

# Andrés Párez-Figueroa

## List of Publications by Year in descending order

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Version: 2024-02-01

32  
papers

1,077  
citations

471509

17  
h-index

414414

32  
g-index

32  
all docs

32  
docs citations

32  
times ranked

1693  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparing three different methods to detect selective loci using dominant markers. <i>Journal of Evolutionary Biology</i> , 2010, 23, 2267-2276.	1.7	177
2	<i>msap</i> : a tool for the statistical analysis of methylation-sensitive amplified polymorphism data. <i>Molecular Ecology Resources</i> , 2013, 13, 522-527.	4.8	130
3	Early detection of population declines: high power of genetic monitoring using effective population size estimators. <i>Evolutionary Applications</i> , 2011, 4, 144-154.	3.1	90
4	Environmental induced methylation changes associated with seawater adaptation in brown trout. <i>Aquaculture</i> , 2013, 392-395, 77-83.	3.5	78
5	Methylation changes associated with early maturation stages in the Atlantic salmon. <i>BMC Genetics</i> , 2011, 12, 86.	2.7	71
6	Allelic diversity for neutral markers retains a higher adaptive potential for quantitative traits than expected heterozygosity. <i>Molecular Ecology</i> , 2015, 24, 4419-4432.	3.9	59
7	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.	1.7	53
8	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.	1.6	46
9	Preserving Population Allele Frequencies in Ex Situ Conservation Programs. <i>Conservation Biology</i> , 2008, 22, 1277-1287.	4.7	40
10	METAPOP: A software for the management and analysis of subdivided populations in conservation programs. <i>Conservation Genetics</i> , 2009, 10, 1097-1099.	1.5	35
11	<i>metapop</i> 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.	4.8	35
12	Optimal Management of Genetic Diversity in Subdivided Populations. <i>Frontiers in Genetics</i> , 2019, 10, 843.	2.3	24
13	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.	1.7	22
14	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.	1.7	22
15	On the Consequences of Purging and Linkage on Fitness and Genetic Diversity. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 171-181.	1.8	22
16	The Action of Purifying Selection, Mutation and Drift on Fitness Epistatic Systems. <i>Genetics</i> , 2009, 183, 299-313.	2.9	21
17	LACK OF NONADDITIVE GENETIC EFFECTS ON EARLY FECUNDITY IN <i>DROSOPHILA MELANOGASTER</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2003, 57, 558-565.	2.3	20
18	Genome-wide methylation study of diploid and triploid brown trout ( <i>Salmo trutta</i> L.). <i>Animal Genetics</i> , 2015, 46, 280-288.	1.7	17

#	ARTICLE	IF	CITATIONS
19	Conflict in outcomes for conservation based on population genetic diversity and genetic divergence approaches: a case study in the Japanese relictual conifer <i>Sciadopitys verticillata</i> (Sciadopityaceae). <i>Conservation Genetics</i> , 2014, 15, 1243-1257.	1.5	14
20	Gene Expression Analyses in Non Muscle Invasive Bladder Cancer Reveals a Role for Alternative Splicing and Tp53 Status. <i>Scientific Reports</i> , 2019, 9, 10362.	3.3	14
21	RNA-seq coupled to proteomic analysis reveals high sperm proteome variation between two closely related marine mussel species. <i>Journal of Proteomics</i> , 2019, 192, 169-187.	2.4	14
22	Population genomics of parallel evolution in gene expression and gene sequence during ecological adaptation. <i>Scientific Reports</i> , 2018, 8, 16147.	3.3	12
23	THE ACTION OF STABILIZING SELECTION, MUTATION, AND DRIFT ON EPISTATIC QUANTITATIVE TRAITS. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 1974-1987.	2.3	11
24	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.	2.4	10
25	Morphological and epigenetic variation in mussels from contrasting environments. <i>Marine Biology</i> , 2018, 165, 1.	1.5	9
26	RNA-seq data from mature male gonads of marine mussels <i>Mytilus edulis</i> and <i>M. galloprovincialis</i> . <i>Data in Brief</i> , 2018, 21, 167-175.	1.0	7
27	Temperature-independent genome-wide DNA methylation profile in turbot post-embryonic development. <i>Journal of Thermal Biology</i> , 2020, 88, 102483.	2.5	7
28	Population structure and effective/census population size ratio in threatened three-spined stickleback populations from an isolated river basin in northwest Spain. <i>Genetica</i> , 2015, 143, 403-411.	1.1	6
29	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.	0.9	4
30	Conserving genomic variability in large mammals: Effect of population fluctuations and variance in male reproductive success on variability in Yellowstone bison. <i>Biological Conservation</i> , 2012, 150, 159-166.	4.1	4
31	LACK OF NONADDITIVE GENETIC EFFECTS ON EARLY FECUNDITY IN <i>DROSOPHILA MELANOGASTER</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2003, 57, 558.	2.3	2
32	Single-cell mtDNA heteroplasmy in colorectal cancer. <i>Genomics</i> , 2022, 114, 110315.	2.9	1