in bighorn sheep (<i>Ovis canadensis</i>). Ecology and Evolution, 2021, 11, 2488-2502.	1.9	4
2	Genomic signatures of divergent selection are associated with social behaviour for spinner dolphin ecotypes. Molecular Ecology, 2021, 30, 1993-2008.	3.9	6
3	<i>Etelis boweni</i> sp. nov., a new cryptic deepwater eteline snapper from the Indo-Pacific (Perciformes: Lutjanidae). Journal of Fish Biology, 2021, 99, 335-344.	1.6	2
4	A new mouse SNP genotyping assay for speed congenics: combining flexibility, affordability, and power. BMC Genomics, 2021, 22, 378.	2.8	8
5	Integrating genomics in population models to forecast translocation success. Restoration Ecology, 2021, 29, e13395.	2.9	13
6	Geospatial genetics: Integrating genetics into marine protection and spatial planning. Aquatic Conservation: Marine and Freshwater Ecosystems, 2021, 31, 2440-2458.	2.0	5
7	Range-Wide Population Structure of 3 Deepwater Eteline Snappers Across the Indo-Pacific Basin. Journal of Heredity, 2020, 111, 471-485.	2.4	6
8	Building a global genomics observatory: Using GEOME (the Genomic Observatories Metadatabase) to expedite and improve deposition and retrieval of genetic data and metadata for biodiversity research. Molecular Ecology Resources, 2020, 20, 1458-1469.	4.8	32
9	Long-lived marine species may be resilient to environmental variability through a temporal portfolio effect. Ecology and Evolution, 2020, 10, 6435-6448.	1.9	1
10	Wireworm (Coleoptera: Elateridae) genomic analysis reveals putative cryptic species, population structure, and adaptation to pest control. Communications Biology, 2020, 3, 489.	4.4	21
11	Phylogenomics of the genus <i>Tursiops</i> and closely related Delphininae reveals extensive reticulation among lineages and provides inference about eco-evolutionary drivers. Molecular Phylogenetics and Evolution, 2020, 146, 106756.	2.7	40
12	Population Genomics Provides Key Insights in Ecology and Evolution. Population Genomics, 2018, , 483-510.	0.5	28
13	Advances in Using Non-invasive, Archival, and Environmental Samples for Population Genomic Studies. Population Genomics, 2018, , 63-99.	0.5	24
14	A bioinformatic pipeline for identifying informative SNP panels for parentage assignment from RADseq data. Molecular Ecology Resources, 2018, 18, 1263-1281.	4.8	45
15	Unbroken: RADseq remains a powerful tool for understanding the genetics of adaptation in natural populations. Molecular Ecology Resources, 2017, 17, 362-365.	4.8	156
16	Age-specific infectious period shapes dynamics of pneumonia in bighorn sheep. Ecology Letters, 2017, 20, 1325-1336.	6.4	39
17	Genomic Methods Take the Plunge: Recent Advances in High-Throughput Sequencing of Marine Mammals. Journal of Heredity, 2016, 107, 481-495.	2.4	50
18	Comparative phylogeography of the ocean planet. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7962-7969.	7.1	190

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19	Phylogeny of deepwater snappers (Genus <i>Etelis</i>) reveals a cryptic species pair in the Indo-Pacific and Pleistocene invasion of the Atlantic. <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 361-371.	2.7	26
20	Harnessing the power of RADseq for ecological and evolutionary genomics. <i>Nature Reviews Genetics</i> , 2016, 17, 81-92.	16.3	1,169
21	Temporal Stability of Genetic Structure in a Mesopelagic Copepod. <i>PLoS ONE</i> , 2015, 10, e0136087.	2.5	21
22	Phylogeographic Analyses of Submesophotic Snappers <i>Etelis coruscans</i> and <i>Etelis œmarshi</i> (Family) Tj ETQq0 0 0 rgBT /Overlock 10 e91665.	2.5	24
23	Multilocus evidence for globally distributed cryptic species and distinct populations across ocean gyres in a mesopelagic copepod. <i>Molecular Ecology</i> , 2014, 23, 5462-5479.	3.9	46
24	Population Genetics in the Conservation of Cetaceans and Primates. <i>Primate Monographs</i> , 2014, , 289-308.	0.8	6
25	Tradeoffs and utility of alternative RADseq methods: Reply to Puritz <i>et al</i> .. <i>Molecular Ecology</i> , 2014, 23, 5943-5946.	3.9	55
26	Recent novel approaches for population genomics data analysis. <i>Molecular Ecology</i> , 2014, 23, 1661-1667.	3.9	113
27	The evolving male: spinner dolphin (<i>Stenella longirostris</i>) ecotypes are divergent at <i>Y</i> chromosome but not mtDNA or autosomal markers. <i>Molecular Ecology</i> , 2013, 22, 2408-2423.	3.9	27
28	ezRAD: a simplified method for genomic genotyping in non-model organisms. <i>PeerJ</i> , 2013, 1, e203.	2.0	184
29	Microsatellites for Next-Generation Ecologists: A Post-Sequencing Bioinformatics Pipeline. <i>PLoS ONE</i> , 2013, 8, e55990.	2.5	49
30	Widespread Dispersal of the Crown-of-Thorns Sea Star, <i>Acanthaster planci</i> , across the Hawaiian Archipelago and Johnston Atoll. <i>Journal of Marine Biology</i> , 2011, 2011, 1-10.	1.0	23
31	Defining Boundaries for Ecosystem-Based Management: A Multispecies Case Study of Marine Connectivity across the Hawaiian Archipelago. <i>Journal of Marine Biology</i> , 2011, 2011, 1-13.	1.0	116
32	Genetic Analyses and Simulations of Larval Dispersal Reveal Distinct Populations and Directional Connectivity across the Range of the Hawaiian Grouper (<i>Epinephelus quernus</i>). <i>Journal of Marine Biology</i> , 2011, 2011, 1-11.	1.0	23
33	Rolling stones and stable homes: social structure, habitat diversity and population genetics of the Hawaiian spinner dolphin (<i>Stenella longirostris</i>). <i>Molecular Ecology</i> , 2010, 19, 732-748.	3.9	92