Tiago R Antao

List of Publications by Year
in descending order

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33 papers	7,277 citations	304701 22 h-index	414395 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 Austronesianâ€“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 (<i>N_e</i>) AND PER REPRODUCTIVE CYCLE (<i>N_b</i>). 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 (<i>N</i>_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	<i>AgeStrucNb</i>: Software for Simulating and Detecting Changes in the Effective Number of Breeders (<i>N</i>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