List of Publications by Year
in descending order

25 papers	2,829 citations	393982 19 h-index	580395 25 g-index
25 all docs	25 docs citations	25 times ranked	5269 citing authors

#	Article	IF	Citations
1	Detecting population declines via monitoring the effective number of breeders (N_b). Molecular Ecology Resources, 2021, 21, 379-393.	2.2	24
2	*AgeStrucNb*: Software for Simulating and Detecting Changes in the Effective Number of Breeders (*N*b). Journal of Heredity, 2020, 111, 491-497.	1.0	3
3	Evidence of Early-Stage Selection on EPAS1 and GPR126 Genes in Andean High Altitude Populations. Scientific Reports, 2017, 7, 13042.	1.6	29
4	Genomic analyses inform on migration events during the peopling of Eurasia. Nature, 2016, 538, 238-242.	13.7	360
5	Selective sweep on human amylase genes postdates the split with Neanderthals. Scientific Reports, 2016, 6, 37198.	1.6	67
6	Multi-layered population structure in Island Southeast Asians. European Journal of Human Genetics, 2016, 24, 1605-1611.	1.4	50
7	Genetic and phenotypic differentiation of an Andean intermediate altitude population. Physiological Reports, 2015, 3, e12376.	0.7	18
8	Plasmodium vivax Diversity and Population Structure across Four Continents. PLoS Neglected Tropical Diseases, 2015, 9, e0003872.	1.3	59
9	Positive selection of AS3MT to arsenic water in Andean populations. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2015, 780, 97-102.	0.4	32
10	Genome-Wide Analysis of Cold Adaptation in Indigenous Siberian Populations. PLoS ONE, 2014, 9, e98076.	1.1	128
11	Effects of Overlapping Generations on Linkage Disequilibrium Estimates of Effective Population Size. Genetics, 2014, 197, 769-780.	1.2	299
12	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.	1.1	48
13	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.	3.3	75
14	A Selective Sweep on a Deleterious Mutation in CPT1A in Arctic Populations. American Journal of Human Genetics, 2014, 95, 584-589.	2.6	119
15	The Andean Adaptive Toolkit to Counteract High Altitude Maladaptation: Genome-Wide and Phenotypic Analysis of the Collas. PLoS ONE, 2014, 9, e93314.	1.1	55
16	Genetic Signatures Reveal High-Altitude Adaptation in a Set of Ethiopian Populations. Molecular Biology and Evolution, 2013, 30, 1877-1888.	3.5	173
17	A Large Plasmodium vivax Reservoir and Little Population Structure in the South Pacific. PLoS ONE, 2013, 8, e66041.	1.1	48
18	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.	1.9	4

#	Article	IF	Citations
19	Policy options for deploying anti-malarial drugs in endemic countries: a population genetics approach. Malaria Journal, 2012, 11, 422.	0.8	13
20	Early detection of population declines: high power of genetic monitoring using effective population size estimators. Evolutionary Applications, 2011, 4, 144-154.	1.5	90
21	Evolutionary parasitology applied to control and elimination policies. Trends in Parasitology, 2011, 27, 233-234.	1.5	8
22	ogaraK: a population genetics simulator for malaria. Bioinformatics, 2011, 27, 1335-1336.	1.8	4
23	Environmental, pharmacological and genetic influences on the spread of drug-resistant malaria. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 1705-1712.	1.2	28
24	LOSITAN: A workbench to detect molecular adaptation based on a F st -outlier method. BMC Bioinformatics, 2008, 9, 323.	1.2	1,044
25	A graphical development and debugging environment for parallel programs. Parallel Computing, 1997, 22, 1747-1770.	1.3	51