

Kathleen E Lotterhos

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

2,905
citations

516710

16
h-index

477307

29
g-index

36
all docs

36
docs citations

36
times ranked

3756
citing authors

#	ARTICLE	IF	CITATIONS
1	Finding the Genomic Basis of Local Adaptation: Pitfalls, Practical Solutions, and Future Directions. <i>American Naturalist</i> , 2016, 188, 379-397.	2.1	663
2	Evaluation of demographic history and neutral parameterization on the performance of <i>ST</i> outlier tests. <i>Molecular Ecology</i> , 2014, 23, 2178-2192.	3.9	472
3	The relative power of genome scans to detect local adaptation depends on sampling design and statistical method. <i>Molecular Ecology</i> , 2015, 24, 1031-1046.	3.9	447
4	Reliable Detection of Loci Responsible for Local Adaptation: Inference of a Null Model through Trimming the Distribution of <i>F_{ST}</i> . <i>American Naturalist</i> , 2015, 186, S24-S36.	2.1	375
5	Convergent local adaptation to climate in distantly related conifers. <i>Science</i> , 2016, 353, 1431-1433.	12.6	303
6	The Importance of Genetic Redundancy in Evolution. <i>Trends in Ecology and Evolution</i> , 2020, 35, 809-822.	8.7	99
7	Responsible <i>RAD</i> : Striving for best practices in population genomic studies of adaptation. <i>Molecular Ecology Resources</i> , 2017, 17, 366-369.	4.8	58
8	The Effect of Neutral Recombination Variation on Genome Scans for Selection. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1851-1867.	1.8	58
9	Composite measures of selection can improve the signal-to-noise ratio in genome scans. <i>Methods in Ecology and Evolution</i> , 2017, 8, 717-727.	5.2	48
10	<i>minotaur</i> : A platform for the analysis and visualization of multivariate results from genome scans with R Shiny. <i>Molecular Ecology Resources</i> , 2017, 17, 33-43.	4.8	45
11	Modularity of genes involved in local adaptation to climate despite physical linkage. <i>Genome Biology</i> , 2018, 19, 157.	8.8	41
12	Inversion invasions: when the genetic basis of local adaptation is concentrated within inversions in the face of gene flow. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, .	4.0	34
13	Seeing the forest for the trees: Assessing genetic offset predictions from gradient forest. <i>Evolutionary Applications</i> , 2022, 15, 403-416.	3.1	32
14	General DNA Methylation Patterns and Environmentally-Induced Differential Methylation in the Eastern Oyster (<i>Crassostrea virginica</i>). <i>Frontiers in Marine Science</i> , 2020, 7, .	2.5	28
15	Ocean Acidification Induces Subtle Shifts in Gene Expression and DNA Methylation in Mantle Tissue of the Eastern Oyster (<i>Crassostrea virginica</i>). <i>Frontiers in Marine Science</i> , 2020, 7, .	2.5	27
16	Fluctuating selection and global change: a synthesis and review on disentangling the roles of climate amplitude, predictability and novelty. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20210727.	2.6	22
17	Comment on "Genomic signals of selection predict climate-driven population declines in a migratory bird". <i>Science</i> , 2018, 361, .	12.6	19
18	Novel and disappearing climates in the global surface ocean from 1800 to 2100. <i>Scientific Reports</i> , 2021, 11, 15535.	3.3	18

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19	Evaluation of rockfish conservation area networks in the United States and Canada relative to the dispersal distance for black rockfish (<i>Sebastes melanostictus</i>). <i>Ecology Letters</i> , 2019, 12, 1073-1083.	10.78	14
20	Breaking RAD: An evaluation of the utility of restriction site associated DNA sequencing for genome scans of adaptation. <i>Molecular Ecology Resources</i> , 2016, 17, 142.	4.8	15
21	Does a complex life cycle affect adaptation to environmental change? Genome-informed insights for characterizing selection across complex life cycle. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20212122.	2.6	14
22	Analysis validation has been neglected in the Age of Reproducibility. <i>PLoS Biology</i> , 2018, 16, e3000070.	5.6	13
23	Invertebrate methylomes provide insight into mechanisms of environmental tolerance and reveal methodological biases. <i>Molecular Ecology Resources</i> , 2022, 22, 1247-1261.	4.8	12
24	Genomic architecture of supergenes: connecting form and function. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, .	4.0	8
25	Ocean acidification alters the diversity and structure of oyster associated microbial communities. <i>Limnology and Oceanography Letters</i> , 2021, 6, 348-359.	3.9	6
26	Nonsignificant isolation by distance implies limited dispersal. <i>Molecular Ecology</i> , 2012, 21, 5637-5639.	3.9	5
27	Evolution in changing seas. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20212443.	2.6	5
28	A novel analytical framework to quantify co- and countergradient variation. <i>Ecology Letters</i> , 2022, 25, 1521-1533.	6.4	4
29	Characterizing the multivariate physiogenomic response to environmental change. <i>Molecular Ecology</i> , 2019, 28, 2711-2714.	3.9	1
30	Parental exposure of Eastern oysters (<i>Crassostrea virginica</i>) to elevated CO ₂ mitigates its negative effects on early larval shell growth and morphology. <i>Limnology and Oceanography</i> , 0, , .	3.1	1