

# Catherine E Grueber

## List of Publications by Year in descending order

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Version: 2024-02-01

90  
papers

4,418  
citations

201575

27  
h-index

118793

62  
g-index

97  
all docs

97  
docs citations

97  
times ranked

6637  
citing authors

#	ARTICLE	IF	CITATIONS
1	Multimodel inference in ecology and evolution: challenges and solutions. <i>Journal of Evolutionary Biology</i> , 2011, 24, 699-711.	0.8	1,772
2	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
3	Heterogeneity in ecological and evolutionary meta-analyses: its magnitude and implications. <i>Ecology</i> , 2016, 97, 3293-3299.	1.5	180
4	Adaptation and conservation insights from the koala genome. <i>Nature Genetics</i> , 2018, 50, 1102-1111.	9.4	163
5	Global Commitments to Conserving and Monitoring Genetic Diversity Are Now Necessary and Feasible. <i>BioScience</i> , 2021, 71, 964-976.	2.2	96
6	Episodic Positive Selection in the Evolution of Avian Toll-Like Receptor Innate Immunity Genes. <i>PLoS ONE</i> , 2014, 9, e89632.	1.1	86
7	Genetic drift outweighs natural selection at toll-like receptor ( <i>TLR</i> ) immunity loci in a reintroduced population of a threatened species. <i>Molecular Ecology</i> , 2013, 22, 4470-4482.	2.0	76
8	Global genetic diversity status and trends: towards a suite of Essential Biodiversity Variables (EBVs) for genetic composition. <i>Biological Reviews</i> , 2022, 97, 1511-1538.	4.7	73
9	Inbreeding Depression Accumulation across Life-History Stages of the Endangered Takahe. <i>Conservation Biology</i> , 2010, 24, 1617-1625.	2.4	67
10	Heterozygosity-fitness correlations and their relevance to studies on inbreeding depression in threatened species. <i>Molecular Ecology</i> , 2008, 17, 3978-3984.	2.0	64
11	Variation at Innate Immunity Toll-Like Receptor Genes in a Bottlenecked Population of a New Zealand Robin. <i>PLoS ONE</i> , 2012, 7, e45011.	1.1	62
12	SEVERE INBREEDING DEPRESSION AND NO EVIDENCE OF PURGING IN AN EXTREMELY INBRED WILD SPECIES-THE CHATHAM ISLAND BLACK ROBIN. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 987-995.	1.1	59
13	Fecal Viral Diversity of Captive and Wild Tasmanian Devils Characterized Using Virion-Enriched Metagenomics and Metatranscriptomics. <i>Journal of Virology</i> , 2019, 93, .	1.5	56
14	A demonstration of conservation genomics for threatened species management. <i>Molecular Ecology Resources</i> , 2020, 20, 1526-1541.	2.2	54
15	Lack of genetic diversity across diverse immune genes in an endangered mammal, the Tasmanian devil ( <i>Sarcophilus harrisii</i> ). <i>Molecular Ecology</i> , 2015, 24, 3860-3872.	2.0	51
16	The imprecision of heterozygosity-fitness correlations hinders the detection of inbreeding and inbreeding depression in a threatened species. <i>Molecular Ecology</i> , 2011, 20, 67-79.	2.0	48
17	From reference genomes to population genomics: comparing three reference-aligned reduced-representation sequencing pipelines in two wildlife species. <i>BMC Genomics</i> , 2019, 20, 453.	1.2	48
18	Increasing generations in captivity is associated with increased vulnerability of Tasmanian devils to vehicle strike following release to the wild. <i>Scientific Reports</i> , 2017, 7, 2161.	1.6	46

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19	Quantifying and managing the loss of genetic variation in a free-ranging population of takahe through the use of pedigrees. <i>Conservation Genetics</i> , 2008, 9, 645-651.	0.8	43
20	Toll-like receptor diversity in 10 threatened bird species: relationship with microsatellite heterozygosity. <i>Conservation Genetics</i> , 2015, 16, 595-611.	0.8	42
21	Looking like the locals - gut microbiome changes post-release in an endangered species. <i>Animal Microbiome</i> , 2019, 1, 8.	1.5	40
22	Founder relationships and conservation management: empirical kinships reveal the effect on breeding programmes when founders are assumed to be unrelated. <i>Animal Conservation</i> , 2019, 22, 348-361.	1.5	40
23	A meta-analysis of birth-origin effects on reproduction in diverse captive environments. <i>Nature Communications</i> , 2018, 9, 1055.	5.8	36
24	Devil Tools & Tech: A Synergy of Conservation Research and Management Practice. <i>Conservation Letters</i> , 2017, 10, 133-138.	2.8	34
25	No evidence of inbreeding depression in a Tasmanian devil insurance population despite significant variation in inbreeding. <i>Scientific Reports</i> , 2017, 7, 1830.	1.6	33
26	Development of a SNP-based assay for measuring genetic diversity in the Tasmanian devil insurance population. <i>BMC Genomics</i> , 2015, 16, 791.	1.2	32
27	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
28	Simulating Retention of Rare Alleles in Small Populations to Assess Management Options for Species with Different Life Histories. <i>Conservation Biology</i> , 2013, 27, 335-344.	2.4	31
29	Allele Retain: a program to assess management options for conserving allelic diversity in small, isolated populations. <i>Molecular Ecology Resources</i> , 2012, 12, 1161-1167.	2.2	29
30	Macronutritional consequences of food generalism in an invasive mammal, the wild boar. <i>Mammalian Biology</i> , 2016, 81, 523-526.	0.8	28
31	Complex problems need detailed solutions: Harnessing multiple data types to inform genetic management in the wild. <i>Evolutionary Applications</i> , 2019, 12, 280-291.	1.5	28
32	Offspring survival changes over generations of captive breeding. <i>Nature Communications</i> , 2021, 12, 3045.	5.8	28
33	Pedigree reconstruction using molecular data reveals an early warning sign of gene diversity loss in an island population of Tasmanian devils ( <i>Sarcophilus harrisi</i> ). <i>Conservation Genetics</i> , 2018, 19, 439-450.	0.8	27
34	Selection on MHC class II supertypes in the New Zealand endemic Hochstetter's frog. <i>BMC Evolutionary Biology</i> , 2015, 15, 63.	3.2	26
35	Genetic impacts of conservation management actions in a critically endangered parrot species. <i>Conservation Genetics</i> , 2020, 21, 869-877.	0.8	26
36	Low genetic diversity and small population size of Takahe ( <i>Porphyrio hochstetteri</i> ) on European arrival in New Zealand. <i>Ibis</i> , 2011, 153, 384-394.	1.0	25

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37	Unexpected positive and negative effects of continuing inbreeding in one of the world's most inbred wild animals. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 154-166.	1.1	25
38	Pedigree analysis reveals a generational decline in reproductive success of captive Tasmanian devil ( <i>Sarcophilus harrisii</i> ): implications for captive management of threatened species. <i>Journal of Heredity</i> , 2017, 108, 488-495.	1.0	25
39	Too much of a good thing? Finding the most informative genetic data set to answer conservation questions. <i>Molecular Ecology Resources</i> , 2019, 19, 659-671.	2.2	25
40	Mixing genetically differentiated populations successfully boosts diversity of an endangered carnivore. <i>Animal Conservation</i> , 2020, 23, 700-712.	1.5	23
41	Genomic insights into a contagious cancer in Tasmanian devils. <i>Trends in Genetics</i> , 2015, 31, 528-535.	2.9	22
42	Characterization of MHC class II B polymorphism in bottlenecked New Zealand saddlebacks reveals low levels of genetic diversity. <i>Immunogenetics</i> , 2013, 65, 619-633.	1.2	21
43	Comparative genomics for biodiversity conservation. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 370-375.	1.9	21
44	The effects of group versus intensive housing on the retention of genetic diversity in insurance populations. <i>BMC Zoology</i> , 2018, 3, .	0.3	21
45	Impact of reduced-representation sequencing protocols on detecting population structure in a threatened marsupial. <i>Molecular Biology Reports</i> , 2019, 46, 5575-5580.	1.0	19
46	Primers for amplification of innate immunity toll-like receptor loci in threatened birds of the Apterygiformes, Gruiformes, Psittaciformes and Passeriformes. <i>Conservation Genetics Resources</i> , 2013, 5, 1043-1047.	0.4	18
47	High blood lead concentrations in captive Tasmanian devils ( <i>Sarcophilus harrisii</i> ): a threat to the conservation of the species?. <i>Australian Veterinary Journal</i> , 2018, 96, 442-449.	0.5	18
48	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
49	The Coalition for Conservation Genetics: Working across organizations to build capacity and achieve change in policy and practice. <i>Conservation Science and Practice</i> , 2022, 4, .	0.9	17
50	Preserving the demographic and genetic integrity of a single source population during multiple translocations. <i>Biological Conservation</i> , 2020, 241, 108318.	1.9	16
51	Impacts of early viability selection on management of inbreeding and genetic diversity in conservation. <i>Molecular Ecology</i> , 2015, 24, 1645-1653.	2.0	15
52	A Tasmanian devil breeding program to support wild recovery. <i>Reproduction, Fertility and Development</i> , 2019, 31, 1296.	0.1	15
53	Isolation and characterization of microsatellite loci from the endangered New Zealand takahe ( <i>Gruiformes; Rallidae; Porphyrio hochstetteri</i> ). <i>Molecular Ecology Resources</i> , 2008, 8, 884-886.	2.2	14
54	Differential patterns of diversity at microsatellite, MHC, and TLR loci in bottlenecked South Island saddleback populations. , 2017, 41, .		14

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55	Reciprocal translocation of small numbers of inbred individuals rescues immunogenetic diversity. <i>Molecular Ecology</i> , 2017, 26, 2660-2673.	2.0	13
56	Are any populations 'safe'? Unexpected reproductive decline in a population of Tasmanian devils free of devil facial tumour disease. <i>Wildlife Research</i> , 2018, 45, 31.	0.7	13
57	Understanding the evolution of viviparity using intraspecific variation in reproductive mode and transitional forms of pregnancy. <i>Biological Reviews</i> , 2022, 97, 1179-1192.	4.7	13
58	Assessing evolutionary processes over time in a conservation breeding program: a combined approach using molecular data, simulations and pedigree analysis. <i>Biodiversity and Conservation</i> , 2021, 30, 1011-1029.	1.2	12
59	Low innate immune-gene diversity in the critically endangered orange-bellied parrot ( <i>Neophema</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	0.2	11
60	Intergenerational effects of nutrition on immunity: a systematic review and meta-analysis. <i>Biological Reviews</i> , 2018, 93, 1108-1124.	4.7	9
61	Comparison of beak and feather disease virus prevalence and immunity-associated genetic diversity over time in an island population of red-crowned parakeets. <i>Archives of Virology</i> , 2016, 161, 811-820.	0.9	8
62	A case for genetic parentage assignment in captive group housing. <i>Conservation Genetics</i> , 2019, 20, 1187-1193.	0.8	8
63	Reducing the Extinction Risk of Populations Threatened by Infectious Diseases. <i>Diversity</i> , 2021, 13, 63.	0.7	8
64	Parallel Tagged Next-Generation Sequencing on Pooled Samples – A New Approach for Population Genetics in Ecology and Conservation. <i>PLoS ONE</i> , 2013, 8, e61471.	1.1	7
65	Landscape-level field data reveal broad-scale effects of a fatal, transmissible cancer on population ecology of the Tasmanian devil. <i>Mammalian Biology</i> , 2018, 91, 41-45.	0.8	7
66	MHC-associated <i>Baylisascaris schroederi</i> load informs the giant panda reintroduction program. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2020, 12, 113-120.	0.6	7
67	Moving from trends to benchmarks by using regression tree analysis to find inbreeding thresholds in a critically endangered bird. <i>Conservation Biology</i> , 2021, 35, 1278-1287.	2.4	7
68	Improved high-throughput MHC typing for non-model species using long-read sequencing. <i>Molecular Ecology Resources</i> , 2022, 22, 862-876.	2.2	7
69	Disentangling the mechanisms of mate choice in a captive koala population. <i>PeerJ</i> , 2018, 6, e5438.	0.9	6
70	MHC-associated mate choice under competitive conditions in captive versus wild Tasmanian devils. <i>Behavioral Ecology</i> , 2019, 30, 1196-1204.	1.0	5
71	Deciphering genetic mate choice: Not so simple in group-housed conservation breeding programs. <i>Evolutionary Applications</i> , 2020, 13, 2179-2189.	1.5	5
72	Investigating inbreeding in a free-ranging, captive population of an Australian marsupial. <i>Conservation Genetics</i> , 2020, 21, 665-675.	0.8	5

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73	Inbreeding depression in one of the last DFTD-free wild populations of Tasmanian devils. PeerJ, 2020, 8, e9220.	0.9	5
74	Response to Britt et al. 2018 "The importance of non-academic co-authors in bridging the conservation genetics gap" Biological Conservation 218, 118-123. Biological Conservation, 2018, 222, 287-288.	1.9	4
75	Assessment of the dunnocks™ introduction to New Zealand using innate immune-gene diversity. Evolutionary Ecology, 2020, 34, 803-820.	0.5	4
76	Characterization of reproductive gene diversity in the endangered Tasmanian devil. Molecular Ecology Resources, 2021, 21, 721-732.	2.2	4
77	Using genomics to fight extinction. Science, 2022, 376, 574-575.	6.0	4
78	DNA metabarcoding reveals a broad dietary range for Tasmanian devils introduced to a naive ecosystem. Ecology and Evolution, 2022, 12, .	0.8	4
79	Population demography and heterozygosity fitness correlations in natural guppy populations: An examination using sexually selected fitness traits. Molecular Ecology, 2017, 26, 4631-4643.	2.0	3
80	Making the best of a bad situation: genetic rescue in the absence of an ideal source population. Animal Conservation, 2017, 20, 14-15.	1.5	3
81	Exploiting genomic synteny in Felidae: cross-species genome alignments and SNV discovery can aid conservation management. BMC Genomics, 2021, 22, 601.	1.2	3
82	First evidence of deviation from Mendelian proportions in a conservation programme. Molecular Ecology, 2021, 30, 3703-3715.	2.0	2
83	How much is enough? Sampling intensity influences estimates of reproductive variance in an introduced population. Ecological Applications, 2021, , e02462.	1.8	2
84	Evolutionary genetics of translocated island populations of birds: data and opportunities. Emu, 2021, 121, 136-146.	0.2	1
85	Using phylogenetics to explore interspecies genetic rescue options for a critically endangered parrot. Conservation Science and Practice, 2021, 3, e483.	0.9	1
86	Functional Diversity within Gut Microbiomes: Implications for Conserving Biodiversity. Conservation, 2021, 1, 311-326.	0.8	1
87	Urban restoration of common species: population genetics of reintroduced native bush rats <i>Rattus fuscipes</i> in Sydney, Australia. Animal Conservation, 2022, 25, 825-836.	1.5	1
88	Devil women. Pacific Conservation Biology, 2018, 24, 271.	0.5	0
89	Genomics for conservation: a case study of behavioral genes in the Tasmanian devil. Conservation Genetics, 2021, 22, 499-512.	0.8	0
90	Genetic analysis of scat samples to inform conservation of the Tasmanian devil. Australian Zoologist, 2020, 40, 492-504.	0.6	0