

Anna Santure

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

2,469
citations

257450

24
h-index

265206

42
g-index

46
all docs

46
docs citations

46
times ranked

3541
citing authors

#	ARTICLE	IF	CITATIONS
1	Parentage and Sibship Inference From Multilocus Genotype Data Under Polygamy. <i>Genetics</i> , 2009, 181, 1579-1594.	2.9	400
2	Variation in recombination frequency and distribution across eukaryotes: patterns and processes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160455.	4.0	306
3	Transposable elements as agents of rapid adaptation may explain the genetic paradox of invasive species. <i>Molecular Ecology</i> , 2015, 24, 2241-2252.	3.9	178
4	On the use of large marker panels to estimate inbreeding and relatedness: empirical and simulation studies of a pedigreed zebra finch population typed at 771 SNPs. <i>Molecular Ecology</i> , 2010, 19, 1439-1451.	3.9	130
5	Fewer invited talks by women in evolutionary biology symposia. <i>Journal of Evolutionary Biology</i> , 2013, 26, 2063-2069.	1.7	120
6	Genomic dissection of variation in clutch size and egg mass in a wild great tit (<i>Parus major</i>) population. <i>Molecular Ecology</i> , 2013, 22, 3949-3962.	3.9	93
7	Genome mapping in intensively studied wild vertebrate populations. <i>Trends in Genetics</i> , 2010, 26, 275-284.	6.7	85
8	Wild GWAS association mapping in natural populations. <i>Molecular Ecology Resources</i> , 2018, 18, 729-738.	4.8	79
9	Partitioning of genetic variation across the genome using multimer methods in a wild bird population. <i>Molecular Ecology</i> , 2013, 22, 3963-3980.	3.9	78
10	Genetic variance in fitness indicates rapid contemporary adaptive evolution in wild animals. <i>Science</i> , 2022, 376, 1012-1016.	12.6	69
11	Characterisation of the transcriptome of a wild great tit <i>Parus major</i> population by next generation sequencing. <i>BMC Genomics</i> , 2011, 12, 283.	2.8	67
12	High genetic diversity in the remnant island population of hihi and the genetic consequences of re-introduction. <i>Molecular Ecology</i> , 2011, 20, 29-45.	3.9	63
13	Replicated analysis of the genetic architecture of quantitative traits in two wild great tit populations. <i>Molecular Ecology</i> , 2015, 24, 6148-6162.	3.9	61
14	The design and cross-population application of a genome-wide SNP chip for the great tit <i>Parus major</i> . <i>Molecular Ecology Resources</i> , 2012, 12, 753-770.	4.8	56
15	Replicated high-density genetic maps of two great tit populations reveal fine-scale genomic departures from sex-equal recombination rates. <i>Heredity</i> , 2014, 112, 307-316.	2.6	53
16	Little Adaptive Potential in a Threatened Passerine Bird. <i>Current Biology</i> , 2019, 29, 889-894.e3.	3.9	53
17	Reference Genomes from Distantly Related Species Can Be Used for Discovery of Single Nucleotide Polymorphisms to Inform Conservation Management. <i>Genes</i> , 2019, 10, 9.	2.4	50
18	A comparison of pedigree, genetic and genomic estimates of relatedness for informing pairing decisions in two critically endangered birds: Implications for conservation breeding programmes worldwide. <i>Evolutionary Applications</i> , 2020, 13, 991-1008.	3.1	48

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19	FINE-SCALE GENETIC STRUCTURE IN A WILD BIRD POPULATION: THE ROLE OF LIMITED DISPERSAL AND ENVIRONMENTALLY BASED SELECTION AS CAUSAL FACTORS. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 3488-3500.	2.3	44
20	The influence of nonrandom extra-pair paternity on heritability estimates derived from wild pedigrees. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1336-1344.	2.3	42
21	Recombination: the good, the bad and the variable. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20170279.	4.0	39
22	Highly Variable Recombinational Landscape Modulates Efficacy of Natural Selection in Birds. <i>Genome Biology and Evolution</i> , 2014, 6, 2061-2075.	2.5	36
23	A high-density SNP chip for genotyping great tit (<i>Parus major</i>) populations and its application to studying the genetic architecture of exploration behaviour. <i>Molecular Ecology Resources</i> , 2018, 18, 877-891.	4.8	36
24	Influence of Mom and Dad: Quantitative Genetic Models for Maternal Effects and Genomic Imprinting. <i>Genetics</i> , 2006, 173, 2297-2316.	2.9	26
25	Expanding the conservation genomics toolbox: Incorporating structural variants to enhance genomic studies for species of conservation concern. <i>Molecular Ecology</i> , 2021, 30, 5949-5965.	3.9	26
26	Genomic data of different resolutions reveal consistent inbreeding estimates but contrasting homozygosity landscapes for the threatened Aotearoa New Zealand hihi. <i>Molecular Ecology</i> , 2021, 30, 6006-6020.	3.9	25
27	The relevance of pedigrees in the conservation genomics era. <i>Molecular Ecology</i> , 2022, 31, 41-54.	3.9	24
28	Polygenic basis for adaptive morphological variation in a threatened Aotearoa New Zealand bird, the hihi (<i>Notiomystis cincta</i>). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20200948.	2.6	23
29	Population structure in the barn swallow, <i>Hirundo rustica</i> : a comparison between neutral DNA markers and quantitative traits. <i>Biological Journal of the Linnean Society</i> , 0, 99, 306-314.	1.6	19
30	Determinants of male floating behaviour and floater reproduction in a threatened population of the hihi (<i>Notiomystis cincta</i>). <i>Evolutionary Applications</i> , 2015, 8, 796-806.	3.1	19
31	No evidence for MHC class II-based disassortative mating in a wild population of great tits. <i>Journal of Evolutionary Biology</i> , 2015, 28, 642-654.	1.7	19
32	The Joint Effects of Selection and Dominance on the $Q \times ST$ vs $F \times ST$ Contrast. <i>Genetics</i> , 2009, 181, 259-276.	2.9	18
33	Can threatened species adapt in a restored habitat? No expected evolutionary response in lay date for the New Zealand hihi. <i>Evolutionary Applications</i> , 2019, 12, 482-497.	3.1	17
34	Building strong relationships between conservation genetics and primary industry leads to mutually beneficial genomic advances. <i>Molecular Ecology</i> , 2016, 25, 5267-5281.	3.9	16
35	Quantitative Genetics of Genomic Imprinting: A Comparison of Simple Variance Derivations, the Effects of Inbreeding, and Response to Selection. <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 131-142.	1.8	12
36	Social and spatial effects on genetic variation between foraging flocks in a wild bird population. <i>Molecular Ecology</i> , 2017, 26, 5807-5819.	3.9	8

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37	The Evolutionary Biology, Ecology and Epidemiology of Coccidia of Passerine Birds. <i>Advances in Parasitology</i> , 2018, 99, 35-60.	3.2	8
38	Genetic Kinship Analyses Reveal That Grayâ€™s Beaked Whales Strand in Unrelated Groups. <i>Journal of Heredity</i> , 2017, 108, 456-461.	2.4	6
39	Hitchhiking consequences for genetic and morphological patterns: the influence of kelp-rafting on a brooding chiton. <i>Biological Journal of the Linnean Society</i> , 2020, 130, 756-770.	1.6	6
40	Consequences of space sharing on individual phenotypes in the New Zealand hihi. <i>Evolutionary Ecology</i> , 2020, 34, 821-839.	1.2	5
41	Finding the adaptive needles in a populationâ€™structured haystack: A case study in a New Zealand mollusc. <i>Journal of Animal Ecology</i> , 2022, 91, 1209-1221.	2.8	3
42	Genomic Imprinting Leads to Less Selectively Maintained Polymorphism on X Chromosomes. <i>Genetics</i> , 2012, 192, 1455-1464.	2.9	2
43	The design and application of a 50 K SNP chip for a threatened Aotearoa New Zealand passerine, the hihi. <i>Molecular Ecology Resources</i> , 2021, , .	4.8	1
44	An ecological model organism flies into the genomics era. <i>Molecular Ecology Resources</i> , 2016, 16, 379-381.	4.8	0
45	Who are you? A framework to identify and report genetic sample mixâ€™ups. <i>Molecular Ecology Resources</i> , 2021, , .	4.8	0