

Joanna L Kelley

List of Publications by Year in descending order

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Version: 2024-02-01

79
papers

12,163
citations

159585

30
h-index

66911

78
g-index

94
all docs

94
docs citations

94
times ranked

25041
citing authors

#	ARTICLE	IF	CITATIONS
1	Pathways to polar adaptation in fishes revealed by long-read sequencing. <i>Molecular Ecology</i> , 2023, 32, 1381-1397.	3.9	8
2	Impacts of heavy metal pollution on the ionomes and transcriptomes of Western mosquitofish (<i>Gambusia affinis</i>). <i>Molecular Ecology</i> , 2022, 31, 1527-1542.	3.9	8
3	Editorial 2022. <i>Molecular Ecology Resources</i> , 2022, 22, 1-8.	4.8	1
4	Long-read isoform sequencing reveals tissue-specific isoform expression between active and hibernating brown bears (<i>Ursus arctos</i>). <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	7
5	Recovering the genomes hidden in museum wet collections. <i>Molecular Ecology Resources</i> , 2022, , .	4.8	4
6	microRNA expression variation as a potential molecular mechanism contributing to adaptation to hydrogen sulphide. <i>Journal of Evolutionary Biology</i> , 2021, 34, 977-988.	1.7	19
7	Sharing and reporting benefits from biodiversity research. <i>Molecular Ecology</i> , 2021, 30, 1103-1107.	3.9	19
8	Editorial 2021. <i>Molecular Ecology Resources</i> , 2021, 21, 1-10.	4.8	1
9	The changing face of genome assemblies: Guidance on achieving high-quality reference genomes. <i>Molecular Ecology Resources</i> , 2021, 21, 641-652.	4.8	44
10	Cold Tolerance of Mountain Stoneflies (Plecoptera: Nemouridae) from the High Rocky Mountains. <i>Western North American Naturalist</i> , 2021, 81, .	0.4	6
11	Big Data in Conservation Genomics: Boosting Skills, Hedging Bets, and Staying Current in the Field. <i>Journal of Heredity</i> , 2021, 112, 313-327.	2.4	10
12	Can offsetting the energetic cost of hibernation restore an active season phenotype in grizzly bears (<i>Ursus arctos horribilis</i>)?. <i>Journal of Experimental Biology</i> , 2021, 224, .	1.7	8
13	Long Reads Are Revolutionizing 20 Years of Insect Genome Sequencing. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	75
14	Epigenetic inheritance of DNA methylation changes in fish living in hydrogen sulfide-rich springs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	36
15	Biological albedo reduction on ice sheets, glaciers, and snowfields. <i>Earth-Science Reviews</i> , 2021, 220, 103728.	9.1	30
16	The biogeographic history of eelpouts and related fishes: Linking phylogeny, environmental change, and patterns of dispersal in a globally distributed fish group. <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107211.	2.7	5
17	The Impacts of Dam Construction and Removal on the Genetics of Recovering Steelhead (<i>Oncorhynchus mykiss</i>) Populations across the Elwha River Watershed. <i>Genes</i> , 2021, 12, 89.	2.4	24
18	Toward a genome sequence for every animal: Where are we now?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	87

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19	Editorial 2020. <i>Molecular Ecology Resources</i> , 2020, 20, 1-7.	4.8	9
20	Macroinvertebrates on glaciers: a key resource for terrestrial food webs?. <i>Ecology</i> , 2020, 101, e02947.	3.2	13
21	Aquatic Insects Are Dramatically Underrepresented in Genomic Research. <i>Insects</i> , 2020, 11, 601.	2.2	35
22	Host plants and <i>Wolbachia</i> shape the population genetics of sympatric herbivore populations. <i>Evolutionary Applications</i> , 2020, 13, 2740-2753.	3.1	13
23	Mountain stoneflies may tolerate warming streams: Evidence from organismal physiology and gene expression. <i>Global Change Biology</i> , 2020, 26, 5524-5538.	9.5	16
24	Convergent evolution of conserved mitochondrial pathways underlies repeated adaptation to extreme environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 16424-16430.	7.1	44
25	Effective study design for comparative functional genomics. <i>Nature Reviews Genetics</i> , 2020, 21, 385-386.	16.3	9
26	Disease swamps molecular signatures of genetic-environmental associations to abiotic factors in Tasmanian devil (<i>Sarcophilus harrisii</i>) populations. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 1392-1408.	2.3	18
27	Bacterial Diversity in Replicated Hydrogen Sulfide-Rich Streams. <i>Microbial Ecology</i> , 2019, 77, 559-573.	2.8	12
28	Nuclear and mitochondrial genomic resources for the meltwater stonefly (Plecoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382 Td (Ne 0.9 5	0.9	5
29	Long-distance dispersal, ice sheet dynamics and mountaintop isolation underlie the genetic structure of glacier ice worms. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190983.	2.6	17
30	Expression analyses of cave mollies (<i>Poecilia mexicana</i>) reveal key genes involved in the early evolution of eye regression. <i>Biology Letters</i> , 2019, 15, 20190554.	2.3	14
31	Hibernation induces widespread transcriptional remodeling in metabolic tissues of the grizzly bear. <i>Communications Biology</i> , 2019, 2, 336.	4.4	61
32	Local ancestry analysis reveals genomic convergence in extremophile fishes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180240.	4.0	18
33	The rising tide of high-quality genomic resources. <i>Molecular Ecology Resources</i> , 2019, 19, 567-569.	4.8	11
34	Transcriptomics of Tasmanian Devil (<i>Sarcophilus Harrisii</i>) Ear Tissue Reveals Homogeneous Gene Expression Patterns across a Heterogeneous Landscape. <i>Genes</i> , 2019, 10, 801.	2.4	6
35	Extreme environments and the origins of biodiversity: Adaptation and speciation in sulphide spring fishes. <i>Molecular Ecology</i> , 2018, 27, 843-859.	3.9	56
36	Whole-genome sequencing reveals the extent of heterozygosity in a preferentially self-fertilizing hermaphroditic vertebrate. <i>Genome</i> , 2018, 61, 241-247.	2.0	15

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37	Molecular evolution and expression of oxygen transport genes in livebearing fishes (Poeciliidae) from hydrogen sulfide rich springs. <i>Genome</i> , 2018, 61, 273-286.	2.0	18
38	Concordant changes in gene expression and nucleotides underlie independent adaptation to hydrogen-sulfide-rich environments. <i>Genome Biology and Evolution</i> , 2018, 10, 2867-2881.	2.5	14
39	How to measure natural selection. <i>Methods in Ecology and Evolution</i> , 2017, 8, 660-662.	5.2	2
40	Complexities of gene expression patterns in natural populations of an extremophile fish (<i>Poecilia</i>). <i>Evolution</i> , 2017, 71, 1000-1010.	3.9	21
41	Responsible RAD: Striving for best practices in population genomic studies of adaptation. <i>Molecular Ecology Resources</i> , 2017, 17, 366-369.	4.8	58
42	The roles of plasticity and evolutionary change in shaping gene expression variation in natural populations of extremophile fish. <i>Molecular Ecology</i> , 2017, 26, 6384-6399.	3.9	33
43	Genome-scale data reveal that endemic <i>Poecilia</i> populations from small sulphidic springs display no evidence of inbreeding. <i>Molecular Ecology</i> , 2017, 26, 4920-4934.	3.9	8
44	Sex-specific differences in transcriptome profiles of brain and muscle tissue of the tropical gar. <i>BMC Genomics</i> , 2017, 18, 283.	2.8	13
45	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.	4.8	322
46	Using NextRAD sequencing to infer movement of herbivores among host plants. <i>PLoS ONE</i> , 2017, 12, e0177742.	2.5	20
47	GBStools: A Statistical Method for Estimating Allelic Dropout in Reduced Representation Sequencing Data. <i>PLoS Genetics</i> , 2016, 12, e1005631.	3.5	30
48	The life aquatic: advances in marine vertebrate genomics. <i>Nature Reviews Genetics</i> , 2016, 17, 523-534.	16.3	69
49	Human enamel thickness and ENAM polymorphism. <i>International Journal of Oral Science</i> , 2016, 8, 93-97.	8.6	29
50	Mechanisms Underlying Adaptation to Life in Hydrogen Sulfide-Rich Environments. <i>Molecular Biology and Evolution</i> , 2016, 33, 1419-1434.	8.9	69
51	The Evolutionary Ecology of Animals Inhabiting Hydrogen Sulfide-Rich Environments. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2016, 47, 239-262.	8.3	54
52	The Genome of the Self-Fertilizing Mangrove Rivulus Fish, <i>Kryptolebias marmoratus</i> : A Model for Studying Phenotypic Plasticity and Adaptations to Extreme Environments. <i>Genome Biology and Evolution</i> , 2016, 8, 2145-2154.	2.5	38
53	Finding the Genomic Basis of Local Adaptation: Pitfalls, Practical Solutions, and Future Directions. <i>American Naturalist</i> , 2016, 188, 379-397.	2.1	663
54	Conservation genomics of natural and managed populations: building a conceptual and practical framework. <i>Molecular Ecology</i> , 2016, 25, 2967-2977.	3.9	141

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55	The Time Scale of Recombination Rate Evolution in Great Apes. <i>Molecular Biology and Evolution</i> , 2016, 33, 928-945.	8.9	92
56	Extreme selective sweeps independently targeted the X chromosomes of the great apes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6413-6418.	7.1	75
57	Inference of Gorilla Demographic and Selective History from Whole-Genome Sequence Data. <i>Molecular Biology and Evolution</i> , 2015, 32, 600-612.	8.9	55
58	Illumina TruSeq Synthetic Long-Reads Empower De Novo Assembly and Resolve Complex, Highly-Repetitive Transposable Elements. <i>PLoS ONE</i> , 2014, 9, e106689.	2.5	180
59	H2S exposure elicits differential expression of candidate genes in fish adapted to sulfidic and non-sulfidic environments. <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2014, 175, 7-14.	1.8	33
60	Genomic inference accurately predicts the timing and severity of a recent bottleneck in a nonmodel insect population. <i>Molecular Ecology</i> , 2014, 23, 136-150.	3.9	40
61	Compact genome of the Antarctic midge is likely an adaptation to an extreme environment. <i>Nature Communications</i> , 2014, 5, 4611.	12.8	128
62	Parallel evolution of cox genes in H2S-tolerant fish as key adaptation to a toxic environment. <i>Nature Communications</i> , 2014, 5, 3873.	12.8	75
63	Positive selection of protective variants for type 2 diabetes from the Neolithic onward: a case study in Central Asia. <i>European Journal of Human Genetics</i> , 2013, 21, 1146-1151.	2.8	35
64	Great ape genetic diversity and population history. <i>Nature</i> , 2013, 499, 471-475.	27.8	768
65	Population Genomic Analysis Reveals a Rich Speciation and Demographic History of Orang-utans (<i>Pongo pygmaeus</i> and <i>Pongo abelii</i>). <i>PLoS ONE</i> , 2013, 8, e77175.	2.5	23
66	Gene expression changes governing extreme dehydration tolerance in an Antarctic insect. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 20744-20749.	7.1	118
67	The Possibility of De Novo Assembly of the Genome and Population Genomics of the Mangrove Rivulus, <i>Kryptolebias marmoratus</i> . <i>Integrative and Comparative Biology</i> , 2012, 52, 737-742.	2.0	11
68	Genomic resources for a model in adaptation and speciation research: characterization of the <i>Poecilia mexicana</i> transcriptome. <i>BMC Genomics</i> , 2012, 13, 652.	2.8	25
69	Systematic underestimation of the age of selected alleles. <i>Frontiers in Genetics</i> , 2012, 3, 165.	2.3	8
70	Association of coagulation-related and inflammation-related genes and factor VIIc levels with stroke: the Cardiovascular Health Study. <i>Journal of Thrombosis and Haemostasis</i> , 2011, 9, 267-274.	3.8	29
71	Classic Selective Sweeps Were Rare in Recent Human Evolution. <i>Science</i> , 2011, 331, 920-924.	12.6	432
72	Functional Diversification and Evolution of Antifreeze Proteins in the Antarctic Fish <i>Lycodichthys dearborni</i> . <i>Journal of Molecular Evolution</i> , 2010, 71, 111-118.	1.8	11

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73	A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010, 467, 1061-1073.	27.8	7,209
74	The CFTR Met 470 Allele Is Associated with Lower Birth Rates in Fertile Men from a Population Isolate. <i>PLoS Genetics</i> , 2010, 6, e1000974.	3.5	21
75	Targeted resequencing of two genes, RAGE and POLL, confirms findings from a genome-wide scan for adaptive evolution and provides evidence for positive selection in additional populations. <i>Human Molecular Genetics</i> , 2009, 18, 779-784.	2.9	7
76	Positive Selection in the Human Genome: From Genome Scans to Biological Significance. <i>Annual Review of Genomics and Human Genetics</i> , 2008, 9, 143-160.	6.2	74
77	Dietary Change and Adaptive Evolution of <i>enamelin</i> in Humans and Among Primates. <i>Genetics</i> , 2008, 178, 1595-1603.	2.9	47
78	Genomic signatures of positive selection in humans and the limits of outlier approaches. <i>Genome Research</i> , 2006, 16, 980-989.	5.5	188
79	Adaptive evolution in the SRZ chemoreceptor families of <i>Caenorhabditis elegans</i> and <i>Caenorhabditis briggsae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4476-4481.	7.1	76