

# Tiago R Antao

## List of Publications by Year in descending order

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Version: 2024-02-01

33  
papers

7,277  
citations

346980

22  
h-index

466096

32  
g-index

33  
all docs

33  
docs citations

33  
times ranked

15149  
citing authors

#	ARTICLE	IF	CITATIONS
1	Detecting population declines via monitoring the effective number of breeders ( <i>N<sub>b</sub></i> ). <i>Molecular Ecology Resources</i> , 2021, 21, 379-393.	2.2	24
2	<i>AgeStrucNb</i> : Software for Simulating and Detecting Changes in the Effective Number of Breeders ( <i>N<sub>b</sub></i> ). <i>Journal of Heredity</i> , 2020, 111, 491-497.	1.0	3
3	Massive introgression drives species radiation at the range limit of <i>Anopheles gambiae</i> . <i>Scientific Reports</i> , 2017, 7, 46451.	1.6	28
4	Evidence of Early-Stage Selection on EPAS1 and GPR126 Genes in Andean High Altitude Populations. <i>Scientific Reports</i> , 2017, 7, 13042.	1.6	29
5	Genomic analyses inform on migration events during the peopling of Eurasia. <i>Nature</i> , 2016, 538, 238-242.	13.7	360
6	Selective sweep on human amylase genes postdates the split with Neanderthals. <i>Scientific Reports</i> , 2016, 6, 37198.	1.6	67
7	Multi-layered population structure in Island Southeast Asians. <i>European Journal of Human Genetics</i> , 2016, 24, 1605-1611.	1.4	50
8	Genetic and phenotypic differentiation of an Andean intermediate altitude population. <i>Physiological Reports</i> , 2015, 3, e12376.	0.7	18
9	<i>Plasmodium vivax</i> Diversity and Population Structure across Four Continents. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003872.	1.3	59
10	Positive selection of AS3MT to arsenic water in Andean populations. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2015, 780, 97-102.	0.4	32
11	Genome-Wide Analysis of Cold Adaptation in Indigenous Siberian Populations. <i>PLoS ONE</i> , 2014, 9, e98076.	1.1	128
12	Effects of Overlapping Generations on Linkage Disequilibrium Estimates of Effective Population Size. <i>Genetics</i> , 2014, 197, 769-780.	1.2	299
13	Adaptive introgression between <i>Anopheles</i> sibling species eliminates a major genomic island but not reproductive isolation. <i>Nature Communications</i> , 2014, 5, 4248.	5.8	143
14	INTERMITTENT BREEDING AND CONSTRAINTS ON LITTER SIZE: CONSEQUENCES FOR EFFECTIVE POPULATION SIZE PER GENERATION ( <i>N<sub>e</sub></i> ) AND PER REPRODUCTIVE CYCLE ( <i>N<sub>b</sub></i> ). <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 1722-1734.	1.1	48
15	Genome-wide evidence of Austronesian-Bantu admixture and cultural reversion in a hunter-gatherer group of Madagascar. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 936-941.	3.3	75
16	A Selective Sweep on a Deleterious Mutation in CPT1A in Arctic Populations. <i>American Journal of Human Genetics</i> , 2014, 95, 584-589.	2.6	119
17	The Andean Adaptive Toolkit to Counteract High Altitude Maladaptation: Genome-Wide and Phenotypic Analysis of the Collas. <i>PLoS ONE</i> , 2014, 9, e93314.	1.1	55
18	Evolution of the Pygmy Phenotype: Evidence of Positive Selection from Genome-wide Scans in African, Asian, and Melanesian Pygmies. <i>Human Biology</i> , 2013, 85, 251-284.	0.4	66

#	ARTICLE	IF	CITATIONS
19	Genetic Signatures Reveal High-Altitude Adaptation in a Set of Ethiopian Populations. <i>Molecular Biology and Evolution</i> , 2013, 30, 1877-1888.	3.5	173
20	A Large <i>Plasmodium vivax</i> Reservoir and Little Population Structure in the South Pacific. <i>PLoS ONE</i> , 2013, 8, e66041.	1.1	48
21	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.	1.9	4
22	Policy options for deploying anti-malarial drugs in endemic countries: a population genetics approach. <i>Malaria Journal</i> , 2012, 11, 422.	0.8	13
23	Early detection of population declines: high power of genetic monitoring using effective population size estimators. <i>Evolutionary Applications</i> , 2011, 4, 144-154.	1.5	90
24	Evolutionary parasitology applied to control and elimination policies. <i>Trends in Parasitology</i> , 2011, 27, 233-234.	1.5	8
25	ogaraK: a population genetics simulator for malaria. <i>Bioinformatics</i> , 2011, 27, 1335-1336.	1.8	4
26	Environmental, pharmacological and genetic influences on the spread of drug-resistant malaria. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 1705-1712.	1.2	28
27	Mcheza: a workbench to detect selection using dominant markers. <i>Bioinformatics</i> , 2011, 27, 1717-1718.	1.8	100
28	interPopula: a Python API to access the HapMap Project dataset. <i>BMC Bioinformatics</i> , 2010, 11, S10.	1.2	0
29	Biopython: freely available Python tools for computational molecular biology and bioinformatics. <i>Bioinformatics</i> , 2009, 25, 1422-1423.	1.8	4,097
30	LOSITAN: A workbench to detect molecular adaptation based on a $F_{st}$ -outlier method. <i>BMC Bioinformatics</i> , 2008, 9, 323.	1.2	1,044
31	BACA: a mitochondrial genome retriever, organizer and visualizer. <i>Molecular Ecology Notes</i> , 2007, 7, 217-220.	1.7	2
32	An experiment in tool integration: The DDBG parallel and distributed debugger. <i>Journal of Systems Architecture</i> , 1999, 45, 897-907.	2.5	12
33	A graphical development and debugging environment for parallel programs. <i>Parallel Computing</i> , 1997, 22, 1747-1770.	1.3	51