

Veronica Fernandes

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

1,589
citations

361413

20
h-index

377865

34
g-index

37
all docs

37
docs citations

37
times ranked

2471
citing authors

#	ARTICLE	IF	CITATIONS
1	The Expansion of mtDNA Haplogroup L3 within and out of Africa. <i>Molecular Biology and Evolution</i> , 2012, 29, 915-927.	8.9	226
2	Dispersals and genetic adaptation of Bantu-speaking populations in Africa and North America. <i>Science</i> , 2017, 356, 543-546.	12.6	188
3	The Arabian Cradle: Mitochondrial Relicts of the First Steps along the Southern Route out of Africa. <i>American Journal of Human Genetics</i> , 2012, 90, 347-355.	6.2	116
4	The Diversity Present in 5140 Human Mitochondrial Genomes. <i>American Journal of Human Genetics</i> , 2009, 84, 628-640.	6.2	114
5	The First Modern Human Dispersals across Africa. <i>PLoS ONE</i> , 2013, 8, e80031.	2.5	86
6	A substantial prehistoric European ancestry amongst Ashkenazi maternal lineages. <i>Nature Communications</i> , 2013, 4, 2543.	12.8	80
7	Extensive Admixture and Selective Pressure Across the Sahel Belt. <i>Genome Biology and Evolution</i> , 2015, 7, 3484-3495.	2.5	68
8	The trans-Saharan slave trade - clues from interpolation analyses and high-resolution characterization of mitochondrial DNA lineages. <i>BMC Evolutionary Biology</i> , 2010, 10, 138.	3.2	60
9	Post-last glacial maximum expansion from Iberia to North Africa revealed by fine characterization of mtDNA H haplogroup in Tunisia. <i>American Journal of Physical Anthropology</i> , 2009, 139, 253-260.	2.1	54
10	Internal Diversification of Mitochondrial Haplogroup R0a Reveals Post-Last Glacial Maximum Demographic Expansions in South Arabia. <i>Molecular Biology and Evolution</i> , 2011, 28, 71-78.	8.9	53
11	Population expansion in the North African Late Pleistocene signalled by mitochondrial DNA haplogroup U6. <i>BMC Evolutionary Biology</i> , 2010, 10, 390.	3.2	52
12	Dynamics of a Dual SARS-CoV-2 Lineage Co-Infection on a Prolonged Viral Shedding COVID-19 Case: Insights into Clinical Severity and Disease Duration. <i>Microorganisms</i> , 2021, 9, 300.	3.6	48
13	Genome-Wide Characterization of Arabian Peninsula Populations: Shedding Light on the History of a Fundamental Bridge between Continents. <i>Molecular Biology and Evolution</i> , 2019, 36, 575-586.	8.9	45
14	Migration of Chadic speaking pastoralists within Africa based on population structure of Chad Basin and phylogeography of mitochondrial L3f haplogroup. <i>BMC Evolutionary Biology</i> , 2009, 9, 63.	3.2	41
15	Near Eastern Neolithic genetic input in a small oasis of the Egyptian Western Desert. <i>American Journal of Physical Anthropology</i> , 2009, 140, 336-346.	2.1	40
16	Genetic Stratigraphy of Key Demographic Events in Arabia. <i>PLoS ONE</i> , 2015, 10, e0118625.	2.5	40
17	The Comoros Show the Earliest Austronesian Gene Flow into the Swahili Corridor. <i>American Journal of Human Genetics</i> , 2018, 102, 58-68.	6.2	32
18	Population history of the Red Sea genetic exchanges between the Arabian Peninsula and East Africa signaled in the mitochondrial DNA HV1 haplogroup. <i>American Journal of Physical Anthropology</i> , 2011, 145, 592-598.	2.1	29

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19	Data from complete mtDNA sequencing of Tunisian centenarians: Testing haplogroup association and the "golden mean" to longevity. <i>Mechanisms of Ageing and Development</i> , 2009, 130, 222-226.	4.6	26
20	Origin and spread of human mitochondrial DNA haplogroup U7. <i>Scientific Reports</i> , 2017, 7, 46044.	3.3	25
21	Papuan mitochondrial genomes and the settlement of Sahul. <i>Journal of Human Genetics</i> , 2020, 65, 875-887.	2.3	24
22	Internal diversification of non-Sub-Saharan haplogroups in Sahelian populations and the spread of pastoralism beyond the Sahara. <i>American Journal of Physical Anthropology</i> , 2017, 164, 424-434.	2.1	23
23	Association of STAT4, TGF β 1, SH2B3 and PTPN22 polymorphisms with autoimmune hepatitis. <i>Experimental and Molecular Pathology</i> , 2018, 105, 279-284.	2.1	17
24	Joint ancestry and association test indicate two distinct pathogenic pathways involved in classical dengue fever and dengue shock syndrome. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006202.	3.0	17
25	Population genetics-informed meta-analysis in seven genes associated with risk to dengue fever disease. <i>Infection, Genetics and Evolution</i> , 2018, 62, 60-72.	2.3	16
26	Evidence of Austronesian Genetic Lineages in East Africa and South Arabia: Complex Dispersal from Madagascar and Southeast Asia. <i>Genome Biology and Evolution</i> , 2019, 11, 748-758.	2.5	15
27	A different view on fine-scale population structure in Western African populations. <i>Human Genetics</i> , 2020, 139, 45-59.	3.8	13
28	Fine Time Scaling of Purifying Selection on Human Nonsynonymous mtDNA Mutations Based on the Worldwide Population Tree and Mother-Child Pairs. <i>Human Mutation</i> , 2015, 36, 1100-1111.	2.5	11
29	Genomic and transcriptomic characterization of the mitochondrial-rich oncocytic phenotype on a thyroid carcinoma background. <i>Mitochondrion</i> , 2019, 46, 123-133.	3.4	10
30	Projecting Ancient Ancestry in Modern-Day Arabians and Iranians: A Key Role of the Past Exposed Arabo-Persian Gulf on Human Migrations. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	6
31	Circum-Saharan Prehistory through the Lens of mtDNA Diversity. <i>Genes</i> , 2022, 13, 533.	2.4	5
32	Host ancestry and dengue fever: from mapping of candidate genes to prediction of worldwide genetic risk. <i>Future Virology</i> , 2018, 13, 647-655.	1.8	3
33	Field and Molecular Epidemiology: How Viral Sequencing Changed Transmission Inferences in the First Portuguese SARS-CoV-2 Infection Cluster. <i>Viruses</i> , 2021, 13, 1116.	3.3	3
34	mtDNA diversity in Sudan (East Africa). <i>Forensic Science International: Genetics Supplement Series</i> , 2008, 1, 257-258.	0.3	2