

Paul A Hohenlohe

List of Publications by Year in descending order

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89
papers

18,459
citations

87843

38
h-index

46771

89
g-index

99
all docs

99
docs citations

99
times ranked

17686
citing authors

#	ARTICLE	IF	CITATIONS
1	Stacks: an analysis tool set for population genomics. <i>Molecular Ecology</i> , 2013, 22, 3124-3140.	2.0	3,077
2	Genome-wide genetic marker discovery and genotyping using next-generation sequencing. <i>Nature Reviews Genetics</i> , 2011, 12, 499-510.	7.7	2,198
3	<i>Stacks</i> : Building and Genotyping Loci <i>De Novo</i> From Short-Read Sequences. <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 171-182.	0.8	1,643
4	Population Genomics of Parallel Adaptation in Threespine Stickleback using Sequenced RAD Tags. <i>PLoS Genetics</i> , 2010, 6, e1000862.	1.5	1,219
5	Genomics and the future of conservation genetics. <i>Nature Reviews Genetics</i> , 2010, 11, 697-709.	7.7	1,181
6	Harnessing the power of RADseq for ecological and evolutionary genomics. <i>Nature Reviews Genetics</i> , 2016, 17, 81-92.	7.7	1,169
7	Genomics and the origin of species. <i>Nature Reviews Genetics</i> , 2014, 15, 176-192.	7.7	850
8	Harnessing genomics for delineating conservation units. <i>Trends in Ecology and Evolution</i> , 2012, 27, 489-496.	4.2	767
9	Genotyping-by-sequencing in ecological and conservation genomics. <i>Molecular Ecology</i> , 2013, 22, 2841-2847.	2.0	469
10	ESTIMATING NONLINEAR SELECTION GRADIENTS USING QUADRATIC REGRESSION COEFFICIENTS: DOUBLE OR NOTHING?. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 2435-2440.	1.1	425
11	Resolving postglacial phylogeography using high-throughput sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 16196-16200.	3.3	412
12	UNDERSTANDING THE EVOLUTION AND STABILITY OF THE G-MATRIX. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 2451-2461.	1.1	356
13	Next-generation RAD sequencing identifies thousands of SNPs for assessing hybridization between rainbow and westslope cutthroat trout. <i>Molecular Ecology Resources</i> , 2011, 11, 117-122.	2.2	323
14	SNP Discovery and Genotyping for Evolutionary Genetics Using RAD Sequencing. <i>Methods in Molecular Biology</i> , 2012, 772, 157-178.	0.4	311
15	Genetic diversity targets and indicators in the CBD post-2020 Global Biodiversity Framework must be improved. <i>Biological Conservation</i> , 2020, 248, 108654.	1.9	285
16	Rapid evolution of a native species following invasion by a congener. <i>Science</i> , 2014, 346, 463-466.	6.0	269
17	Population genomics for wildlife conservation and management. <i>Molecular Ecology</i> , 2021, 30, 62-82.	2.0	258
18	Multiple Sex-Associated Regions and a Putative Sex Chromosome in Zebrafish Revealed by RAD Mapping and Population Genomics. <i>PLoS ONE</i> , 2012, 7, e40701.	1.1	211

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19	Extensive linkage disequilibrium and parallel adaptive divergence across threespine stickleback genomes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 395-408.	1.8	190
20	Using Population Genomics to Detect Selection in Natural Populations: Key Concepts and Methodological Considerations. <i>International Journal of Plant Sciences</i> , 2010, 171, 1059-1071.	0.6	165
21	Genomic patterns of introgression in rainbow and westslope cutthroat trout illuminated by overlapping paired-end RAD sequencing. <i>Molecular Ecology</i> , 2013, 22, 3002-3013.	2.0	162
22	Rapid evolutionary response to a transmissible cancer in Tasmanian devils. <i>Nature Communications</i> , 2016, 7, 12684.	5.8	162
23	Unbroken: RADseq remains a powerful tool for understanding the genetics of adaptation in natural populations. <i>Molecular Ecology Resources</i> , 2017, 17, 362-365.	2.2	156
24	Conservation genomics of natural and managed populations: building a conceptual and practical framework. <i>Molecular Ecology</i> , 2016, 25, 2967-2977.	2.0	141
25	Post-2020 goals overlook genetic diversity. <i>Science</i> , 2020, 367, 1083-1085.	6.0	132
26	Adaptive divergence despite strong genetic drift: genomic analysis of the evolutionary mechanisms causing genetic differentiation in the island fox (<i>Urocyon littoralis</i>). <i>Molecular Ecology</i> , 2016, 25, 2176-2194.	2.0	114
27	DRIFT PROMOTES SPECIATION BY SEXUAL SELECTION. <i>Evolution; International Journal of Organic Evolution</i> , 2009, 63, 583-594.	1.1	96
28	Limits to gene flow in marine animals with planktonic larvae: models of <i>Littorina</i> species around Point Conception, California. <i>Biological Journal of the Linnean Society</i> , 2004, 82, 169-187.	0.7	91
29	MIPoD: A Hypothesis-Testing Framework for Microevolutionary Inference from Patterns of Divergence. <i>American Naturalist</i> , 2008, 171, 366-385.	1.0	84
30	Contemporary Demographic Reconstruction Methods Are Robust to Genome Assembly Quality: A Case Study in Tasmanian Devils. <i>Molecular Biology and Evolution</i> , 2019, 36, 2906-2921.	3.5	84
31	Population Genomics: Advancing Understanding of Nature. <i>Population Genomics</i> , 2018, , 3-79.	0.2	70
32	RAD sequencing yields a high success rate for westslope cutthroat and rainbow trout species-specific diagnostic SNP assays. <i>Molecular Ecology Resources</i> , 2012, 12, 653-660.	2.2	64
33	Population Genomic Analysis of Model and Nonmodel Organisms Using Sequenced RAD Tags. <i>Methods in Molecular Biology</i> , 2012, 888, 235-260.	0.4	56
34	Trade-offs and utility of alternative RADseq methods: Reply to Puritz <i>et al.</i> . <i>Molecular Ecology</i> , 2014, 23, 5943-5946.	2.0	55
35	Conservation implications of limited genetic diversity and population structure in Tasmanian devils (<i>Sarcophilus harrisii</i>). <i>Conservation Genetics</i> , 2017, 18, 977-982.	0.8	50
36	Infection of the fittest: devil facial tumour disease has greatest effect on individuals with highest reproductive output. <i>Ecology Letters</i> , 2017, 20, 770-778.	3.0	50

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37	Large-effect loci affect survival in Tasmanian devils (<i>Sarcophilus harrisi</i>) infected with a transmissible cancer. <i>Molecular Ecology</i> , 2018, 27, 4189-4199.	2.0	45
38	A bioinformatic pipeline for identifying informative SNP panels for parentage assignment from RAD-seq data. <i>Molecular Ecology Resources</i> , 2018, 18, 1263-1281.	2.2	45
39	Cryptic Patterns of Speciation in Cryptic Primates: Microendemic Mouse Lemurs and the Multispecies Coalescent. <i>Systematic Biology</i> , 2021, 70, 203-218.	2.7	42
40	Dimensionality of mate choice, sexual isolation, and speciation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 16583-16588.	3.3	41
41	Conserving adaptive potential: lessons from Tasmanian devils and their transmissible cancer. <i>Conservation Genetics</i> , 2019, 20, 81-87.	0.8	41
42	Intercontinental genomic parallelism in multiple three-spined stickleback adaptive radiations. <i>Nature Ecology and Evolution</i> , 2021, 5, 251-261.	3.4	41
43	Vive la résistance: genome-wide selection against introduced alleles in invasive hybrid zones. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161380.	1.2	40
44	Mixed population genomics support for the central marginal hypothesis across the invasive range of the cane toad (<i>Rhinella marina</i>) in Australia. <i>Molecular Ecology</i> , 2016, 25, 4161-4176.	2.0	38
45	Tracing the rise of malignant cell lines: Distribution, epidemiology and evolutionary interactions of two transmissible cancers in Tasmanian devils. <i>Evolutionary Applications</i> , 2019, 12, 1772-1780.	1.5	37
46	Genomics and introgression: Discovery and mapping of thousands of species-diagnostic SNPs using RAD sequencing. <i>Environmental Epigenetics</i> , 2015, 61, 146-154.	0.9	35
47	Individual and temporal variation in pathogen load predicts long-term impacts of an emerging infectious disease. <i>Ecology</i> , 2019, 100, e02613.	1.5	33
48	Population Genomic Analysis of North American Eastern Wolves (<i>Canis lycaon</i>) Supports Their Conservation Priority Status. <i>Genes</i> , 2018, 9, 606.	1.0	32
49	Effective population size remains a suitable, pragmatic indicator of genetic diversity for all species, including forest trees. <i>Biological Conservation</i> , 2021, 253, 108906.	1.9	32
50	Developmental dissociation in morphological evolution of the stickleback opercle. <i>Evolution & Development</i> , 2012, 14, 326-337.	1.1	30
51	The genomic basis of tumor regression in Tasmanian devils (<i>Sarcophilus harrisi</i>). <i>Genome Biology and Evolution</i> , 2018, 10, 3012-3025.	1.1	30
52	The ecology of an adaptive radiation of three-spined stickleback from North Uist, Scotland. <i>Molecular Ecology</i> , 2016, 25, 4319-4336.	2.0	29
53	Population Genomics Provides Key Insights in Ecology and Evolution. <i>Population Genomics</i> , 2018, , 483-510.	0.2	28
54	Rate of intersexual interactions affects injury likelihood in Tasmanian devil contact networks. <i>Behavioral Ecology</i> , 2019, 30, 1087-1095.	1.0	25

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55	A transmissible cancer shifts from emergence to endemism in Tasmanian devils. <i>Science</i> , 2020, 370, .	6.0	24
56	Comment on "Whole-genome sequence analysis shows two endemic species of North American wolf are admixtures of the coyote and gray wolf". <i>Science Advances</i> , 2017, 3, e1602250.	4.7	22
57	Spontaneous Tumor Regression in Tasmanian Devils Associated with <i>RASL11A</i> Activation. <i>Genetics</i> , 2020, 215, 1143-1152.	1.2	22
58	Trait dimensionality explains widespread variation in local adaptation. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20141570.	1.2	21
59	High genomic diversity and candidate genes under selection associated with range expansion in eastern coyote (<i>Canis latrans</i>) populations. <i>Ecology and Evolution</i> , 2018, 8, 12641-12655.	0.8	21
60	Wireworm (Coleoptera: Elateridae) genomic analysis reveals putative cryptic species, population structure, and adaptation to pest control. <i>Communications Biology</i> , 2020, 3, 489.	2.0	21
61	Sharing and reporting benefits from biodiversity research. <i>Molecular Ecology</i> , 2021, 30, 1103-1107.	2.0	19
62	The devil is in the details: Genomics of transmissible cancers in Tasmanian devils. <i>PLoS Pathogens</i> , 2018, 14, e1007098.	2.1	18
63	Authors' Reply to Letter to the Editor: Continued improvement to genetic diversity indicator for CBD. <i>Conservation Genetics</i> , 2021, 22, 533-536.	0.8	18
64	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.	1.1	18
65	Infectious disease and sickness behaviour: tumour progression affects interaction patterns and social network structure in wild Tasmanian devils. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20202454.	1.2	16
66	Life history of <i>Littorina scutulata</i> and <i>L. plena</i> , sibling gastropod species with planktotrophic larvae. <i>Invertebrate Biology</i> , 2002, 121, 25-37.	0.3	15
67	GENETIC REGULATORY NETWORK MOTIFS CONSTRAIN ADAPTATION THROUGH CURVATURE IN THE LANDSCAPE OF MUTATIONAL (CO)VARIANCE. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 950-964.	1.1	14
68	Natural re-colonization and admixture of wolves (<i>Canis lupus</i>) in the US Pacific Northwest: challenges for the protection and management of rare and endangered taxa. <i>Heredity</i> , 2019, 122, 133-149.	1.2	13
69	Darwin, the devil, and the management of transmissible cancers. <i>Conservation Biology</i> , 2021, 35, 748-751.	2.4	13
70	Comparative landscape genetics reveals differential effects of environment on host and pathogen genetic structure in Tasmanian devils (<i>Sarcophilus harrisii</i>) and their transmissible tumour. <i>Molecular Ecology</i> , 2020, 29, 3217-3233.	2.0	9
71	Contemporary and historical selection in Tasmanian devils (<i>Sarcophilus harrisii</i>) support novel, polygenic response to transmissible cancer. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20210577.	1.2	9
72	Full Mitochondrial Genome Sequence of the Sugar Beet Wireworm <i>Limonius californicus</i> (Coleoptera: Elateridae), a Common Agricultural Pest. <i>Genome Announcements</i> , 2016, 4, .	0.8	7

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73	The Population Genomics of Parallel Adaptation: Lessons from Threespine Stickleback. <i>Population Genomics</i> , 2019, , 249-276.	0.2	7
74	Wildlife Population Genomics: Applications and Approaches. <i>Population Genomics</i> , 2020, , 3-59.	0.2	7
75	Development and characterization of fourteen novel microsatellite markers for the chestnut short-tailed fruit bat (<i>Carollia castanea</i>), and cross-amplification to related species. <i>PeerJ</i> , 2016, 4, e2465.	0.9	7
76	Ecological genomics in full colour. <i>Molecular Ecology</i> , 2014, 23, 5129-5131.	2.0	6
77	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.	1.0	6
78	Spatial variation in gene expression of Tasmanian devil facial tumors despite minimal host transcriptomic response to infection. <i>BMC Genomics</i> , 2021, 22, 698.	1.2	6
79	Hybridization and range expansion in tamarisk beetles (<i>Diorhabda</i> spp.) introduced to North America for classical biological control. <i>Evolutionary Applications</i> , 2022, 15, 60-77.	1.5	6
80	The role of neutral and adaptive genomic variation in population diversification and speciation in two ground squirrel species of conservation concern. <i>Molecular Ecology</i> , 2021, 30, 4673-4694.	2.0	5
81	Emergence, transmission and evolution of an uncommon enemy: Tasmanian devil facial tumour disease. , 2019, , 321-341.		4
82	Considering all the evidence: a reply to Sefc and Koblmüller (2016). <i>Biology Letters</i> , 2016, 12, 20151009.	1.0	3
83	Population Genomics Training for the Next Generation of Conservation Geneticists: ConGen 2018 Workshop. <i>Journal of Heredity</i> , 2020, 111, 227-236.	1.0	3
84	Combining Harvest and Genetics to Estimate Reproduction in Wolves. <i>Journal of Wildlife Management</i> , 2020, 84, 492-504.	0.7	2
85	Population Genomics of Wildlife Cancer. <i>Population Genomics</i> , 2020, , 385-416.	0.2	2
86	Estimation of the strength of mate preference from mated pairs observed in the wild. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 29-41.	1.1	2
87	A Publish-Subscribe Model of Genetic Networks. <i>PLoS ONE</i> , 2008, 3, e3245.	1.1	1
88	Long-lived marine species may be resilient to environmental variability through a temporal portfolio effect. <i>Ecology and Evolution</i> , 2020, 10, 6435-6448.	0.8	1
89	Panmixia in spiders (<i>Mecaphesa celer</i> , Thomisidae) despite fragmented habitat at Craters of the Moon in Idaho. <i>Ecological Entomology</i> , 0, , .	1.1	0