Tiago R Antao

List of Publications by Year in descending order

33 papers	7,277 citations	304743 22 h-index	414414 32 g-index
33 all docs	33 docs citations	33 times ranked	13627 citing authors

#	Article	IF	Citations
1	Biopython: freely available Python tools for computational molecular biology and bioinformatics. Bioinformatics, 2009, 25, 1422-1423.	4.1	4,097
2	LOSITAN: A workbench to detect molecular adaptation based on a F st -outlier method. BMC Bioinformatics, 2008, 9, 323.	2.6	1,044
3	Genomic analyses inform on migration events during the peopling of Eurasia. Nature, 2016, 538, 238-242.	27.8	360
4	Effects of Overlapping Generations on Linkage Disequilibrium Estimates of Effective Population Size. Genetics, 2014, 197, 769-780.	2.9	299
5	Genetic Signatures Reveal High-Altitude Adaptation in a Set of Ethiopian Populations. Molecular Biology and Evolution, 2013, 30, 1877-1888.	8.9	173
6	Adaptive introgression between Anopheles sibling species eliminates a major genomic island but not reproductive isolation. Nature Communications, 2014, 5, 4248.	12.8	143
7	Genome-Wide Analysis of Cold Adaptation in Indigenous Siberian Populations. PLoS ONE, 2014, 9, e98076.	2.5	128
8	A Selective Sweep on a Deleterious Mutation in CPT1A in Arctic Populations. American Journal of Human Genetics, 2014, 95, 584-589.	6.2	119
9	Mcheza: a workbench to detect selection using dominant markers. Bioinformatics, 2011, 27, 1717-1718.	4.1	100
10	Early detection of population declines: high power of genetic monitoring using effective population size estimators. Evolutionary Applications, 2011, 4, 144-154.	3.1	90
11	Genome-wide evidence of Austronesian–Bantu admixture and cultural reversion in a hunter-gatherer group of Madagascar. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 936-941.	7.1	75
12	Selective sweep on human amylase genes postdates the split with Neanderthals. Scientific Reports, 2016, 6, 37198.	3.3	67
13	Evolution of the Pygmy Phenotype: Evidence of Positive Selection from Genome-wide Scans in African, Asian, and Melanesian Pygmies. Human Biology, 2013, 85, 251-284.	0.2	66
14	Plasmodium vivax Diversity and Population Structure across Four Continents. PLoS Neglected Tropical Diseases, 2015, 9, e0003872.	3.0	59
15	The Andean Adaptive Toolkit to Counteract High Altitude Maladaptation: Genome-Wide and Phenotypic Analysis of the Collas. PLoS ONE, 2014, 9, e93314.	2.5	55
16	A graphical development and debugging environment for parallel programs. Parallel Computing, 1997, 22, 1747-1770.	2.1	51
17	Multi-layered population structure in Island Southeast Asians. European Journal of Human Genetics, 2016, 24, 1605-1611.	2.8	50
18	A Large Plasmodium vivax Reservoir and Little Population Structure in the South Pacific. PLoS ONE, 2013, 8, e66041.	2.5	48

#	Article	IF	Citations
19	INTERMITTENT BREEDING AND CONSTRAINTS ON LITTER SIZE: CONSEQUENCES FOR EFFECTIVE POPULATION SIZE PER GENERATION (N_e) AND PER REPRODUCTIVE CYCLE (N_b). Evolution; International Journal of Organic Evolution, 2014, 68, 1722-1734.	2.3	48
20	Positive selection of AS3MT to arsenic water in Andean populations. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2015, 780, 97-102.	1.0	32
21	Evidence of Early-Stage Selection on EPAS1 and GPR126 Genes in Andean High Altitude Populations. Scientific Reports, 2017, 7, 13042.	3.3	29
22	Environmental, pharmacological and genetic influences on the spread of drug-resistant malaria. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 1705-1712.	2.6	28
23	Massive introgression drives species radiation at the range limit of Anopheles gambiae. Scientific Reports, 2017, 7, 46451.	3.3	28
24	Detecting population declines via monitoring the effective number of breeders (N_b). Molecular Ecology Resources, 2021, 21, 379-393.	4.8	24
25	Genetic and phenotypic differentiation of an Andean intermediate altitude population. Physiological Reports, 2015, 3, e12376.	1.7	18
26	Policy options for deploying anti-malarial drugs in endemic countries: a population genetics approach. Malaria Journal, 2012, 11, 422.	2.3	13
27	An experiment in tool integration: The DDBG parallel and distributed debugger. Journal of Systems Architecture, 1999, 45, 897-907.	4.3	12
28	Evolutionary parasitology applied to control and elimination policies. Trends in Parasitology, 2011, 27, 233-234.	3.3	8
29	ogaraK: a population genetics simulator for malaria. Bioinformatics, 2011, 27, 1335-1336.	4.1	4
30	Conserving genomic variability in large mammals: Effect of population fluctuations and variance in male reproductive success on variability in Yellowstone bison. Biological Conservation, 2012, 150, 159-166.	4.1	4
31	*AgeStrucNb*: Software for Simulating and Detecting Changes in the Effective Number of Breeders (N_b). Journal of Heredity, 2020, 111, 491-497.	2.4	3
32	BACA: a mitochondrial genome retriever, organizer and visualizer. Molecular Ecology Notes, 2007, 7, 217-220.	1.7	2
33	interPopula: a Python API to access the HapMap Project dataset. BMC Bioinformatics, 2010, 11, S10.	2.6	0