

Armando Caballero

List of Publications by Year in descending order

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127
papers

7,441
citations

94381

37
h-index

64755

79
g-index

136
all docs

136
docs citations

136
times ranked

9135
citing authors

#	ARTICLE	IF	CITATIONS
1	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. <i>Nature Genetics</i> , 2018, 50, 381-389.	9.4	1,332
2	Developments in the prediction of effective population size. <i>Heredity</i> , 1994, 73, 657-679.	1.2	528
3	Interrelations between effective population size and other pedigree tools for the management of conserved populations. <i>Genetical Research</i> , 2000, 75, 331-343.	0.3	362
4	Analysis of genetic diversity for the management of conserved subdivided populations. <i>Conservation Genetics</i> , 2002, 3, 289-299.	0.8	299
5	Genomic mutation rates for lifetime reproductive output and lifespan in <i>Caenorhabditis elegans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 3823-3827.	3.3	256
6	Prediction and estimation of effective population size. <i>Heredity</i> , 2016, 117, 193-206.	1.2	254
7	Characterization and conservation of genetic diversity in subdivided populations. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2005, 360, 1367-1378.	1.8	208
8	Developments in predicting the effective size of subdivided populations. <i>Heredity</i> , 1999, 82, 212-226.	1.2	180
9	Comparing three different methods to detect selective loci using dominant markers. <i>Journal of Evolutionary Biology</i> , 2010, 23, 2267-2276.	0.8	177
10	PARALLEL EVOLUTION OF LOCAL ADAPTATION AND REPRODUCTIVE ISOLATION IN THE FACE OF GENE FLOW. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 935-949.	1.1	165
11	Recent Demographic History Inferred by High-Resolution Analysis of Linkage Disequilibrium. <i>Molecular Biology and Evolution</i> , 2020, 37, 3642-3653.	3.5	141
12	Molecular characterization of breeds and its use in conservation. <i>Livestock Science</i> , 2009, 120, 174-195.	0.6	140
13	Impact of Amplified Fragment Length Polymorphism Size Homoplasmy on the Estimation of Population Genetic Diversity and the Detection of Selective Loci. <i>Genetics</i> , 2008, 179, 539-554.	1.2	129
14	ESTIMATING SEXUAL SELECTION AND SEXUAL ISOLATION EFFECTS FROM MATING FREQUENCIES. <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 30-36.	1.1	126
15	Properties of spontaneous mutations affecting quantitative traits. <i>Genetical Research</i> , 1999, 74, 341-350.	0.3	118
16	Management of genetic diversity of subdivided populations in conservation programmes. <i>Conservation Genetics</i> , 2010, 11, 409-419.	0.8	117
17	Management of Subdivided Populations in Conservation Programs: Development of a Novel Dynamic System. <i>Genetics</i> , 2008, 179, 683-692.	1.2	108
18	Nonallopatric and parallel origin of local reproductive barriers between two snail ecotypes. <i>Molecular Ecology</i> , 2004, 13, 3415-3424.	2.0	104

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19	Effective Size and Polymorphism of Linked Neutral Loci in Populations Under Directional Selection. <i>Genetics</i> , 1998, 149, 2105-2117.	1.2	94
20	Systems of mating to reduce inbreeding in selected populations. <i>Animal Science</i> , 1996, 62, 431-442.	1.3	93
21	PHYLOGENETIC EVIDENCE FOR MULTIPLE SYMPATRIC ECOLOGICAL DIVERSIFICATION IN A MARINE SNAIL. <i>Evolution; International Journal of Organic Evolution</i> , 2007, 61, 1600-1612.	1.1	93
22	Allelic Diversity and Its Implications for the Rate of Adaptation. <i>Genetics</i> , 2013, 195, 1373-1384.	1.2	91
23	Variation After a Selective Sweep in a Subdivided Population. <i>Genetics</i> , 2005, 169, 475-483.	1.2	76
24	Inbreeding load and purging: implications for the short-term survival and the conservation management of small populations. <i>Heredity</i> , 2017, 118, 177-185.	1.2	75
25	Bottleneck Effect on Genetic Variance: A Theoretical Investigation of the Role of Dominance. <i>Genetics</i> , 1998, 150, 435-447.	1.2	70
26	Allelic diversity for neutral markers retains a higher adaptive potential for quantitative traits than expected heterozygosity. <i>Molecular Ecology</i> , 2015, 24, 4419-4432.	2.0	59
27	The Nature of Genetic Variation for Complex Traits Revealed by GWAS and Regional Heritability Mapping Analyses. <i>Genetics</i> , 2015, 201, 1601-1613.	1.2	58
28	Managing Individuals' Contributions to Maximize the Allelic Diversity Maintained in Small, Conserved Populations. <i>Conservation Biology</i> , 2004, 18, 1358-1367.	2.4	55
29	A simulation study on the performance of differentiation-based methods to detect selected loci using linked neutral markers. <i>Journal of Evolutionary Biology</i> , 2012, 25, 1364-1376.	0.8	53
30	Selection Response in Finite Populations. <i>Genetics</i> , 1996, 144, 1961-1974.	1.2	53
31	Neutral genetic diversity as a useful tool for conservation biology. <i>Conservation Genetics</i> , 2021, 22, 541-545.	0.8	49
32	ESTIMATING SEXUAL SELECTION AND SEXUAL ISOLATION EFFECTS FROM MATING FREQUENCIES. <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 30.	1.1	48
33	ON THE PERSISTENCE AND PERVASIVENESS OF A NEW MUTATION. <i>Evolution; International Journal of Organic Evolution</i> , 2003, 57, 2644-2646.	1.1	46
34	Comparing the estimation properties of different statistics for measuring sexual isolation from mating frequencies. <i>Biological Journal of the Linnean Society</i> , 2005, 85, 307-318.	0.7	46
35	An evaluation of inbreeding measures using a whole-genome sequenced cattle pedigree. <i>Heredity</i> , 2021, 126, 410-423.	1.2	46
36	Genetic variation for shell traits in a direct-developing marine snail involved in a putative sympatric ecological speciation process. <i>Evolutionary Ecology</i> , 2007, 21, 635-650.	0.5	41

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37	Strategies for increasing fixation probabilities of recessive mutations. <i>Genetical Research</i> , 1991, 58, 129-138.	0.3	40
38	Preserving Population Allele Frequencies in Ex Situ Conservation Programs. <i>Conservation Biology</i> , 2008, 22, 1277-1287.	2.4	40
39	A comparison of management strategies for conservation with regard to population fitness. <i>Conservation Genetics</i> , 2001, 2, 121-131.	0.8	39
40	RELATIVE ROLE OF GENETIC DETERMINATION AND PLASTIC RESPONSE DURING ONTOGENY FOR SHELL-SHAPE TRAITS SUBJECTED TO DIVERSIFYING SELECTION. <i>Evolution; International Journal of Organic Evolution</i> , 2009, 63, 1356-1363.	1.1	39
41	Impact of precocious male parr on the effective size of a wild population of Atlantic salmon. <i>Freshwater Biology</i> , 2008, 53, 2375-2384.	1.2	38
42	A note on using biased parameter values and non-random mating to reduce rates of inbreeding in selection programmes. <i>Animal Science</i> , 1994, 59, 465-468.	1.3	37
43	Response to selection from new mutation and effective size of partially inbred populations. I. Theoretical results. <i>Genetical Research</i> , 1995, 66, 213-225.	0.3	36
44	A new method for the partition of allelic diversity within and between subpopulations. <i>Conservation Genetics</i> , 2010, 11, 2219-2229.	0.8	36
45	METAPOP—A software for the management and analysis of subdivided populations in conservation programs. <i>Conservation Genetics</i> , 2009, 10, 1097-1099.	0.8	35
46	Evaluating the Relationship between Evolutionary Divergence and Phylogenetic Accuracy in AFLP Data Sets. <i>Molecular Biology and Evolution</i> , 2010, 27, 988-1000.	3.5	35
47	<scp>metapop</scp>2: Reimplementation of software for the analysis and management of subdivided populations using gene and allelic diversity. <i>Molecular Ecology Resources</i> , 2019, 19, 1095-1100.	2.2	35
48	On the estimation of inbreeding depression using different measures of inbreeding from molecular markers. <i>Evolutionary Applications</i> , 2021, 14, 416-428.	1.5	35
49	Inferring the Nature of Missing Heritability in Human Traits Using Data from the GWAS Catalog. <i>Genetics</i> , 2019, 212, 891-904.	1.2	34
50	Population genetics: Surviving under mutation pressure. <i>Current Biology</i> , 1998, 8, R235-R237.	1.8	31
51	Estimation of genetic purging under competitive conditions. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1856-1870.	1.1	31
52	The value of genomic relationship matrices to estimate levels of inbreeding. <i>Genetics Selection Evolution</i> , 2021, 53, 42.	1.2	31
53	Accumulation of deleterious mutations and equalization of parental contributions in the conservation of genetic resources. <i>Heredity</i> , 2001, 86, 480-488.	1.2	30
54	Predictions of response to selection caused by angling in a wild population of Atlantic salmon (<i>Salmo salar</i>). <i>Freshwater Biology</i> , 2010, 55, 923-930.	1.2	29

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55	Average Dominance for Polygenes: Drawbacks of Regression Estimates. <i>Genetics</i> , 1997, 147, 1487-1490.	1.2	29
56	Relaxation of Selection With Equalization of Parental Contributions in Conservation Programs: An Experimental Test With <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2006, 172, 1043-1054.	1.2	28
57	Response to selection from new mutation and effective size of partially inbred populations. II. Experiments with <i>Drosophila melanogaster</i> . <i>Genetical Research</i> , 1995, 66, 227-240.	0.3	27
58	Quantitative variation as a tool for detecting human-induced impacts on genetic diversity. <i>Biological Conservation</i> , 2005, 124, 1-13.	1.9	25
59	Genetic impact of the Prestige oil spill in wild populations of a poor dispersal marine snail from intertidal rocky shores. <i>Marine Pollution Bulletin</i> , 2008, 56, 270-281.	2.3	25
60	Accumulation of mutations affecting body weight in inbred mouse lines. <i>Genetical Research</i> , 1995, 65, 145-149.	0.3	24
61	Homoplasmy and Distribution of AFLP Fragments: An Analysis In Silico of the Genome of Different Species. <i>Molecular Biology and Evolution</i> , 2010, 27, 1139-1151.	3.5	24
62	Optimal Management of Genetic Diversity in Subdivided Populations. <i>Frontiers in Genetics</i> , 2019, 10, 843.	1.1	24
63	Estimates of recent and historical effective population size in turbot, seabream, seabass and carp selective breeding programmes. <i>Genetics Selection Evolution</i> , 2021, 53, 85.	1.2	23
64	Inferences on genome-wide deleterious mutation rates in inbred populations of <i>Drosophila</i> and mice. <i>Genetica</i> , 1998, 102/103, 229-239.	0.5	22
65	Mutation-selection balance accounting for genetic variation for viability in <i>Drosophila melanogaster</i> deduced from an inbreeding and artificial selection experiment. <i>Journal of Evolutionary Biology</i> , 2004, 17, 528-541.	0.8	22
66	The evolutionary forces maintaining a wild polymorphism of <i>Littorina saxatilis</i> : model selection by computer simulations. <i>Journal of Evolutionary Biology</i> , 2005, 18, 191-202.	0.8	22
67	On the Consequences of Purging and Linkage on Fitness and Genetic Diversity. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 171-181.	0.8	22
68	The Action of Purifying Selection, Mutation and Drift on Fitness Epistatic Systems. <i>Genetics</i> , 2009, 183, 299-313.	1.2	21
69	The estimates of effective population size based on linkage disequilibrium are virtually unaffected by natural selection. <i>PLoS Genetics</i> , 2022, 18, e1009764.	1.5	21
70	Long-term exhaustion of the inbreeding load in <i>Drosophila melanogaster</i> . <i>Heredity</i> , 2021, 127, 373-383.	1.2	20
71	Genetic discontinuity associated with an environmentally induced barrier to gene exchange in the marine snail <i>Littorina saxatilis</i> . <i>Marine Ecology - Progress Series</i> , 2008, 357, 175-184.	0.9	20
72	Genomic distribution of AFLP markers relative to gene locations for different eukaryotic species. <i>BMC Genomics</i> , 2013, 14, 528.	1.2	19

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73	Reviewing the consequences of genetic purging on the success of rescue programs. <i>Conservation Genetics</i> , 2022, 23, 1-17.	0.8	19
74	Gene-Expression Changes Caused by Inbreeding Protect Against Inbreeding Depression in <i>Drosophila</i> . <i>Genetics</i> , 2012, 192, 161-172.	1.2	18
75	The accuracy of a heritability estimator using molecular information. <i>Conservation Genetics</i> , 2007, 8, 1189-1198.	0.8	17
76	A parallel optimization approach for controlling allele diversity in conservation schemes. <i>Mathematical Biosciences</i> , 2003, 183, 161-173.	0.9	16
77	Habitat-dependent Ecotype Micro-distribution at the Mid-shore in Natural Populations of <i>Littorina saxatilis</i> . <i>Hydrobiologia</i> , 2005, 548, 307-311.	1.0	16
78	Genetic variation in restored Atlantic salmon (<i>Salmo salar</i> L.) populations in the Ulla and LÃ©rez rivers, Galicia, Spain. <i>ICES Journal of Marine Science</i> , 2006, 63, 1290-1296.	1.2	16
79	The mutational rate of <i>Drosophila</i> viability decline: tinkering with old data. <i>Genetical Research</i> , 2002, 80, 99-105.	0.3	15
80	Analysis of the Estimators of the Average Coefficient of Dominance of Deleterious Mutations. <i>Genetics</i> , 2004, 168, 1053-1069.	1.2	14
81	Prediction of the minimum effective size of a population viable in the long term. <i>Biodiversity and Conservation</i> , 2022, 31, 2763-2780.	1.2	14
82	Effect of linkage on the control of inbreeding in selection programmes. <i>Genetics Selection Evolution</i> , 2000, 32, 249-64.	1.2	13
83	Joint Prediction of the Effective Population Size and the Rate of Fixation of Deleterious Mutations. <i>Genetics</i> , 2016, 204, 1267-1279.	1.2	13
84	Accelerated inbreeding depression suggests synergistic epistasis for deleterious mutations in <i>Drosophila melanogaster</i> . <i>Heredity</i> , 2019, 123, 709-722.	1.2	13
85	Mate Choice Contributes to the Maintenance of Shell Color Polymorphism in a Marine Snail via Frequency-Dependent Sexual Selection. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	13
86	Population genomics of parallel evolution in gene expression and gene sequence during ecological adaptation. <i>Scientific Reports</i> , 2018, 8, 16147.	1.6	12
87	Survival rates of mutant genes under artificial selection using individual and family information. <i>Journal of Genetics</i> , 1996, 75, 63-80.	0.4	11
88	The Effect of Antagonistic Pleiotropy on the Estimation of the Average Coefficient of Dominance of Deleterious Mutations. <i>Genetics</i> , 2005, 171, 2097-2112.	1.2	11
89	Palliating the impact of fixation of a major gene on the genetic variation of artificially selected polygenes. <i>Genetical Research</i> , 2006, 88, 105-118.	0.3	11
90	THE ACTION OF STABILIZING SELECTION, MUTATION, AND DRIFT ON EPISTATIC QUANTITATIVE TRAITS. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 1974-1987.	1.1	11

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91	Can parallel ecological speciation be detected with phylogenetic analyses?. <i>Molecular Phylogenetics and Evolution</i> , 2017, 116, 149-156.	1.2	11
92	Untangling the contribution of genetic and environmental effects to shell differentiation across an environmental cline in a marine snail. <i>Journal of Experimental Marine Biology and Ecology</i> , 2019, 513, 27-34.	0.7	11
93	Genetic Differentiation and Estimation of Effective Population Size and Migration Rates in Two Sympatric Ecotypes of the Marine Snail <i>Littorina saxatilis</i> . <i>Journal of Heredity</i> , 2005, 96, 460-464.	1.0	10
94	Genetic diversity and effective size of the Atlantic salmon <i>Salmo salar</i> L. inhabiting the River Eo (Spain) following a stock collapse. <i>Journal of Fish Biology</i> , 2008, 72, 1933-1944.	0.7	10
95	The relationship between hatching rate and number of embryos of the brood pouch in <i>Littorina saxatilis</i> . <i>Journal of Sea Research</i> , 2008, 60, 223-225.	0.6	10
96	The relative contribution of band number to phylogenetic accuracy in AFLP data sets. <i>Journal of Evolutionary Biology</i> , 2011, 24, 2346-2356.	0.8	9
97	Dietary effects on shell growth and shape in an intertidal marine snail, <i>Littorina saxatilis</i> . <i>Journal of Molluscan Studies</i> , 2012, 78, 213-216.	0.4	9
98	Are transcriptional responses to inbreeding a functional response to alleviate inbreeding depression?. <i>Fly</i> , 2013, 7, 8-12.	0.9	9
99	A Note on the Inbreeding Effective Population Size. <i>Evolution; International Journal of Organic Evolution</i> , 1992, 46, 1969.	1.1	8
100	An experimental evaluation with <i>Drosophila melanogaster</i> of a novel dynamic system for the management of subdivided populations in conservation programs. <i>Heredity</i> , 2011, 106, 765-774.	1.2	8
101	Lack of early laboratory postzygotic reproductive isolation between two ecotypes of <i>Littorina saxatilis</i> (Mollusca, Gastropoda) showing strong premating sexual isolation. <i>Hydrobiologia</i> , 2011, 675, 13-18.	1.0	8
102	The time of detection of recessive visible genes with non-random mating. <i>Genetical Research</i> , 1992, 60, 201-207.	0.3	7
103	A NOTE ON THE INBREEDING EFFECTIVE POPULATION SIZE. <i>Evolution; International Journal of Organic Evolution</i> , 1992, 46, 1969-1972.	1.1	7
104	Application of Reproduction Technologies to the Conservation of Genetic Resources. <i>Conservation Biology</i> , 2000, 14, 1831-1836.	2.4	7
105	ON THE PERSISTENCE AND PERVASIVENESS OF A NEW MUTATION. <i>Evolution; International Journal of Organic Evolution</i> , 2003, 57, 2644.	1.1	7
106	Efficiency in prediction of response in selection index experiments. <i>Journal of Animal Breeding and Genetics</i> , 1989, 106, 187-194.	0.8	6
107	The value of targeting recombination as a strategy against coronavirus diseases. <i>Heredity</i> , 2020, 125, 169-172.	1.2	6
108	An experimental evaluation of the usefulness of secondary traits in index selection, using <i>Drosophila melanogaster</i> . <i>Journal of Animal Breeding and Genetics</i> , 1987, 104, 175-179.	0.8	5

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109	An experimental assessment of artificial within-family selection for fitness in conservation programs. <i>Conservation Genetics</i> , 2013, 14, 1149-1159.	0.8	5
110	Efficiency of Conservation Management Methods for Subdivided Populations under Local Adaptation. <i>Journal of Heredity</i> , 2013, 104, 554-564.	1.0	5
111	Candidate Transcriptomic Sources of Inbreeding Depression in <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2013, 8, e70067.	1.1	5
112	Analysis and Management of Gene and Allelic Diversity in Subdivided Populations Using the Software Program METAPOP. <i>Methods in Molecular Biology</i> , 2012, 888, 261-275.	0.4	4
113	Application of Reproduction Technologies to the Conservation of Genetic Resources. <i>Conservation Biology</i> , 2000, 14, 1831-1836.	2.4	4
114	The cumulative effect of artificial selection on the reduction of population effective size. <i>Journal of Animal Breeding and Genetics</i> , 1990, 107, 180-187.	0.8	3
115	AFLPM ax : a user-friendly application for computing the optimal number of amplified fragment length polymorphism markers needed in phylogenetic reconstruction. <i>Molecular Ecology Resources</i> , 2012, 12, 566-569.	2.2	3
116	Impact of deep coalescence and recombination on the estimation of phylogenetic relationships among species using AFLP markers. <i>Molecular Phylogenetics and Evolution</i> , 2014, 76, 102-109.	1.2	3
117	The risk of forcing inbreeding in conservation programmes: a reply to Theodorou and Couvet. <i>Heredity</i> , 2017, 119, 51-53.	1.2	3
118	Highly pleiotropic variants of human traits are enriched in genomic regions with strong background selection. <i>Human Genetics</i> , 2021, 140, 1343-1351.	1.8	3
119	A Note on the Change in Gene Frequency of a Selected Allele in Partial Full-Sib Mating Populations. <i>Genetics</i> , 1996, 142, 649-650.	1.2	3
120	Prediction of fitness under different breeding designs in conservation programs. <i>Animal Conservation</i> , 2023, 26, 86-102.	1.5	3
121	Estimation of the upper limit of the mutation rate and mean heterozygous effect of deleterious mutations. <i>Genetical Research</i> , 2006, 88, 137.	0.3	2
122	GWESHS: A Genome-Wide Effect Sizes and Heritability Screener. <i>Genes</i> , 2019, 10, 558.	1.0	2
123	Looking for a successful translocation: the case of <i>Astragalus edulis</i> . <i>Mediterranean Botany</i> , 0, 42, e68048.	0.9	2
124	Analysis of the biases in the estimation of deleterious mutation parameters from natural populations at mutation-selection balance. <i>Genetical Research</i> , 2006, 88, 177.	0.3	1
125	Inferences on genome-wide deleterious mutation rates in inbred populations of <i>Drosophila</i> and mice. <i>Contemporary Issues in Genetics and Evolution</i> , 1998, , 229-239.	0.9	1
126	A First Insight into the In Silico Evaluation of the Accuracy of AFLP Markers for Phylogenetic Reconstruction. <i>Lecture Notes in Computer Science</i> , 2009, , 1143-1146.	1.0	0

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127	Obituary in memoriam of Professor William G. (Bill) Hill. <i>Heredity</i> , 2022, 128, 77-78.	1.2	0