Luisa Pereira

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

200 6,093 42 71 g-index

218 7,110 4.5 S-47 ext. papers ext. citations avg, IF L-index

#	Paper	IF	Citations
200	SARS-CoV-2 reinfection in a healthcare worker: First case in Portugal confirmed by viral genome sequencing <i>Porto Biomedical Journal</i> , 2022 , 7, e171	1.1	
199	InfectionCMA: A Cell MicroArray Approach for Efficient Biomarker Screening in In Vitro Infection Assays <i>Pathogens</i> , 2022 , 11,	4.5	1
198	The Upper Digestive Tract Microbiome and Oesophageal Squamous Cell Carcinoma: Epidemiology, Pathogenesis, and Clinical Implications in Africa. <i>Pathobiology</i> , 2021 , 88, 141-155	3.6	2
197	Genetic variation patterns of Ethalassemia in western Andalusia (Spain) reveal a structure of specific mutations within the Iberian Peninsula. <i>Annals of Human Biology</i> , 2021 , 1-31	1.7	
196	Chromogranin A and NSE in cystic pancreatic neuroendocrine tumors. <i>Clinics and Research in Hepatology and Gastroenterology</i> , 2021 , 45, 101601	2.4	1
195	Peer support programs in the fields of medicine and nursing: a systematic search and narrative review. <i>Canadian Medical Education Journal</i> , 2021 , 12, 113-125	1	3
194	Field and Molecular Epidemiology: How Viral Sequencing Changed Transmission Inferences in the First Portuguese SARS-CoV-2 Infection Cluster. <i>Viruses</i> , 2021 , 13,	6.2	1
193	A second endoscopic ultrasound with fine-needle aspiration for cytology identifies high-risk pancreatic cysts overlooked by current guidelines. <i>Diagnostic Cytopathology</i> , 2021 , 49, 109-118	1.4	1
192	Chitinase 3-like-1 and fibronectin in the cargo of extracellular vesicles shed by human macrophages influence pancreatic cancer cellular response to gemcitabine. <i>Cancer Letters</i> , 2021 , 501, 210-223	9.9	20
191	Sub-Saharan African information potential to unveil adaptations to infectious disease. <i>Human Molecular Genetics</i> , 2021 , 30, R138-R145	5.6	0
190	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,	4.9	18
189	African genetic diversity and adaptation inform a precision medicine agenda. <i>Nature Reviews Genetics</i> , 2021 , 22, 284-306	30.1	20
188	Shedding Light on the African Enigma: In Vitro Testing of Coevolution. <i>Microorganisms</i> , 2021 , 9,	4.9	4
187	Papuan mitochondrial genomes and the settlement of Sahul. <i>Journal of Human Genetics</i> , 2020 , 65, 875-8	8 4 .73	11
186	The effects of cannabinoids on glioblastoma growth: A systematic review with meta-analysis of animal model studies. <i>European Journal of Pharmacology</i> , 2020 , 876, 173055	5.3	6
185	The mitogenome portrait of Umbria in Central Italy as depicted by contemporary inhabitants and pre-Roman remains. <i>Scientific Reports</i> , 2020 , 10, 10700	4.9	4
184	Methylation changes at the imprinted locus in pancreatic cystic neoplasms are important for the diagnosis of malignant cysts. <i>World Journal of Gastrointestinal Oncology</i> , 2020 , 12, 1056-1064	3.4	2

(2019-2020)

183	Excellent Accuracy of Glucose Level in Cystic Fluid for Diagnosis of Pancreatic Mucinous Cysts. <i>Digestive Diseases and Sciences</i> , 2020 , 65, 2071-2078	4	23	
182	A different view on fine-scale population structure in Western African populations. <i>Human Genetics</i> , 2020 , 139, 45-59	6.3	6	
181	The prognostic value of NRF2 in breast cancer patients: a systematic review with meta-analysis. Breast Cancer Research and Treatment, 2020 , 179, 523-532	4.4	9	
180	Human Genomic Diversity Where the Mediterranean Joins the Atlantic. <i>Molecular Biology and Evolution</i> , 2020 , 37, 1041-1055	8.3	7	
179	On the almost sure limit theorem for the joint version of maxima and minima of non-stationary random fields. <i>Communications in Statistics - Theory and Methods</i> , 2020 , 1-11	0.5		
178	Gastric Microbiome Diversities in Gastric Cancer Patients from Europe and Asia Mimic the Human Population Structure and Are Partly Driven by Microbiome Quantitative Trait Loci. <i>Microorganisms</i> , 2020 , 8,	4.9	7	
177	Psilocybin as a New Approach to Treat Depression and Anxiety in the Context of Life-Threatening Diseases-A Systematic Review and Meta-Analysis of Clinical Trials. <i>Biomedicines</i> , 2020 , 8,	4.8	16	
176	Population structure of modern-day Italians reveals patterns of ancient and archaic ancestries in Southern Europe. <i>Science Advances</i> , 2019 , 5, eaaw3492	14.3	30	
175	Profiling of lung microbiota discloses differences in adenocarcinoma and squamous cell carcinoma. <i>Scientific Reports</i> , 2019 , 9, 12838	4.9	31	
174	Genome-wide analysis of Corsican population reveals a close affinity with Northern and Central Italy. <i>Scientific Reports</i> , 2019 , 9, 13581	4.9	4	
173	Development of a carboxymethyl xylan film containing licorice essential oil with antioxidant properties to inhibit the growth of foodborne pathogens. <i>LWT - Food Science and Technology</i> , 2019 , 111, 218-225	5.4	24	
172	Star anise (Illicium verum Hook. f.) essential oil: Antioxidant properties and antibacterial activity against Acinetobacter baumannii. <i>Flavour and Fragrance Journal</i> , 2019 , 34, 260-270	2.5	14	
171	IPCAPS: an R package for iterative pruning to capture population structure. <i>Source Code for Biology and Medicine</i> , 2019 , 14, 2	1.9	4	
170	A dispersal of Homo sapiens from southern to eastern Africa immediately preceded the out-of-Africa migration. <i>Scientific Reports</i> , 2019 , 9, 4728	4.9	31	
169	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	8.3	18	
168	A meta-analytic perspective on Arcobacter spp. antibiotic resistance. <i>Journal of Global Antimicrobial Resistance</i> , 2019 , 16, 130-139	3.4	12	
167	On the almost sure convergence for the joint version of maxima and minima of stationary sequences. <i>Statistics and Probability Letters</i> , 2019 , 154, 108540	0.6	2	
166	Expression and Clinical Relevance of SOX9 in Gastric Cancer. <i>Disease Markers</i> , 2019 , 2019, 8267021	3.2	13	

165	Genetic testing microforceps biopsy in pancreatic cysts: Systematic review and meta-analysis. <i>World Journal of Gastroenterology</i> , 2019 , 25, 3450-3467	5.6	3
164	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	3.9	10
163	Investigating the resolution of ancestry testing in geographic regions characterized by high population admixture. <i>Forensic Science International: Genetics Supplement Series</i> , 2019 , 7, 12-13	0.5	
162	Association of Leukotriene A4 Hydrolase with Tuberculosis Susceptibility Using Genomic Data in Portugal. <i>Microorganisms</i> , 2019 , 7,	4.9	3
161	Statistical methods for assessing the contagion of spatial extreme events among regions. <i>Communications in Statistics - Theory and Methods</i> , 2019 , 48, 3208-3218	0.5	1
160	Genomic and transcriptomic characterization of the mitochondrial-rich oncocytic phenotype on a thyroid carcinoma background. <i>Mitochondrion</i> , 2019 , 46, 123-133	4.9	7
159	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	4.5	7
158	Reconstructing an African haploid genome from the 18th century. <i>Nature Genetics</i> , 2018 , 50, 199-205	36.3	12
157	NIS expression in thyroid tumors, relation with prognosis clinicopathological and molecular features. <i>Endocrine Connections</i> , 2018 , 7, 78-90	3.5	35
156	The Comoros Show the Earliest Austronesian Gene Flow into the Swahili Corridor. <i>American Journal of Human Genetics</i> , 2018 , 102, 58-68	11	17
155	On the Asymptotic Locations of the Largest and Smallest Extremes of a Stationary Sequence. Journal of Theoretical Probability, 2018 , 31, 853-866	0.5	O
154	Interactions between the major bioactive polyphenols of berries: effects on antioxidant properties. <i>European Food Research and Technology</i> , 2018 , 244, 175-185	3.4	22
153	Host ancestry and dengue fever: from mapping of candidate genes to prediction of worldwide genetic risk. <i>Future Virology</i> , 2018 , 13, 647-655	2.4	2
152	CRABP1, C1QL1 and LCN2 are biomarkers of differentiated thyroid carcinoma, and predict extrathyroidal extension. <i>BMC Cancer</i> , 2018 , 18, 68	4.8	15
151	On the maxima and minima of complete and incomplete samples from nonstationary random fields. <i>Statistics and Probability Letters</i> , 2018 , 137, 124-134	0.6	2
150	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	4.8	11
149	Genetic history of the African Sahelian populations. <i>Hla</i> , 2018 , 91, 153-166	1.9	8
148	Phytochemical characterization, and evaluation of rheological and antioxidant properties of commercially available juices of berries. <i>Journal of Berry Research</i> , 2018 , 8, 11-23	2	5

(2016-2018)

147	Association of STAT4, TGFI, SH2B3 and PTPN22 polymorphisms with autoimmune hepatitis. Experimental and Molecular Pathology, 2018 , 105, 279-284	4.4	10
146	Effects of red clover on perimenopausal and postmenopausal women@ blood lipid profile: A meta-analysis. <i>Climacteric</i> , 2018 , 21, 446-453	3.1	15
145	Afadin Downregulation by Induces Epithelial to Mesenchymal Transition in Gastric Cells. <i>Frontiers in Microbiology</i> , 2018 , 9, 2712	5.7	12
144	Almost Sure Convergence for the Maximum of Nonstationary Random Fields. <i>Journal of Theoretical Probability</i> , 2017 , 30, 996-1013	0.5	4
143	Origin and spread of human mitochondrial DNA haplogroup U7. Scientific Reports, 2017, 7, 46044	4.9	15
142	TERT, BRAF, and NRAS in Primary Thyroid Cancer and Metastatic Disease. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2017 , 102, 1898-1907	5.6	77
141	Dispersals and genetic adaptation of Bantu-speaking populations in Africa and North America. <i>Science</i> , 2017 , 356, 543-546	33.3	128
140	Reconciling evidence from ancient and contemporary genomes: a major source for the European Neolithic within Mediterranean Europe. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017 , 284,	4.4	17
139	A genetic chronology for the Indian Subcontinent points to heavily sex-biased dispersals. <i>BMC Evolutionary Biology</i> , 2017 , 17, 88	3	43
138	Can Cranberries Contribute to Reduce the Incidence of Urinary Tract Infections? A Systematic Review with Meta-Analysis and Trial Sequential Analysis of Clinical Trials. <i>Journal of Urology</i> , 2017 , 198, 614-621	2.5	50
137	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	2.5	14
136	Clustering of high values in random fields. <i>Extremes</i> , 2017 , 20, 807-838	0.7	10
135	Genetic Structure of the Western and Eastern African Sahel/Savannah Belt and the Role of Nomadic Pastoralists as Inferred from the Variation of D-Loop Mitochondrial DNA Sequences. <i>Human Biology</i> , 2017 , 89, 281	1.2	8
134	OSBPL10, RXRA and lipid metabolism confer African-ancestry protection against dengue haemorrhagic fever in admixed Cubans. <i>PLoS Pathogens</i> , 2017 , 13, e1006220	7.6	41
133	GLUT1, MCT1/4 and CD147 overexpression supports the metabolic reprogramming in papillary renal cell carcinoma. <i>Histology and Histopathology</i> , 2017 , 32, 1029-1040	1.4	8
132	QmihR: Pipeline for Quantification of Microbiome in Human RNA-seq. <i>Advances in Intelligent Systems and Computing</i> , 2017 , 173-179	0.4	2
131	Genetic Structure of the Western and Eastern African Sahel/Savannah Belt and the Role of Nomadic Pastoralists as Inferred from the Variation of D-Loop Mitochondrial DNA Sequences. <i>Human Biology</i> , 2017 , 89, 281-302	1.2	0
130	Dependence matrices for spatial extreme events. <i>Communications in Statistics - Theory and Methods</i> , 2016 , 45, 6321-6341	0.5	

129	Resolving the ancestry of Austronesian-speaking populations. <i>Human Genetics</i> , 2016 , 135, 309-26	6.3	51
128	Quantifying the legacy of the Chinese Neolithic on the maternal genetic heritage of Taiwan and Island Southeast Asia. <i>Human Genetics</i> , 2016 , 135, 363-376	6.3	20
127	A Genetic Perspective on African Prehistory. Vertebrate Paleobiology and Paleoanthropology, 2016, 383	3- 403	10
126	60,000 years of interactions between Central and Eastern Africa documented by major African mitochondrial haplogroup L2. <i>Scientific Reports</i> , 2015 , 5, 12526	4.9	25
125	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, 1100-11	4.7	9
124	Extensive Admixture and Selective Pressure Across the Sahel Belt. <i>Genome Biology and Evolution</i> , 2015 , 7, 3484-95	3.9	42
123	Dependence of maxima in space. <i>Journal of Physics: Conference Series</i> , 2015 , 574, 012021	0.3	1
122	Radiocarbon Dating the Beginning of the Neolithic in Iberia: New Results, New Problems. <i>Journal of Mediterranean Archaeology</i> , 2015 , 28, 105-131	1.9	55
121	Genetic stratigraphy of key demographic events in Arabia. <i>PLoS ONE</i> , 2015 , 10, e0118625	3.7	31
120	Early Holocenic and Historic mtDNA African Signatures in the Iberian Peninsula: The Andalusian Region as a Paradigm. <i>PLoS ONE</i> , 2015 , 10, e0139784	3.7	15
119	Bacteremia due to Campylobacter in renal transplantation: a case report and review of literature. <i>Transplant Infectious Disease</i> , 2014 , 16, 1007-11	2.7	11
118	On the Multivariate Upcrossings Index. Communications in Statistics - Theory and Methods, 2014 , 43, 12	776:1529	2
117	Global human frequencies of predicted nuclear pathogenic variants and the role played by protein hydrophobicity in pathogenicity potential. <i>Scientific Reports</i> , 2014 , 4, 7155	4.9	5
116	Estimating the upcrossings index. <i>Test</i> , 2013 , 22, 549-579	1.1	1
115	A founder SDHB mutation in Portuguese paraganglioma patients. <i>Endocrine-Related Cancer</i> , 2013 , 20, L23-6	5.7	10
114	Asymptotic Location of Largest Values of a Stationary Random Field. <i>Communications in Statistics - Theory and Methods</i> , 2013 , 42, 4513-4524	0.5	3
113	The genetic impact of the lake chad basin population in North Africa as documented by mitochondrial diversity and internal variation of the L3e5 haplogroup. <i>Annals of Human Genetics</i> , 2013 , 77, 513-23	2.2	14
112	A substantial prehistoric European ancestry amongst Ashkenazi maternal lineages. <i>Nature Communications</i> , 2013 , 4, 2543	17.4	62

111	The first modern human dispersals across Africa. <i>PLoS ONE</i> , 2013 , 8, e80031	3.7	78
110	Evaluating purifying selection in the mitochondrial DNA of various mammalian species. <i>PLoS ONE</i> , 2013 , 8, e58993	3.7	33
109	On the Maximum and Minimum of a Stationary Random Field 2013 , 337-345		1
108	Point processes of exceedances by random fields. <i>Journal of Statistical Planning and Inference</i> , 2012 , 142, 773-779	0.8	7
107	Pleistocene-Holocene boundary in Southern Arabia from the perspective of human mtDNA variation. <i>American Journal of Physical Anthropology</i> , 2012 , 149, 291-8	2.5	30
106	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. <i>BMC Cancer</i> , 2012 , 12, 53	4.8	64
105	Mitochondrial DNA signals of late glacial recolonization of Europe from near eastern refugia. <i>American Journal of Human Genetics</i> , 2012 , 90, 915-24	11	123
104	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, 347-55	11	93
103	The Expansion of mtDNA Haplogroup L3 within and out of Africa. <i>Molecular Biology and Evolution</i> , 2012 , 29, 915-27	8.3	168
102	Mitochondrial genomes from modern horses reveal the major haplogroups that underwent domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 2449-54	11.5	157
101	From Networks to Trees. Advances in Intelligent and Soft Computing, 2012, 129-136		
100	Human neutral genetic variation and forensic STR data. <i>PLoS ONE</i> , 2012 , 7, e49666	3.7	41
99	Comparing phylogeny and the predicted pathogenicity of protein variations reveals equal purifying selection across the global human mtDNA diversity. <i>American Journal of Human Genetics</i> , 2011 , 88, 433-	9 ¹¹	85
98	PopAffiliator: online calculator for individual affiliation to a major population group based on 17 autosomal short tandem repeat genotype profile. <i>International Journal of Legal Medicine</i> , 2011 , 125, 629-36	3.1	36
97	Population history of the Red Seagenetic exchanges between the Arabian Peninsula and East Africa signaled in the mitochondrial DNA HV1 haplogroup. <i>American Journal of Physical Anthropology</i> , 2011 , 145, 592-8	2.5	22
96	Internal diversification of mitochondrial haplogroup R0a reveals post-last glacial maximum demographic expansions in South Arabia. <i>Molecular Biology and Evolution</i> , 2011 , 28, 71-8	8.3	45
95	Genetic structure of pastoral and farmer populations in the African Sahel. <i>Molecular Biology and Evolution</i> , 2011 , 28, 2491-500	8.3	33
94	Linking the sub-Saharan and West Eurasian gene pools: maternal and paternal heritage of the Tuareg nomads from the African Sahel. <i>European Journal of Human Genetics</i> , 2010 , 18, 915-23	5.3	39

93	The genome-wide structure of the Jewish people. <i>Nature</i> , 2010 , 466, 238-42	50.4	295
92	Predictors of uncontrolled hypertension and antihypertensive medication nonadherence. <i>Journal of Cardiovascular Disease Research (discontinued)</i> , 2010 , 1, 196-202	0.5	45
91	Icelandic population data for the STR loci in the AMPFISTR SGM Plus system and the PowerPlex Y-system. <i>Forensic Science International: Genetics</i> , 2010 , 4, e101-3	4.3	5
90	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	50
89	Population expansion in the North African late Pleistocene signalled by mitochondrial DNA haplogroup U6. <i>BMC Evolutionary Biology</i> , 2010 , 10, 390	3	48
88	Blood pressure control and antihypertensive pharmacotherapy patterns in a hypertensive population of Eastern Central Region of Portugal. <i>BMC Health Services Research</i> , 2010 , 10, 349	2.9	3
87	Clustering of upcrossings of high values. <i>Journal of Statistical Planning and Inference</i> , 2010 , 140, 1003-1	0128	2
86	On the extremal behavior of a nonstationary normal random field. <i>Journal of Statistical Planning and Inference</i> , 2010 , 140, 3567-3576	0.8	9
85	Local population structure in Arabian Peninsula revealed by Y-STR diversity. <i>Human Heredity</i> , 2009 , 68, 45-54	1.1	30
84	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, 222-6	5.6	21
83	CSA: an efficient algorithm to improve circular DNA multiple alignment. <i>BMC Bioinformatics</i> , 2009 , 10, 230	3.6	32
82	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	34
81	Out of Arabia-the settlement of island Soqotra as revealed by mitochondrial and Y chromosome genetic diversity. <i>American Journal of Physical Anthropology</i> , 2009 , 138, 439-47	2.5	35
80	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, 253-60	2.5	47
79	Near eastern neolithic genetic input in a small oasis of the Egyptian Western Desert. <i>American Journal of Physical Anthropology</i> , 2009 , 140, 336-46	2.5	31
78	The asymptotic location of the maximum of a stationary random field. <i>Statistics and Probability Letters</i> , 2009 , 79, 2166-2169	0.6	9
77	The diversity present in 5140 human mitochondrial genomes. <i>American Journal of Human Genetics</i> , 2009 , 84, 628-40	11	100
76	Response to Yao et´al <i>American Journal of Human Genetics</i> , 2009 , 85, 933	11	78

(2006-2009)

75	MtDNA GeneExtractor: a computer tool for mtDNA gene/region information extraction. <i>Mitochondrion</i> , 2009 , 9, 36-40	4.9	1
74	The dawn of human matrilineal diversity. American Journal of Human Genetics, 2008, 82, 1130-40	11	322
73	Mutation C11994T in the mitochondrial ND4 gene is not a cause of low sperm motility in Portugal. <i>Fertility and Sterility</i> , 2008 , 89, 738-41	4.8	22
72	Heterogeneity in coding mtDNA mutation rates: Implications in forensic genetics. <i>Forensic Science International: Genetics Supplement Series</i> , 2008 , 1, 274-276	0.5	1
71	mtDNA diversity in Sudan (East Africa). <i>Forensic Science International: Genetics Supplement Series</i> , 2008 , 1, 257-258	0.5	2
70	A worldwide database of autosomal markers used by the forensic community. <i>Forensic Science International: Genetics Supplement Series</i> , 2008 , 1, 656-657	0.5	4
69	A SNaPshot multiplex typing strategy for mtDNA identification of mouse inbred strains. <i>Forensic Science International: Genetics Supplement Series</i> , 2008 , 1, 596-597	0.5	
68	Evidence for variable selective pressures at a large secondary structure of the human mitochondrial DNA control region. <i>Molecular Biology and Evolution</i> , 2008 , 25, 2759-70	8.3	43
67	Counting the founders: the matrilineal genetic ancestry of the Jewish Diaspora. <i>PLoS ONE</i> , 2008 , 3, e20	063. ₇	77
66	Multidimensional outlier-proneness of dependent data and the extremal index. <i>Statistical Methodology</i> , 2008 , 5, 72-82		
65	Specificity of mtDNA-directed PCR-influence of NUclear MTDNA insertion (NUMT) contamination in routine samples and techniques. <i>International Journal of Legal Medicine</i> , 2008 , 122, 341-5	3.1	20
64	Identification of mouse inbred strains through mitochondrial DNA single-nucleotide extension. <i>Electrophoresis</i> , 2008 , 29, 4795-802	3.6	7
63	Regional differences in the distribution of the sub-Saharan, West Eurasian, and South Asian mtDNA lineages in Yemen. <i>American Journal of Physical Anthropology</i> , 2008 , 136, 128-37	2.5	47
62	How to compute the extremal index of stationary random fields. <i>Statistics and Probability Letters</i> , 2008 , 78, 1301-1304	0.6	15
61	Characterizing partial AZFc deletions of the Y chromosome with amplicon-specific sequence markers. <i>BMC Genomics</i> , 2007 , 8, 342	4.5	25
60	No evidence for an mtDNA role in sperm motility: data from complete sequencing of asthenozoospermic males. <i>Molecular Biology and Evolution</i> , 2007 , 24, 868-74	8.3	55
59	mtDNA phylogeny and evolution of laboratory mouse strains. <i>Genome Research</i> , 2007 , 17, 293-8	9.7	78
58	Usefulness of microchip electrophoresis for the analysis of mitochondrial DNA in forensic and ancient DNA studies. <i>Electrophoresis</i> , 2006 , 27, 5101-9	3.6	16

57	Islands inside an island: reproductive isolates on Jerba island. <i>American Journal of Human Biology</i> , 2006 , 18, 149-53	2.7	29
56	Genetic signatures of a Mediterranean influence in Iberian Peninsula sheep husbandry. <i>Molecular Biology and Evolution</i> , 2006 , 23, 1420-6	8.3	73
55	The matrilineal ancestry of Ashkenazi Jewry: portrait of a recent founder event. <i>American Journal of Human Genetics</i> , 2006 , 78, 487-97	11	120
54	RepeatAround: a software tool for finding and visualizing repeats in circular genomes and its application to a human mtDNA database. <i>Mitochondrion</i> , 2006 , 6, 218-24	4.9	8
53	Mitochondrial DNA pseudogenes in the nuclear genome as possible sources of contamination. <i>International Congress Series</i> , 2006 , 1288, 697-699		2
52	Sampling efficiency for Amerindian female lineages. <i>International Congress Series</i> , 2006 , 1288, 322-324		
51	Extended Northern Portuguese database on 21 autosomal STRs used in genetic identification. <i>International Congress Series</i> , 2006 , 1288, 364-366		5
50	mtDNA lineages in two Tunisian Berber communities: Comparing diversities between villages and towns. <i>International Congress Series</i> , 2006 , 1288, 121-123		5
49	Analysis of inter-specific mitochondrial DNA diversity for accurate species identification. <i>International Congress Series</i> , 2006 , 1288, 103-105		5
48	The Islamization of Iberian Peninsula: A demographic shift or a cultural change? Search for an answer using extant and ancient DNA from Mftola (Southeast Portugal). <i>International Congress Series</i> , 2006 , 1288, 828-830		2
47	Limiting crossing probabilities of random fields. Journal of Applied Probability, 2006, 43, 884-891	0.8	14
46	Evaluating the forensic informativeness of mtDNA haplogroup H sub-typing on a Eurasian scale. <i>Forensic Science International</i> , 2006 , 159, 43-50	2.6	15
45	Data for Y-chromosome haplotypes defined by 17 STRs (AmpFLSTR Yfiler) in two Tunisian Berber communities. <i>Forensic Science International</i> , 2006 , 160, 80-3	2.6	31
44	Female gene pools of Berber and Arab neighboring communities in central Tunisia: microstructure of mtDNA variation in North Africa. <i>Human Biology</i> , 2005 , 77, 61-70	1.2	42
43	African female heritage in Iberia: a reassessment of mtDNA lineage distribution in present times. <i>Human Biology</i> , 2005 , 77, 213-29	1.2	29
42	Data for 15 autosomal STR markers (Powerplex 16 System) from two Tunisian populations: Kesra (Berber) and Zriba (Arab). <i>Forensic Science International</i> , 2005 , 147, 101-6	2.6	18
41	Y-chromosomal STR haplotypes in three ethnic groups and one cosmopolitan population from Tunisia. <i>Forensic Science International</i> , 2005 , 152, 95-9	2.6	25
40	Pros and cons in the use of SNPs in forensic kinship investigation: a comparative analysis with STRs. <i>Forensic Science International</i> , 2005 , 150, 17-21	2.6	101

(2003-2005)

39	The mtDNA catalogue of all Portuguese autochthonous goat (Capra hircus) breeds: high diversity of female lineages at the western fringe of European distribution. <i>Molecular Ecology</i> , 2005 , 14, 2313-8	5.7	50
38	Human mtDNA haplogroups and reduced male fertility: real association or hidden population substructuring. <i>Journal of Developmental and Physical Disabilities</i> , 2005 , 28, 241-7		29
37	mtDNA single macrodeletions associated with myopathies: absence of haplogroup-related increased risk. <i>Journal of Inherited Metabolic Disease</i> , 2005 , 28, 769-78	5.4	3
36	MtDNA diversity among four Portuguese autochthonous dog breeds: a fine-scale characterisation. <i>BMC Genetics</i> , 2005 , 6, 37	2.6	20
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34	High-resolution mtDNA evidence for the late-glacial resettlement of Europe from an Iberian refugium. <i>Genome Research</i> , 2005 , 15, 19-24	9.7	121
33	Predicting sampling saturation of mtDNA haplotypes: an application to an enlarged Portuguese database. <i>International Journal of Legal Medicine</i> , 2004 , 118, 132-6	3.1	57
32	Pattern of mtDNA variation in three populations from SB Tomle Prlicipe. <i>Annals of Human Genetics</i> , 2004 , 68, 40-54	2.2	29
31	Standardisation of nomenclature for dog mtDNA D-loop: a prerequisite for launching a Canis familiaris database. <i>Forensic Science International</i> , 2004 , 141, 99-108	2.6	50
30	GATA C4 allele 17 as a marker for sub-Saharan origin of Y-chromosome lineages. <i>International Congress Series</i> , 2004 , 1261, 281-283		
29	Genotyping inconsistencies and null alleles using AmpFLSTR[] Identifiler[] and Powerplex[] 16 kits. <i>International Congress Series</i> , 2004 , 1261, 176-178		2
28	Subdividing mtDNA haplogroup H based on coding-region polymorphisms study in Iberia. <i>International Congress Series</i> , 2004 , 1261, 416-418		4
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22	Differential slave trade to Europe and Brazil from the western and eastern African coasts as registered in the mtDNA pool. <i>International Congress Series</i> , 2003 , 1239, 49-52		

21	Phylogeny of the mtDNA haplogroup U6. Analysis of the sequences observed in North Africa and Iberia. <i>International Congress Series</i> , 2003 , 1239, 491-493		2
20	An evaluation of the proportion of identical Y-STR haplotypes due to recurrent mutation. <i>International Congress Series</i> , 2003 , 1239, 57-60		2
19	Multiplex STR genotyping: comparison study, population data and new sequence information. <i>International Congress Series</i> , 2003 , 1239, 131-135		8
18	Mitochondrial portrait of the Cabo Verde archipelago: the Senegambian outpost of Atlantic slave trade. <i>Annals of Human Genetics</i> , 2002 , 66, 49-60	2.2	55
17	Bantu and European Y-lineages in Sub-Saharan Africa. <i>Annals of Human Genetics</i> , 2002 , 66, 369-378	2.2	42
16	Mismatch distribution analysis of Y-STR haplotypes as a tool for the evaluation of identity-by-state proportions and significance of matchesthe European picture. <i>Forensic Science International</i> , 2002 , 130, 147-55	2.6	11
15	The asymptotic locations of the maximum and minimum of stationary sequences. <i>Journal of Statistical Planning and Inference</i> , 2002 , 104, 287-295	0.8	7
14	Results of the 1999-2000 collaborative exercise and proficiency testing program on mitochondrial DNA of the GEP-ISFG: an inter-laboratory study of the observed variability in the heteroplasmy level of hair from the same donor. <i>Forensic Science International</i> , 2002 , 125, 1-7	2.6	41
13	VWA STR genotyping: further inconsistencies between Perkin-Elmer and Promega kits. <i>International Journal of Legal Medicine</i> , 2001 , 115, 97-9	3.1	23
12	Limit distribution for point processes of high local maxima. <i>Journal of Statistical Planning and Inference</i> , 2001 , 97, 227-233	0.8	2
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10	Prehistoric and historic traces in the mtDNA of Mozambique: insights into the Bantu expansions and the slave trade. <i>Annals of Human Genetics</i> , 2001 , 65, 439-458	2.2	148
9	Phylogeography of the human mitochondrial haplogroup L3e: a snapshot of African prehistory and Atlantic slave trade. <i>Annals of Human Genetics</i> , 2001 , 65, 549-563	2.2	72
8	Y-chromosome mismatch distributions in Europe. <i>Molecular Biology and Evolution</i> , 2001 , 18, 1259-71	8.3	24
7	Prehistoric and historic traces in the mtDNA of Mozambique: insights into the Bantu expansions and the slave trade. <i>Annals of Human Genetics</i> , 2001 , 65, 439-58	2.2	45
6	Diversity of mtDNA lineages in Portugal: not a genetic edge of European variation. <i>Annals of Human Genetics</i> , 2000 , 64, 491-506	2.2	103
5	Y-chromosomal diversity in Europe is clinal and influenced primarily by geography, rather than by language. <i>American Journal of Human Genetics</i> , 2000 , 67, 1526-43	11	471
4	Clinal variation of YAP+ Y-chromosome frequencies in Western Iberia. <i>Human Biology</i> , 2000 , 72, 937-44	1.2	9

LIST OF PUBLICATIONS

3	Detection of additional structural variation at the FES/FPS system and population data from S. Tomle Prlicipe and North Portugal. <i>International Journal of Legal Medicine</i> , 1999 , 112, 204-6	3.1	1
2	Failed PCR amplifications of MBP-STR alleles due to polymorphism in the primer annealing region. <i>International Journal of Legal Medicine</i> , 1996 , 108, 313-5	3.1	25
1	A methodology for unsupervised clustering using iterative pruning to capture fine-scale structure		2