

# 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	Harnessing the power of RADseq for ecological and evolutionary genomics. <i>Nature Reviews Genetics</i> , 2016, 17, 81-92.	16.3	1,169
2	Comparative phylogeography of the ocean planet. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 7962-7969.	7.1	190
3	ezRAD: a simplified method for genomic genotyping in non-model organisms. <i>PeerJ</i> , 2013, 1, e203.	2.0	184
4	Unbroken: RADseq remains a powerful tool for understanding the genetics of adaptation in natural populations. <i>Molecular Ecology Resources</i> , 2017, 17, 362-365.	4.8	156
5	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
6	Recent novel approaches for population genomics data analysis. <i>Molecular Ecology</i> , 2014, 23, 1661-1667.	3.9	113
7	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
8	Trade-offs and utility of alternative RADseq methods: Reply to Puritz et al.. <i>Molecular Ecology</i> , 2014, 23, 5943-5946.	3.9	55
9	Genomic Methods Take the Plunge: Recent Advances in High-Throughput Sequencing of Marine Mammals. <i>Journal of Heredity</i> , 2016, 107, 481-495.	2.4	50
10	Microsatellites for Next-Generation Ecologists: A Post-Sequencing Bioinformatics Pipeline. <i>PLoS ONE</i> , 2013, 8, e55990.	2.5	49
11	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
12	A bioinformatic pipeline for identifying informative SNP panels for parentage assignment from RADseq data. <i>Molecular Ecology Resources</i> , 2018, 18, 1263-1281.	4.8	45
13	Phylogenomics of the genus <i>Tursiops</i> and closely related Delphininae reveals extensive reticulation among lineages and provides inference about eco-evolutionary drivers. <i>Molecular Phylogenetics and Evolution</i> , 2020, 146, 106756.	2.7	40
14	Age-specific infectious period shapes dynamics of pneumonia in bighorn sheep. <i>Ecology Letters</i> , 2017, 20, 1325-1336.	6.4	39
15	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. <i>Molecular Ecology Resources</i> , 2020, 20, 1458-1469.	4.8	32
16	Population Genomics Provides Key Insights in Ecology and Evolution. <i>Population Genomics</i> , 2018, , 483-510.	0.5	28
17	The evolving male: spinner dolphin ( <i>Stenella longirostris</i> ) ecotypes are divergent at Y chromosome but not mtDNA or autosomal markers. <i>Molecular Ecology</i> , 2013, 22, 2408-2423.	3.9	27
18	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

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19	Phylogeographic Analyses of Submesophotic Snappers <i>Etelis coruscans</i> and <i>Etelis æmarshi</i> (Family) Tj ETQq1 1 0.784314 rgBT /Ov e91665.	2.5	24
20	Advances in Using Non-invasive, Archival, and Environmental Samples for Population Genomic Studies. <i>Population Genomics</i> , 2018, , 63-99.	0.5	24
21	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
22	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
23	Temporal Stability of Genetic Structure in a Mesopelagic Copepod. <i>PLoS ONE</i> , 2015, 10, e0136087.	2.5	21
24	Wireworm (Coleoptera: Elateridae) genomic analysis reveals putative cryptic species, population structure, and adaptation to pest control. <i>Communications Biology</i> , 2020, 3, 489.	4.4	21
25	Integrating genomics in population models to forecast translocation success. <i>Restoration Ecology</i> , 2021, 29, e13395.	2.9	13
26	A new mouse SNP genotyping assay for speed congenics: combining flexibility, affordability, and power. <i>BMC Genomics</i> , 2021, 22, 378.	2.8	8
27	Population Genetics in the Conservation of Cetaceans and Primates. <i>Primate Monographs</i> , 2014, , 289-308.	0.8	6
28	Range-Wide Population Structure of 3 Deepwater Eteline Snappers Across the Indo-Pacific Basin. <i>Journal of Heredity</i> , 2020, 111, 471-485.	2.4	6
29	Genomic signatures of divergent selection are associated with social behaviour for spinner dolphin ecotypes. <i>Molecular Ecology</i> , 2021, 30, 1993-2008.	3.9	6
30	Geospatial genetics: Integrating genetics into marine protection and spatial planning. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2021, 31, 2440-2458.	2.0	5
31	Genomic association with pathogen carriage in bighorn sheep ( <i>Ovis canadensis</i> ). <i>Ecology and Evolution</i> , 2021, 11, 2488-2502.	1.9	4
32	<i>Etelis boweni</i> sp. nov., a new cryptic deepwater eteline snapper from the Indo-Pacific (Perciformes: Lutjanidae). <i>Journal of Fish Biology</i> , 2021, 99, 335-344.	1.6	2
33	Long-lived marine species may be resilient to environmental variability through a temporal portfolio effect. <i>Ecology and Evolution</i> , 2020, 10, 6435-6448.	1.9	1