Francesc Calafell

List of Publications by Year
in descending order

218 papers	10,209 citations	23565 58 h-index	46795 89 g-index
227 all docs	227 docs citations	227 times ranked	9608 citing authors

#	Article	IF	Citations
1	Trading Genes along the Silk Road: mtDNA Sequences and the Origin of Central Asian Populations. American Journal of Human Genetics, 1998, 63, 1824-1838.	6.2	295
2	Statistical Power Analysis of Neutrality Tests Under Demographic Expansions, Contractions and Bottlenecks With Recombination. Genetics, 2008, 179, 555-567.	2.9	242
3	High-Resolution Analysis of Human Y-Chromosome Variation Shows a Sharp Discontinuity and Limited Gene Flow between Northwestern Africa and the Iberian Peninsula. American Journal of Human Genetics, 2001, 68, 1019-1029.	6.2	234
4	A Natural History of FUT2 Polymorphism in Humans. Molecular Biology and Evolution, 2009, 26, 1993-2003.	8.9	209
5	A Global Haplotype Analysis of the Myotonic Dystrophy Locus: Implications for the Evolution of Modern Humans and for the Origin of Myotonic Dystrophy Mutations. American Journal of Human Genetics, 1998, 62, 1389-1402.	6.2	197
6	Geographic Patterns of mtDNA Diversity in Europe. American Journal of Human Genetics, 2000, 66, 262-278.	6.2	194
7	Human mitochondrial DNA variation and the origin of Basques. Annals of Human Genetics, 1995, 59, 63-81.	0.8	191
8	Origins and Divergence of the Roma (Gypsies). American Journal of Human Genetics, 2001, 69, 1314-1331.	6.2	188
9	Gene mapping in Gypsies identifies a novel demyelinating neuropathy on chromosome 8q24. Nature Genetics, 1996, 14, 214-217.	21.4	185
10	Potential Transmission of Human Polyomaviruses through the Gastrointestinal Tract after Exposure to Virions or Viral DNA. Journal of Virology, 2001, 75, 10290-10299.	3.4	175
11	The Genetic Legacy of Religious Diversity and Intolerance: Paternal Lineages of Christians, Jews, and Muslims in the Iberian Peninsula. American Journal of Human Genetics, 2008, 83, 725-736.	6.2	174
12	Balancing Selection Is the Main Force Shaping the Evolution of Innate Immunity Genes. Journal of Immunology, 2008, 181, 1315-1322.	0.8	173
13	Admixture, migrations, and dispersals in Central Asia: evidence from maternal DNA lineages. European Journal of Human Genetics, 2004, 12, 495-504.	2.8	145
14	Short tandem repeat polymorphism evolution in humans. European Journal of Human Genetics, 1998, 6, 38-49.	2.8	142
15	On the Origins and Admixture of Malagasy: New Evidence from High-Resolution Analyses of Paternal and Maternal Lineages. Molecular Biology and Evolution, 2009, 26, 2109-2124.	8.9	142
16	From Asia to Europe: mitochondrial DNA sequence variability in Bulgarians and Turks. Annals of Human Genetics, 1996, 60, 35-49.	0.8	141
17	Neandertal Evolutionary Genetics: Mitochondrial DNA Data from the Iberian Peninsula. Molecular Biology and Evolution, 2005, 22, 1077-1081.	8.9	139
18	Mutation rates at Y chromosome specific microsatellites. Human Mutation, 2005, 26, 520-528.	2.5	133

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19	Geographic variation in human mitochondrial DNA control region sequence: the population history of Turkey and its relationship to the European populations. Molecular Biology and Evolution, 1996, 13, 1067-1077.	8.9	128
20	Genetic studies of the Roma (Gypsies): a review. BMC Medical Genetics, 2001, 2, 5.	2.1	126
21	Alu insertion polymorphisms in NW Africa and the Iberian Peninsula: evidence for a strong genetic boundary through the Gibraltar Straits. Human Genetics, 2000, 107, 312-319.	3.8	124
22	Joining the Pillars of Hercules: mtDNA Sequences Show Multidirectional Gene Flow in the Western Mediterranean. Annals of Human Genetics, 2003, 67, 312-328.	0.8	123
23	Sex-Specific Migration Patterns in Central Asian Populations, Revealed by Analysis of Y-Chromosome Short Tandem Repeats and mtDNA. American Journal of Human Genetics, 1999, 65, 208-219.	6.2	119
24	Microsatellite variation and the differentiation of modern humans. Human Genetics, 1996, 99, 1-7.	3.8	115
25	Genetic and Demographic Implications of the Bantu Expansion: Insights from Human Paternal Lineages. Molecular Biology and Evolution, 2009, 26, 1581-1589.	8.9	114
26	Principal component analysis of gene frequencies and the origin of Basques. American Journal of Physical Anthropology, 1994, 93, 201-215.	2.1	105
27	Variation in Short Tandem Repeats Is Deeply Structured by Genetic Background on the Human Y Chromosome. American Journal of Human Genetics, 1999, 65, 1623-1638.	6.2	105
28	Insights into the Demographic History of African Pygmies from Complete Mitochondrial Genomes. Molecular Biology and Evolution, 2011, 28, 1099-1110.	8.9	105
29	Population genetics of a functional variant of the dopamine Î²-hydroxylase gene (DBH). American Journal of Medical Genetics Part A, 1997, 74, 374-379.	2.4	104
30	Genetic structure of north-west Africa revealed by STR analysis. European Journal of Human Genetics, 2000, 8, 360-366.	2.8	104
31	Genetic origin, admixture, and asymmetry in maternal and paternal human lineages in Cuba. BMC Evolutionary Biology, 2008, 8, 213.	3.2	101
32	Sequence diversity of the control region of mitochondrial DNA in Tuscany and its implications for the peopling of Europe. , 1996, 100, 443-460.		97
33	Paternal and maternal lineages in the Balkans show a homogeneous landscape over linguistic barriers, except for the isolated Aromuns. Annals of Human Genetics, 2006, 70, 459-487.	0.8	97
34	High resolution Y chromosome typing: 19 STRs amplified in three multiplex reactions. Forensic Science International, 2002, 125, 42-51.	2.2	93
35	A Recent Shift from Polygyny to Monogamy in Humans Is Suggested by the Analysis of Worldwide Y-Chromosome Diversity. Journal of Molecular Evolution, 2003, 57, 85-97.	1.8	90
36	Mitochondrial DNA reveals a strong phylogeographic structure in the badger across Eurasia. Molecular Ecology, 2006, 15, 1007-1020.	3.9	89

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37	Evolutionary dynamics of the human ABO gene. Human Genetics, 2008, 124, 123-135.	3.8	85
38	Mitochondrial DNA Heterogeneity in Tunisian Berbers. Annals of Human Genetics, 2004, 68, 222-233.	0.8	83
39	Extreme population differences across Neuregulin 1 gene, with implications for association studies. Molecular Psychiatry, 2006, 11, 66-75.	7.9	83
40	Population Genetics of Y-Chromosome Short Tandem Repeats in Humans. Journal of Molecular Evolution, 1997, 45, 265-270.	1.8	82
41	The portability of tagSNPs across populations: A worldwide survey. Genome Research, 2006, 16, 323-330.	5.5	82
42	Association of the CTLA4 promoter region (â^'1661G allele) with type 1 diabetes in the South Moroccan population. Genes and Immunity, 2003, 4, 132-137.	4.1	81
43	A highly divergent mtDNA sequence in a Neandertal individual from Italy. Current Biology, 2006, 16, R630-R632.	3.9	80
44	HLA class I and class II DNA typing and the origin of Basques. Tissue Antigens, 1998, 51, 30-40.	1.0	76
45	Human mitochondrial DNA sequence variation in the Moroccan population of the Souss area. Annals of Human Biology, 2001, 28, 295-307.	1.0	76
46	Micro-Phylogeographic and Demographic History of Portuguese Male Lineages. Annals of Human Genetics, 2006, 70, 181-194.	0.8	76
47	MtDNA from extinct Tainos and the peopling of the Caribbean. Annals of Human Genetics, 2001, 65, 137-151.	0.8	75
48	The Analysis of Variation of mtDNA Hypervariable Region 1 Suggests That Eastern and Western Pygmies Diverged before the Bantu Expansion. American Naturalist, 2004, 163, 212-226.	2.1	73
49	Population history of north Africa: evidence from classical genetic markers. Human Biology, 1997, 69, 295-311.	0.2	71
50	Insights into the western Bantu dispersal: mtDNA lineage analysis in Angola. Human Genetics, 2004, 115, 439-47.	3.8	70
51	The Y chromosome as the most popular marker in genetic genealogy benefits interdisciplinary research. Human Genetics, 2017, 136, 559-573.	3.8	69
52	Mitochondrial DNA from preâ€€Columbian Ciboneys from Cuba and the prehistoric colonization of the Caribbean. American Journal of Physical Anthropology, 2003, 121, 97-108.	2.1	68
53	Mitochondrial DNA of an Iberian Neandertal suggests a population affinity with other European Neandertals. Current Biology, 2006, 16, R629-R630.	3.9	68
54	Patterns of inter- and intra-group genetic diversity in the Vlax Roma as revealed by Y chromosome and mitochondrial DNA lineages. European Journal of Human Genetics, 2001, 9, 97-104.	2.8	67

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55	High level of male-biased Scandinavian admixture in Greenlandic Inuit shown by Y-chromosomal analysis. Human Genetics, 2003, 112, 353-363.	3.8	66
56	Asian Origin for the Worldwide-Spread Mutational Event in Machado-Joseph Disease. Archives of Neurology, 2007, 64, 1502.	4.5	65
57	Combined epigenetic and intraspecific variation of theDRD4andSERTgenes influence novelty seeking behavior in great titParus major. Epigenetics, 2015, 10, 516-525.	2.7	65
58	Mitochondrial DNA variation and the origin of the Europeans. Human Genetics, 1997, 99, 443-449.	3.8	61
59	SNP analysis to results (SNPator): a web-based environment oriented to statistical genomics analyses upon SNP data. Bioinformatics, 2008, 24, 1643-1644.	4.1	61
60	Reconstructing the Indian Origin and Dispersal of the European Roma: A Maternal Genetic Perspective. PLoS ONE, 2011, 6, e15988.	2.5	61
61	Georgian and Kurd mtDNA sequence analysis shows a lack of correlation between languages and female genetic lineages. , 2000, 112, 5-16.		60
62	Identification of a Novel Founder Mutation in the DYSF Gene Causing Clinical Variability in the Spanish Population. Archives of Neurology, 2005, 62, 1256.	4.5	57
63	The Genetics of the Pre-Roman Iberian Peninsula: A mtDNA Study of Ancient Iberians. Annals of Human Genetics, 2005, 69, 535-548.	0.8	56
64	Phylogeography of the human mitochondrial L1c haplogroup: Genetic signatures of the prehistory of Central Africa. Molecular Phylogenetics and Evolution, 2007, 43, 635-644.	2.7	56
65	Worldwide Genetic Analysis of the CFTR Region. American Journal of Human Genetics, 2001, 68, 103-117.	6.2	55
66	Effectiveness of hand hygiene and provision of information in preventing influenza cases requiring hospitalization. Preventive Medicine, 2012, 54, 434-439.	3.4	52
67	Evolution of the O alleles of the human ABO blood group gene. Transfusion, 2004, 44, 707-715.	1.6	49
68	Allele Frequencies for 20 Microsatellites in a Worldwide Population Survey. Human Heredity, 1997, 47, 189-196.	0.8	47
69	A tale of two islands: population history and mitochondrial DNA sequence variation of Bioko and SÃ£o TomÃ©, Gulf of Guinea. Annals of Human Genetics, 1997, 61, 507-518.	0.8	45
70	Sequence Variability of a Human Pseudogene. Genome Research, 2001, 11, 1071-1085.	5.5	45
71	A Perspective on the History of the Iberian Gypsies Provided by Phylogeographic Analysis of Yâ€Chromosome Lineages. Annals of Human Genetics, 2008, 72, 215-227.	0.8	45
72	Mendelian genes for Parkinson's disease contribute to the sporadic forms of the diseaseâ€. Human Molecular Genetics, 2015, 24, 2023-2034.	2.9	45

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73	Prion susceptibility and protective alleles exhibit marked geographic differences. Human Mutation, 2003, 22, 104-105.	2.5	43
74	Brief communication: mtDNA variation in North Cameroon: Lack of asian lineages and implications for back migration from Asia to subâ€Saharan Africa. American Journal of Physical Anthropology, 2005, 128, 678-681.	2.1	43
75	A genome-wide survey does not show the genetic distinctiveness of Basques. Human Genetics, 2010, 127, 455-458.	3.8	43
76	Allele frequencies of 13 short tandem repeats in population samples from the Iberian Peninsula and Northern Africa. International Journal of Legal Medicine, 2000, 113, 208-214.	2.2	42
77	The west side story:MEFVhaplotype in Spanish FMF patients and controls, and evidence of high LD and a recombination â€œhot-spotâ€•at theMEFVlocus. Human Mutation, 2004, 23, 399-399.	2.5	42
78	Y-chromosome diversity in Catalan surname samples: insights into surname origin and frequency. European Journal of Human Genetics, 2015, 23, 1549-1557.	2.8	42
79	Fragmentation of Contaminant and Endogenous DNA in Ancient Samples Determined by Shotgun Sequencing; Prospects for Human Palaeogenomics. PLoS ONE, 2011, 6, e24161.	2.5	42
80	Spatial patterns of cystic fibrosis mutation spectra in European populations. European Journal of Human Genetics, 2003, 11, 385-394.	2.8	41
81	Linguistic and maternal genetic diversity are not correlated in Native Mexicans. Human Genetics, 2009, 126, 521-531.	3.8	40
82	Mitochondrial DNA structure in North Africa reveals a genetic discontinuity in the Nile Valley. American Journal of Physical Anthropology, 2011, 145, 107-117.	2.1	40
83	A tale of two islands: population history and mitochondrial DNA sequence variation of Bioko and SÃ£o TomÃ©, Gulf of Guinea. Annals of Human Genetics, 1997, 61, 507-518.	0.8	40
84	Association study between Alzheimer?s disease and genes involved in A? biosynthesis, aggregation and degradation: suggestive results with BACE1. Journal of Neurology, 2003, 250, 956-961.	3.6	39
85	Sequence Variability of a Human Pseudogene. Genome Research, 2001, 11, 1071-1085.	5.5	39
86	Can a Place of Origin of the Main Cystic Fibrosis Mutations Be Identified?. American Journal of Human Genetics, 2002, 70, 257-264.	6.2	37
87	Allelic and genotypic associations of DRD2 TaqI A polymorphism with heroin dependence in Spanish subjects: a case control study. Behavioral and Brain Functions, 2007, 3, 25.	3.3	37
88	Consistency of metagenomic assignment programs in simulated and real data. BMC Bioinformatics, 2014, 15, 90.	2.6	37
89	Alu insertion polymorphisms in the Balkans and the origins of the Aromuns. Annals of Human Genetics, 2004, 68, 120-127.	0.8	35
90	A genomic analysis identifies a novel component in the genetic structure of sub-Saharan African populations. European Journal of Human Genetics, 2011, 19, 84-88.	2.8	35

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91	High mitochondrial sequence diversity in linguistic isolates of the Alps. American Journal of Human Genetics, 1996, 59, 1363-75.	6.2	34
92	Y chromosome STR haplotypes in four populations from northwest Africa. International Journal of Legal Medicine, 2000, 114, 36-40.	2.2	33
93	Comparative Genetics of Functional Trinucleotide Tandem Repeats in Humans and Apes. Journal of Molecular Evolution, 2004, 59, 329-339.	1.8	33
94	Genetic Heterogeneity in Algerian Human Populations. PLoS ONE, 2015, 10, e0138453.	2.5	33
95	A multistep mutation mechanism drives the evolution of the CAG repeat at MJD/SCA3 locus. European Journal of Human Genetics, 2006, 14, 932-940.	2.8	31
96	Recombination Gives a New Insight in the Effective Population Size and the History of the Old World Human Populations. Molecular Biology and Evolution, 2012, 29, 25-30.	8.9	31
97	Dynamics of CAG repeat loci revealed by the analysis of their variability. Human Mutation, 2003, 21, 61-70.	2.5	30
98	The prion protein gene in humans revisited: Lessons from a worldwide resequencing study. Genome Research, 2005, 16, 231-239.	5.5	29
99	Sequence variation and genetic evolution at the human F12 locus: mapping quantitative trait nucleotides that influence FXII plasma levels. Human Molecular Genetics, 2010, 19, 517-525.	2.9	28
100	Length and repeat-sequence variation in 58 STRs and 94 SNPs in two Spanish populations. Forensic Science International: Genetics, 2017, 30, 66-70.	3.1	28
101	European Roma groups show complex West Eurasian admixture footprints and a common South Asian genetic origin. PLoS Genetics, 2019, 15, e1008417.	3.5	28
102	Do Basque- and Caucasian- Speaking Populations Share Non-Indo-European Ancestors?. European Journal of Human Genetics, 1995, 3, 256-263.	2.8	28
103	mtDNA hypervariable region II (HVII) sequences in human evolution studies. European Journal of Human Genetics, 2000, 8, 964-974.	2.8	27
104	Blood Biochemistry Reflects Seasonal Nutritional and Reproductive Constraints in the Eurasian Badger (Meles meles). Physiological and Biochemical Zoology, 2001, 74, 450-460.	1.5	27
105	Haplotype Evolution and Linkage Disequilibrium: A Simulation Study. Human Heredity, 2001, 51, 85-96.	0.8	27
106	Estimating the Ancestral Recombinations Graph (ARG) as Compatible Networks of SNP Patterns. Journal of Computational Biology, 2008, 15, 1133-1153.	1.6	27
107	Recent human evolution has shaped geographical differences in susceptibility to disease. BMC Genomics, 2011, 12, 55.	2.8	27
108	Analysis of the R1b-DF27 haplogroup shows that a large fraction of Iberian Y-chromosome lineages originated recently in situ. Scientific Reports, 2017, 7, 7341.	3.3	27

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109	Genetic and Geographical Variability in Cystic Fibrosis: Evolutionary Considerations. Novartis Foundation Symposium, 1996, 197, 97-118.	1.1	27
110	Signatures of Selection in the Human Olfactory Receptor OR5I1 Gene. Molecular Biology and Evolution, 2007, 25, 144-154.	8.9	26
111	Yâ€chromosome diversity in Native Mexicans reveals continental transition of genetic structure in the Americas. American Journal of Physical Anthropology, 2012, 148, 395-405.	2.1	26
112	Signatures of Evolutionary Adaptation in Quantitative Trait Loci Influencing Trace Element Homeostasis in Liver. Molecular Biology and Evolution, 2016, 33, 738-754.	8.9	26
113	Genetic history of cystic fibrosis mutations in Italy. I. Regional distribution. Annals of Human Genetics, 1997, 61, 411-424.	0.8	26
114	Classifying humans. Nature Genetics, 2003, 33, 435-436.	21.4	25
115	Joint analysis of candidate genes related to Alzheimer's disease in a Spanish population. Psychiatric Genetics, 2003, 13, 85-90.	1.1	25
116	People from Ibiza: an unexpected isolate in the Western Mediterranean. European Journal of Human Genetics, 2019, 27, 941-951.	2.8	25
117	Cisâ€acting factors promoting the CAG intergenerational instability in Machadoâ€“Joseph disease. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 439-446.	1.7	24
118	Whole Y-chromosome sequences reveal an extremely recent origin of the most common North African paternal lineage E-M183 (M81). Scientific Reports, 2017, 7, 15941.	3.3	24
119	Ancient DNA of Phoenician remains indicates discontinuity in the settlement history of Ibiza. Scientific Reports, 2018, 8, 17567.	3.3	24
120	Cystic fibrosis mutations and associated haplotypes in Bulgaria - a comparative population genetic study. Human Genetics, 1997, 99, 513-520.	3.8	23
121	Extreme individual marker FST values do not imply population-specific selection in humans: the NRG1 example. Human Genetics, 2007, 121, 759-762.	3.8	23
122	Genetic adaptation of the antibacterial human innate immunity network. BMC Evolutionary Biology, 2011, 11, 202.	3.2	23
123	Surname and Y chromosome in Southern Europe: a case study with Colom/Colombo. European Journal of Human Genetics, 2012, 20, 211-216.	2.8	23
124	MtDNA from extinct Tainos and the peopling of the Caribbean. Annals of Human Genetics, 2001, 65, 137-51.	0.8	23
125	No Major Host Genetic Risk Factor Contributed to A(H1N1)2009 Influenza Severity. PLoS ONE, 2015, 10, e0135983.	2.5	22
126	HLA evidence for the lack of genetic heterogeneity in Basques. Annals of Human Genetics, 1998, 62, 123-132.	0.8	21

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127	TNFA-TNFB haplotypes modify susceptibility to type I diabetes mellitus independently of HLA class II in a Moroccan population. Tissue Antigens, 2003, 61, 72-79.	1.0	21
128	Haplotype tagging efficiency in worldwide populations in CTLA4 gene. Genes and Immunity, 2005, 6, 646-657.	4.1	21
129	Recent Radiation of R-M269 and High Y-STR Haplotype Resemblance Confirmed. Annals of Human Genetics, 2014, 78, 253-254.	0.8	21
130	An assessment of a massively parallel sequencing approach for the identification of individuals from mass graves of the Spanish Civil War (1936â€“1939). Electrophoresis, 2016, 37, 2841-2847.	2.4	21
131	The probability distribution of the number of loci indicating exclusion in a core set of STR markers. International Journal of Legal Medicine, 2000, 114, 61-65.	2.2	20
132	Interrogating 11 Fast-Evolving Genes for Signatures of Recent Positive Selection in Worldwide Human Populations. Molecular Biology and Evolution, 2009, 26, 2285-2297.	8.9	20
133	Population history of Corsica: a linguistic and genetic analysis. Annals of Human Biology, 1996, 23, 237-251.	1.0	19
134	Recent Insertion of an Alu Element Within a Polymorphic Human-Specific Alu Insertion. Molecular Biology and Evolution, 2001, 18, 85-88.	8.9	19
135	Decay of linkage disequilibrium within genes across HGDP-CEPH human samples: most population isolates do not show increased LD. BMC Genomics, 2009, 10, 338.	2.8	19
136	The Genetic History of the Iberian Peninsula: A Simulation. Current Anthropology, 1993, 34, 735-745.	1.6	19
137	A New Method for Extracting Skin Microbes Allows Metagenomic Analysis of Whole-Deep Skin. PLoS ONE, 2013, 8, e74914.	2.5	19
138	Mountains and genes: population history of the Pyrenees. Human Biology, 1994, 66, 823-42.	0.2	19
139	Assessing the signatures of selection in PRNP from polymorphism data: results support Kreitman and Di Rienzo's opinion. Trends in Genetics, 2005, 21, 389-391.	6.7	18
140	Similarity in Recombination Rate Estimates Highly Correlates with Genetic Differentiation in Humans. PLoS ONE, 2011, 6, e17913.	2.5	18
141	Y-chromosomal sequences of diverse Indian populations and the ancestry of the Andamanese. Human Genetics, 2017, 136, 499-510.	3.8	18
142	Deletion pattern in the dystrophin gene in Turks and a comparison with Europeans and Indians. Annals of Human Genetics, 2000, 64, 33-40.	0.8	17
143	Isolated populations as treasure troves in genetic epidemiology: the case of the Basques. European Journal of Human Genetics, 2009, 17, 1490-1494.	2.8	17
144	STR data for 21 loci in northwestern Africa. Forensic Science International, 2001, 116, 41-51.	2.2	16

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145	PKLR-GBA region shows almost complete linkage disequilibrium over 70Âkb in a set of worldwide populations. Human Genetics, 2002, 110, 532-544.	3.8	16
146	Understanding the dynamics of Spinocerebellar Ataxia 8 (SCA8) locus through a comparative genetic approach in humans and apes. Neuroscience Letters, 2003, 336, 143-146.	2.1	16
147	Search for genetic association between IgA nephropathy and candidate genes selected by function or by gene mapping at loci IGAN2 and IGAN3. Nephrology Dialysis Transplantation, 2012, 27, 2328-2337.	0.7	16
148	The genetic landscape of Mediterranean North African populations through complete mtDNA sequences. Annals of Human Biology, 2018, 45, 98-104.	1.0	16
149	Recent Common Origin, Reduced Population Size, and Marked Admixture Have Shaped European Roma Genomes. Molecular Biology and Evolution, 2020, 37, 3175-3187.	8.9	16
150	Basic glossary on genetic epidemiology. Journal of Epidemiology and Community Health, 2003, 57, 480-482.	3.7	15
151	A Common Haplotype Associated with the Basque 2362AG-TCATCT Mutation in the Muscular Calpain-3 Gene. Human Biology, 2004, 76, 731-741.	0.2	15
152	The Mediterranean Paradox for Susceptibility Factors in Coronary Heart Disease Extends to Genetics. Annals of Human Genetics, 2007, 72, 070807042352002-???.	0.8	15
153	A New Method to Reconstruct Recombination Events at a Genomic Scale. PLoS Computational Biology, 2010, 6, e1001010.	3.2	14
154	IRiS: Construction of ARG networks at genomic scales. Bioinformatics, 2011, 27, 2448-2450.	4.1	14
155	Characterization of the Iberian Y chromosome haplogroup R-DF27 in Northern Spain. Forensic Science International: Genetics, 2017, 27, 142-148.	3.1	14
156	The Counteracting Effects of Demography on Functional Genomic Variation: The Roma Paradigm. Molecular Biology and Evolution, 2021, 38, 2804-2817.	8.9	14
157	Genealogy reconstruction from short tandem repeat genotypes in an Amazonian population. , 1999, 108, 137-146.		13
158	Allele Frequencies in a Worldwide Survey of a CA Repeat in the First Intron of the CFTR Gene. Human Heredity, 1999, 49, 15-20.	0.8	13
159	Geographic stratification of linkage disequilibrium: a worldwide population study in a region of chromosome 22. Human Genomics, 2004, 1, 399.	2.9	13
160	Genetic analysis of the presumptive blood from Louis XVI, king of France. Forensic Science International: Genetics, 2011, 5, 459-463.	3.1	13
161	Staphylococcus prevails in the skin microbiota of longâ€term immunodeficient mice. Environmental Microbiology, 2012, 14, 2087-2098.	3.8	13
162	Genetic comparison of the head of Henri IV and the presumptive blood from Louis XVI (both Kings of) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.2	13

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163	Patterns of genetic structure and adaptive positive selection in the Lithuanian population from high-density SNP data. Scientific Reports, 2019, 9, 9163.	3.3	13
164	Reconstruction of Prehistory on the Basis of Genetic Data. American Journal of Human Genetics, 2000, 66, 1177-1179.	6.2	12
165	Basic molecular genetics for epidemiologists. Journal of Epidemiology and Community Health, 2003, 57, 398-400.	3.7	12
166	Microsatellite Variation and Evolutionary History of PCDHX/Y Gene Pair Within the Xq21.3/Yp11.2 Hominid-Specific Homology Block. Molecular Biology and Evolution, 2004, 21, 2092-2101.	8.9	12
167	Human F7 sequence is split into three deep clades that are related to FVII plasma levels. Human Genetics, 2006, 118, 741-751.	3.8	12
168	Human pseudogenes of the ABO family show a complex evolutionary dynamics and loss of function. Glycobiology, 2009, 19, 583-591.	2.5	12
169	Minimizing recombinations in consensus networks for phylogeographic studies. BMC Bioinformatics, 2009, 10, S72.	2.6	12
170	Direct Sequencing from the Minimal Number of DNA Molecules Needed to Fill a 454 Picotiterplate. PLoS ONE, 2014, 9, e97379.	2.5	12
171	Structure of Linkage Disequilibrium in Humans: Genome Factors and Population Stratification. Cold Spring Harbor Symposia on Quantitative Biology, 2003, 68, 79-88.	1.1	12
172	Admixture and sexual bias in the population settlement of La RÃ©union Island (Indian Ocean). American Journal of Physical Anthropology, 2008, 136, 100-107.	2.1	11
173	Y-Chromosome Analysis in Individuals Bearing the Basarab Name of the First Dynasty of Wallachian Kings. PLoS ONE, 2012, 7, e41803.	2.5	11
174	Genetic origins, singularity, and heterogeneity of Basques. Current Biology, 2021, 31, 2167-2177.e4.	3.9	11
175	Allele frequencies of markers LDLR, GYPA, D7S8, HBGG, GC, HLA-DQA1 and D1S80 in the general and minority populations of Costa Rica. Forensic Science International, 2001, 124, 1-4.	2.2	10
176	An evolutionary approach to the medical implications of the tumor necrosis factor receptor superfamily member 13B (TNFRSF13B) gene. Genes and Immunity, 2009, 10, 566-578.	4.1	10
177	Deletion pattern in the dystrophin gene in Turks and a comparison with Europeans and Indians. Annals of Human Genetics, 2000, 64, 33-40.	0.8	10
178	Profiles of accepted mutation: from neutrality in a pseudogene to disease-causing mutation on its homologous gene. Human Genetics, 2001, 109, 7-10.	3.8	9
179	FABSIM: a software for generating F ST distributions with various ascertainment biases. Bioinformatics, 2008, 24, 2790-2791.	4.1	9
180	Detection of major genes underlying several quantitative traits associated with a common disease using different ascertainment schemes. Genetic Epidemiology, 1997, 14, 809-814.	1.3	8

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181	Second GHEP-ISFG exercise for DVI: â€œDNA-ledâ€•victimsâ€™ identification in a simulated air crash. Forensic Science International: Genetics, 2021, 53, 102527.	3.1	8
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