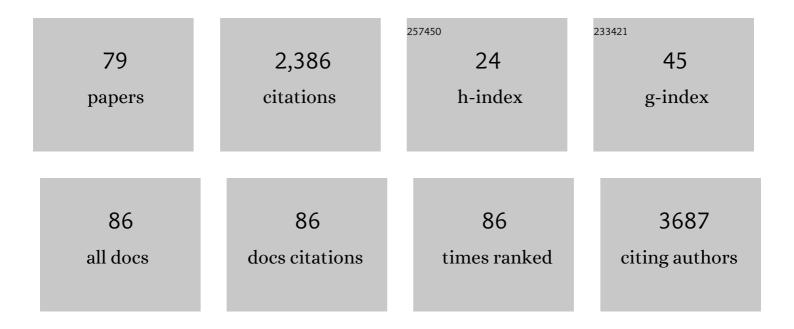
Filipe Pereira

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Revealing the History of Sheep Domestication Using Retrovirus Integrations. Science, 2009, 324, 532-536.	12.6	402
2	A Paradigm for Virus–Host Coevolution: Sequential Counter-Adaptations between Endogenous and Exogenous Retroviruses. PLoS Pathogens, 2007, 3, e170.	4.7	135
3	Identification of Species with DNA-Based Technology: Current Progress and Challenges. Recent Patents on DNA & Gene Sequences, 2008, 2, 187-200.	0.7	109
4	Evolutionary dynamics of the SARS-CoV-2 ORF8 accessory gene. Infection, Genetics and Evolution, 2020, 85, 104525.	2.3	102
5	Tracing the History of Goat Pastoralism: New Clues from Mitochondrial and Y Chromosome DNA in North Africa. Molecular Biology and Evolution, 2009, 26, 2765-2773.	8.9	96
6	Genetic Signatures of a Mediterranean Influence in Iberian Peninsula Sheep Husbandry. Molecular Biology and Evolution, 2006, 23, 1420-1426.	8.9	94
7	Association of G-quadruplex forming sequences with human mtDNA deletion breakpoints. BMC Genomics, 2014, 15, 677.	2.8	91
8	Forensic genetics and genomics: Much more than just a human affair. PLoS Genetics, 2017, 13, e1006960.	3.5	71
9	Mitochondrial DNA Rearrangements in Health and Disease-A Comprehensive Study. Human Mutation, 2014, 35, 1-14.	2.5	67
10	Mitochondrial DNA deletions are associated with non-B DNA conformations. Nucleic Acids Research, 2012, 40, 7606-7621.	14.5	64
11	Digital PCR methods improve detection sensitivity and measurement precision of low abundance mtDNA deletions. Scientific Reports, 2016, 6, 25186.	3.3	63
12	The mtDNA catalogue of all Portuguese autochthonous goat (Capra hircus) breeds: high diversity of female lineages at the western fringe of European distribution. Molecular Ecology, 2005, 14, 2313-2318.	3.9	54
13	Actinobacteria Isolated From Laminaria ochroleuca: A Source of New Bioactive Compounds. Frontiers in Microbiology, 2019, 10, 683.	3.5	54
14	Identification of species by multiplex analysis of variable-length sequences. Nucleic Acids Research, 2010, 38, e203-e203.	14.5	53
15	MitoBreak: the mitochondrial DNA breakpoints database. Nucleic Acids Research, 2014, 42, D1261-D1268.	14.5	51
16	A new autosomal STR nineplex for canine identification and parentage testing. Electrophoresis, 2009, 30, 417-423.	2.4	48
17	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
18	New Method for the Simultaneous Identification of Cow, Sheep, Goat, and Water Buffalo in Dairy Products by Analysis of Short Species-Specific Mitochondrial DNA Targets. Journal of Agricultural and Food Chemistry, 2012, 60, 10480-10485.	5.2	45

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19	New Insights into the Phylogeny and Worldwide Dispersion of Two Closely Related Nematode Species, Bursaphelenchus xylophilus and Bursaphelenchus mucronatus. PLoS ONE, 2013, 8, e56288.	2.5	43
20	Epistatic interactions modulate the evolution of mammalian mitochondrial respiratory complex components. BMC Genomics, 2009, 10, 266.	2.8	33
21	Comparative Analysis of the Adhesive Proteins of the Adult Stalked Goose Barnacle Pollicipes pollicipes (Cirripedia: Pedunculata). Marine Biotechnology, 2019, 21, 38-51.	2.4	33
22	Data for Y-chromosome haplotypes defined by 17 STRs (AmpFLSTR® Yfilerâ,,¢) in two Tunisian Berber communities. Forensic Science International, 2006, 160, 80-83.	2.2	31
23	SARS-CoV-2 variants combining spike mutations and the absence of ORF8 may be more transmissible and require close monitoring. Biochemical and Biophysical Research Communications, 2021, 550, 8-14.	2.1	31
24	The mitogenomic phylogeny of the Elasmobranchii (Chondrichthyes). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 867-878.	0.7	30
25	Biodegradation of mono-, di- and trifluoroacetate by microbial cultures with different origins. New Biotechnology, 2018, 43, 23-29.	4.4	29
26	MtDNA diversity among four Portuguese autochthonous dog breeds: a fine-scale characterisation. BMC Genetics, 2005, 6, 37.	2.7	24
27	Mitochondrial lineages reveal intense gene flow between Iberian wild boars and South Iberian pig breeds. Animal Genetics, 2012, 43, 35-41.	1.7	24
28	Splice-Break: exploiting an RNA-seq splice junction algorithm to discover mitochondrial DNA deletion breakpoints and analyses of psychiatric disorders. Nucleic Acids Research, 2019, 47, e59-e59.	14.5	22
29	A framework for the development of STR genotyping in domestic animal species: Characterization and population study of 12 canine X $\hat{a}\in\epsilon$ hromosome loci. Electrophoresis, 2010, 31, 303-308.	2.4	21
30	Species assignment in forensics and the challenge of hybrids. Forensic Science International: Genetics, 2020, 48, 102333.	3.1	21
31	Usefulness of microchip electrophoresis for the analysis of mitochondrial DNA in forensic and ancient DNA studies. Electrophoresis, 2006, 27, 5101-5109.	2.4	20
32	Genetic profiles and sex identification of found-dead wolves determined by the use of an 11-loci PCR multiplex. Forensic Science International: Genetics, 2010, 4, 68-72.	3.1	20
33	Diversity and Bioactive Potential of Actinobacteria Isolated from a Coastal Marine Sediment in Northern Portugal. Microorganisms, 2020, 8, 1691.	3.6	20
34	Mitochondrial <scp>DNA</scp> variation of domestic sheep (<i>Ovis aries</i>) in Kenya. Animal Genetics, 2016, 47, 377-381.	1.7	19
35	Species identification in forensic samples using the SPInDel approach: A GHEP-ISFG inter-laboratory collaborative exercise. Forensic Science International: Genetics, 2017, 28, 219-224.	3.1	19
36	Evolution of the NET (NocA, Nlz, Elbow, TLP-1) protein family in metazoans: insights from expression data and phylogenetic analysis. Scientific Reports, 2016, 6, 38383.	3.3	17

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37	SARS-CoV-2 variants lacking a functional ORF8 may reduce accuracy of serological testing. Journal of Immunological Methods, 2021, 488, 112906.	1.4	17
38	SARS-CoV-2 variants lacking ORF8 occurred in farmed mink and pangolin. Gene, 2021, 784, 145596.	2.2	17
39	SPI n D el: a multifunctional workbench for species identification using insertion/deletion variants. Molecular Ecology Resources, 2012, 12, 1190-1195.	4.8	15
40	Identification of plant species using variable length chloroplast DNA sequences. Forensic Science International: Genetics, 2018, 36, 1-12.	3.1	15
41	A Guide for Mitochondrial DNA Analysis in Non-Human Forensic Investigations~!2010-01-07~!2010-04-02~!2010-05-17~!. The Open Forensic Science Journal, 2010, 3, 33-44.	0.8	15
42	The risks of using "species-specific―PCR assays in wildlife research: The case of red fox (Vulpes vulpes) identification in Tasmania. Forensic Science International: Genetics, 2014, 11, e9-e11.	3.1	13
43	Metagenomic Composition Analysis of an Ancient Sequenced Polar Bear Jawbone from Svalbard. Genes, 2018, 9, 445.	2.4	13
44	The dispersion and detection patterns of mt DNA â€assigned red fox Vulpes vulpes scats in Tasmania are anomalous. Journal of Applied Ecology, 2014, 51, 1033-1040.	4.0	10
45	Amphibians on the hotspot: Molecular biology and conservation in the South American Atlantic Rainforest. PLoS ONE, 2019, 14, e0224320.	2.5	9
46	State-of-the-Art and Future Prospects of Canine STR-Based Genotyping~!2010-01-07~!2010-04-02~!2010-05-17~!. The Open Forensic Science Journal, 2010, 3, 45-52.	0.8	9
47	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
48	EbolaID: An Online Database of Informative Genomic Regions for Ebola Identification and Treatment. PLoS Neglected Tropical Diseases, 2016, 10, e0004757.	3.0	8
49	mtDNA lineages in two Tunisian Berber communities: Comparing diversities between villages and towns. International Congress Series, 2006, 1288, 121-123.	0.2	7
50	Analysis of inter-specific mitochondrial DNA diversity for accurate species identification. International Congress Series, 2006, 1288, 103-105.	0.2	7
51	Opportunistically acquired evidence is unsuitable data to model fox (<i>Vulpes vulpes</i>) distribution in Tasmania. Wildlife Society Bulletin, 2014, 38, 757-766.	1.6	6
52	The genetic diversity and phylogeography of Mexican domestic sheep. Small Ruminant Research, 2020, 187, 106109.	1.2	6
53	Identification of mtDNA Lineages ofSus scrofaby Multiplex Single Base Extension for the Authentication of Processed Food Products. Journal of Agricultural and Food Chemistry, 2011, 59, 6920-6926.	5.2	5
54	A method to assemble DNA fragments mimicking junctions of transgenic elements: Application to the AquAdvantage salmon. Food Control, 2017, 82, 179-183.	5.5	5

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55	Molecular Evolution of DNA Topoisomerase III Beta (TOP3B) in Metazoa. Journal of Molecular Evolution, 2021, 89, 384-395.	1.8	5
56	Evolutionary History of TOPIIA Topoisomerases in Animals. Journal of Molecular Evolution, 2022, 90, 149-165.	1.8	5
57	Geographical contrasts of Yâ€chromosomal haplogroups from wild and domestic goats reveal ancient migrations and recent introgressions. Molecular Ecology, 2022, 31, 4364-4380.	3.9	5
58	A multiplex PCR assay for identification of the red fox (Vulpes vulpes) using the mitochondrial ribosomal RNA genes. Conservation Genetics Resources, 2015, 7, 45-48.	0.8	4
59	Design and evaluation of PCR primers for amplification of four chloroplast DNA regions in plants. Conservation Genetics Resources, 2017, 9, 9-12.	0.8	4
60	A Guide for Mitochondrial DNA Analysis in Non-Human Forensic Investigations. The Open Forensic Science Journal, 2012, 3, 33-44.	0.8	4
61	Molecular dynamics and intrinsic disorder analysis of the SARS-CoV-2 Nsp1 structural changes caused by substitution and deletion mutations. Molecular Simulation, 2022, 48, 1192-1201.	2.0	4
62	Relative Y-STR mutation rates estimated from the variance inside SNP defined lineages. International Congress Series, 2006, 1288, 82-84.	0.2	3
63	A new autosomal STR multiplex for canine genotyping. Forensic Science International: Genetics Supplement Series, 2008, 1, 628-629.	0.3	3
64	Results of the GHEP-ISFG collaborative exercise for the taxonomic identification of forensic samples using the SPInDel method. Forensic Science International: Genetics Supplement Series, 2015, 5, e184-e185.	0.3	3
65	A proposal for standardization of transgenic reference sequences used in food forensics. Forensic Science International: Genetics, 2017, 29, e26-e28.	3.1	3
66	The HIV oligonucleotide database (HIVoligoDB). Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	3
67	Did â€~precautionary' 1080 baiting have a realistic potential to eradicate <scp>R</scp> ed <scp>F</scp> ox (<i><scp>V</scp>ulpes vulpes</i>) in <scp>T</scp> asmania without <i>in situ</i> monitoring data?. Ecological Management and Restoration, 2014, 15, 196-203.	1.5	2
68	The mitochondrial genome of the pinewood nematode (Bursaphelenchus xylophilus) lineage introduced in Europe. Mitochondrial DNA, 2014, 25, 420-421.	0.6	2
69	The shark panel: An InDel multiplex for shark species identification. Forensic Science International: Genetics Supplement Series, 2015, 5, e430-e432.	0.3	2
70	Applications of DNA-Based Methods in Food Forensics. Security Science and Technology, 2016, , 493-517.	0.5	2
71	Trends in anecdotal fox sightings in Tasmania accounted for by psychological factors. Conservation Biology, 2017, 31, 1450-1458.	4.7	2
72	Quantification of <i>Neurospora crassa</i> mitochondrial DNA using quantitative realâ€ŧime PCR. Letters in Applied Microbiology, 2020, 71, 171-178.	2.2	2

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73	Species identification in routine casework samples using the SPInDel kit. Forensic Science International: Genetics Supplement Series, 2019, 7, 180-181.	0.3	1
74	State-of-the-Art and Future Prospects of Canine STR-Based Genotyping. The Open Forensic Science Journal, 2012, 3, 45-52.	0.8	1
75	Genetic and DNA-Based Techniques. Comprehensive Analytical Chemistry, 2013, , 195-220.	1.3	0
76	Genetic diversity of freshwater fishes from the South American Atlantic Rainforest: The case study of the genus Phalloceros. Forensic Science International: Genetics Supplement Series, 2015, 5, e608-e610.	0.3	0
77	Reply to Sarre et al. "Defining specificity in DNA detection of wildlife― Forensic Science International: Genetics, 2015, 16, e1-e2.	3.1	0
78	Probing the potential of the Shark Panel InDel multiplex v2.0 on the forensic identification of batoid elasmobranchs. Forensic Science International: Genetics Supplement Series, 2017, 6, e221-e223.	0.3	0
79	Revisiting the Neurospora crassa mitochondrial genome. Letters in Applied Microbiology, 2021, 73, 495-505.	2.2	Ο