## Pedro A Soares

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3739892/publications.pdf

Version: 2024-02-01

76 papers

4,913 citations

32 h-index 98798 67 g-index

79 all docs

79 docs citations

79 times ranked 6383 citing authors

#	Article	IF	CITATIONS
1	A glimpse at an early stage of microbe domestication revealed in the variable genome of <i>Torulaspora delbrueckii</i> , an emergent industrial yeast. Molecular Ecology, 2023, 32, 2396-2412.	3.9	12
2	Uncovering Novel Plasma Membrane Carboxylate Transporters in the Yeast Cyberlindnera jadinii. Journal of Fungi (Basel, Switzerland), 2022, 8, 51.	3.5	3
3	Whole-Genome Sequencing and Annotation of the Yeast Clavispora santaluciae Reveals Important Insights about Its Adaptation to the Vineyard Environment. Journal of Fungi (Basel, Switzerland), 2022, 8, 52.	3.5	2
4	Ancient DNA at the edge of the world: Continental immigration and the persistence of Neolithic male lineages in Bronze Age Orkney. Proceedings of the National Academy of Sciences of the United States of America, 2022, $119$ , .	7.1	12
5	Improvement of Torulaspora delbrueckii Genome Annotation: Towards the Exploitation of Genomic Features of a Biotechnologically Relevant Yeast. Journal of Fungi (Basel, Switzerland), 2021, 7, 287.	3 <b>.</b> 5	10
6	Biotechnological Importance of TorulasporaÂdelbrueckii: From the Obscurity to the Spotlight. Journal of Fungi (Basel, Switzerland), 2021, 7, 712.	3.5	22
7	Biomolecular insights into North African-related ancestry, mobility and diet in eleventh-century Al-Andalus. Scientific Reports, 2021, 11, 18121.	3.3	8
8	Expanding the Knowledge on the Skillful Yeast Cyberlindnera jadinii. Journal of Fungi (Basel,) Tj ETQq0 0 0 rgBT	Overlock	10 <u>Tf</u> 50 462 <sup>-</sup>
9	BAGS: An automated Barcode, Audit & System for DNA barcode reference libraries.  Molecular Ecology Resources, 2021, 21, 573-583.	4.8	33
10	Population Analysis and Evolution of Saccharomyces cerevisiae Mitogenomes. Microorganisms, 2020, 8, 1001.	3.6	1
11	Phylogeography of 27,000 SARS-CoV-2 Genomes: Europe as the Major Source of the COVID-19 Pandemic. Microorganisms, 2020, 8, 1678.	3.6	21
12	Carboxylic Acid Transporters in <i>Candida</i> Pathogenesis. MBio, 2020, 11, .	4.1	22
13	Evolutionary analysis of Mycobacterium bovis genotypes across Africa suggests co-evolution with livestock and humans. PLoS Neglected Tropical Diseases, 2020, 14, e0008081.	3.0	16
14	An Efficient and User-Friendly Implementation of the Founder Analysis Methodology. Advances in Intelligent Systems and Computing, 2020, , 121-128.	0.6	0
15	On Methodological issues in the Indo-European debate By Michel Danino. Journal of Biosciences, 2019, 44, 1.	1.1	0
16	Untangling Neolithic and Bronze Age mitochondrial lineages in South Asia. Annals of Human Biology, 2019, 46, 140-144.	1.0	1
17	Maternal relationships within an Iron Age burial at the High Pasture Cave, Isle of Skye, Scotland. Journal of Archaeological Science, 2019, 110, 104978.	2.4	6
18	A dispersal of Homo sapiens from southern to eastern Africa immediately preceded the out-of-Africa migration. Scientific Reports, 2019, 9, 4728.	3.3	49

#	Article	IF	CITATIONS
19	The genomic history of the Iberian Peninsula over the past 8000 years. Science, 2019, 363, 1230-1234.	12.6	340
20	Rectifying long-standing misconceptions about the Ï-statistic for molecular dating. PLoS ONE, 2019, 14, e0212311.	2.5	15
21	Deep segregation in the open ocean: MacaronesiaÂas an evolutionary hotspot for low dispersal marine invertebrates. Molecular Ecology, 2019, 28, 1784-1800.	3.9	20
22	Association of Leukotriene A4 Hydrolase with Tuberculosis Susceptibility Using Genomic Data in Portugal. Microorganisms, 2019, 7, 650.	3.6	14
23	The acetate uptake transporter family motif "NPAPLGL(M/S)―is essential for substrate uptake. Fungal Genetics and Biology, 2019, 122, 1-10.	2.1	17
24	Evidence of Austronesian Genetic Lineages in East Africa and South Arabia: Complex Dispersal from Madagascar and Southeast Asia. Genome Biology and Evolution, 2019, 11, 748-758.	2.5	15
25	Methodological issues in the Indo-European debate Michel Danino. Journal of Biosciences, 2019, 44, .	1.1	0
26	ONCE UPON A TIME IN THE WEST:., 2018, , 153-191.		2
27	Mitogenome Diversity in Sardinians: A Genetic Window onto an Island's Past. Molecular Biology and Evolution, 2017, 34, 1230-1239.	8.9	61
28	Origin and spread of human mitochondrial DNA haplogroup U7. Scientific Reports, 2017, 7, 46044.	3.3	25
29	Reconciling evidence from ancient and contemporary genomes: a major source for the European Neolithic within Mediterranean Europe. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20161976.	2.6	22
30	A genetic chronology for the Indian Subcontinent points to heavily sex-biased dispersals. BMC Evolutionary Biology, 2017, 17, 88.	3.2	59
31	OSBPL10, RXRA and lipid metabolism confer African-ancestry protection against dengue haemorrhagic fever in admixed Cubans. PLoS Pathogens, 2017, 13, e1006220.	4.7	51
32	Assembling and auditing a comprehensive <scp>DNA</scp> barcode reference library for European marine fishes. Journal of Fish Biology, 2016, 89, 2741-2754.	1.6	30
33	Mapping human dispersals into the Horn of Africa from Arabian Ice Age refugia using mitogenomes. Scientific Reports, 2016, 6, 25472.	3.3	40
34	Palaeogenomics: Mitogenomes and Migrations in Europe's Past. Current Biology, 2016, 26, R243-R246.	3.9	15
35	Resolving the ancestry of Austronesian-speaking populations. Human Genetics, 2016, 135, 309-326.	3.8	71
36	Quantifying the legacy of the Chinese Neolithic on the maternal genetic heritage of Taiwan and Island Southeast Asia. Human Genetics, 2016, 135, 363-376.	3.8	28

#	Article	IF	Citations
37	A Genetic Perspective on African Prehistory. Vertebrate Paleobiology and Paleoanthropology, 2016, , 383-405.	0.5	15
38	ARCHAEOGENETIC AND PALAEOGENETIC EVIDENCE FOR METAL AGE MOBILITY IN EUROPE. , 2016, , 351-384.		2
39	Fine Time Scaling of Purifying Selection on Human Nonsynonymous mtDNA Mutations Based on the Worldwide Population Tree and Mother-Child Pairs. Human Mutation, 2015, 36, 1100-1111.	2.5	11
40	Archaeogenetics., 2015,, 26-54.		1
41	Extensive Admixture and Selective Pressure Across the Sahel Belt. Genome Biology and Evolution, 2015, 7, 3484-3495.	2.5	68
42	Genetic Stratigraphy of Key Demographic Events in Arabia. PLoS ONE, 2015, 10, e0118625.	2.5	40
43	Early Holocenic and Historic mtDNA African Signatures in the Iberian Peninsula: The Andalusian Region as a Paradigm. PLoS ONE, 2015, 10, e0139784.	2.5	18
44	60,000 years of interactions between Central and Eastern Africa documented by major African mitochondrial haplogroup L2. Scientific Reports, 2015, 5, 12526.	3.3	33
45	Mosaic maternal ancestry in the Great Lakes region of East Africa. Human Genetics, 2015, 134, 1013-1027.	3.8	18
46	Global human frequencies of predicted nuclear pathogenic variants and the role played by protein hydrophobicity in pathogenicity potential. Scientific Reports, 2014, 4, 7155.	3.3	8
47	A founder SDHB mutation in Portuguese paraganglioma patients. Endocrine-Related Cancer, 2013, 20, L23-L26.	3.1	12
48	Genetic and archaeological perspectives on the initial modern human colonization of southern Asia. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 10699-10704.	7.1	246
49	The Genetic Impact of the Lake Chad Basin Population in North Africa as Documented by Mitochondrial Diversity and Internal Variation of the L3e5 Haplogroup. Annals of Human Genetics, 2013, 77, 513-523.	0.8	17
50	A substantial prehistoric European ancestry amongst Ashkenazi maternal lineages. Nature Communications, 2013, 4, 2543.	12.8	80
51	The First Modern Human Dispersals across Africa. PLoS ONE, 2013, 8, e80031.	2.5	86
52	Evaluating Purifying Selection in the Mitochondrial DNA of Various Mammalian Species. PLoS ONE, 2013, 8, e58993.	2.5	39
53	The Expansion of mtDNA Haplogroup L3 within and out of Africa. Molecular Biology and Evolution, 2012, 29, 915-927.	8.9	226
54	Mitochondrial genomes from modern horses reveal the major haplogroups that underwent domestication. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2449-2454.	7.1	198

#	Article	IF	CITATIONS
55	Pleistoceneâ∈Holocene boundary in Southern Arabia from the perspective of human mtDNA variation. American Journal of Physical Anthropology, 2012, 149, 291-298.	2.1	37
56	Somatic mitochondrial DNA mutations in cancer escape purifying selection and high pathogenicity mutations lead to the oncocytic phenotype: pathogenicity analysis of reported somatic mtDNA mutations in tumors. BMC Cancer, 2012, 12, 53.	2.6	75
57	Mitochondrial DNA Signals of Late Glacial Recolonization of Europe from Near Eastern Refugia. American Journal of Human Genetics, 2012, 90, 915-924.	6.2	150
58	The Arabian Cradle: Mitochondrial Relicts of the First Steps along the Southern Route out of Africa. American Journal of Human Genetics, 2012, 90, 347-355.	6.2	116
59	Ancient Voyaging and Polynesian Origins. American Journal of Human Genetics, 2011, 88, 239-247.	6.2	161
60	Comparing Phylogeny and the Predicted Pathogenicity of Protein Variations Reveals Equal Purifying Selection across the Global Human mtDNA Diversity. American Journal of Human Genetics, 2011, 88, 433-439.	6.2	103
61	Population history of the Red Sea—genetic exchanges between the Arabian Peninsula and East Africa signaled in the mitochondrial DNA HV1 haplogroup. American Journal of Physical Anthropology, 2011, 145, 592-598.	2.1	29
62	Population Genetic Structure in Indian Austroasiatic Speakers: The Role of Landscape Barriers and Sex-Specific Admixture. Molecular Biology and Evolution, 2011, 28, 1013-1024.	8.9	135
63	Genetic Structure of Pastoral and Farmer Populations in the African Sahel. Molecular Biology and Evolution, 2011, 28, 2491-2500.	8.9	43
64	Population expansion in the North African Late Pleistocene signalled by mitochondrial DNA haplogroup U6. BMC Evolutionary Biology, 2010, 10, 390.	3.2	52
65	The Archaeogenetics of Europe. Current Biology, 2010, 20, R174-R183.	3.9	210
66	A common MYBPC3 (cardiac myosin binding protein C) variant associated with cardiomyopathies in South Asia. Nature Genetics, 2009, 41, 187-191.	21.4	245
67	Correcting for Purifying Selection: An Improved Human Mitochondrial Molecular Clock. American Journal of Human Genetics, 2009, 84, 740-759.	6.2	643
68	A multiplex primer extension assay for the rapid identification of paternal lineages in domestic goat (Capra hircus): Laying the foundations for a detailed caprine Y chromosome phylogeny. Molecular Phylogenetics and Evolution, 2008, 49, 663-668.	2.7	8
69	Complete Mitochondrial Genome Sequence of the Tyrolean Iceman. Current Biology, 2008, 18, 1687-1693.	3.9	101
70	Climate Change and Postglacial Human Dispersals in Southeast Asia. Molecular Biology and Evolution, 2008, 25, 1209-1218.	8.9	186
71	Evidence for Variable Selective Pressures at a Large Secondary Structure of the Human Mitochondrial DNA Control Region. Molecular Biology and Evolution, 2008, 25, 2759-2770.	8.9	47
72	A Mitochondrial Stratigraphy for Island Southeast Asia. American Journal of Human Genetics, 2007, 80, 29-43.	6.2	228

#	Article	IF	CITATIONS
73	Relative Y-STR mutation rates estimated from the variance inside SNP defined lineages. International Congress Series, 2006, 1288, 82-84.	0.2	3
74	Mutational Spectrum and Linkage Disequilibrium Patterns at the Ornithine Transcarbamylase Gene (OTC). Annals of Human Genetics, 2006, 70, 797-801.	0.8	8
75	Phylogeography and Ethnogenesis of Aboriginal Southeast Asians. Molecular Biology and Evolution, 2006, 23, 2480-2491.	8.9	153
76	Evolutionary insights derived from comprehensive analyses of DNA barcoding diversity in marine members of the superorder Peracarida (Crustacea: Malacostraca). Frontiers in Marine Science, 0, 6, .	2.5	0