Francesc Calafell

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.

214 8,603 56 83 g-index

227 9,415 5 5.41 ext. papers ext. citations avg, IF L-index

#	Paper	IF	Citations
214	A forensic population database in El Salvador: 58 STRs and 94 SNPs. <i>Forensic Science International: Genetics</i> , 2021 , 57, 102646	4.3	O
213	Whole-exome analysis in Tunisian Imazighen and Arabs shows the impact of demography in functional variation. <i>Scientific Reports</i> , 2021 , 11, 21125	4.9	1
212	The Counteracting Effects of Demography on Functional Genomic Variation: The Roma Paradigm. <i>Molecular Biology and Evolution</i> , 2021 , 38, 2804-2817	8.3	4
211	Genetic origins, singularity, and heterogeneity of Basques. <i>Current Biology</i> , 2021 , 31, 2167-2177.e4	6.3	5
210	Admixture Has Shaped Romani Genetic Diversity in Clinically Relevant Variants. <i>Frontiers in Genetics</i> , 2021 , 12, 683880	4.5	3
209	Autosomal genetics and Y-chromosome haplogroup L1b-M317 reveal Mount Lebanon Maronites as a persistently non-emigrating population. <i>European Journal of Human Genetics</i> , 2021 , 29, 581-592	5.3	
208	Second GHEP-ISFG exercise for DVI: "DNA-led" victimsPidentification in a simulated air crash. <i>Forensic Science International: Genetics</i> , 2021 , 53, 102527	4.3	1
207	The Y Chromosome. <i>Evolutionary Studies</i> , 2021 , 121-136	2.5	
206	Recent Common Origin, Reduced Population Size, and Marked Admixture Have Shaped European Roma Genomes. <i>Molecular Biology and Evolution</i> , 2020 , 37, 3175-3187	8.3	4
205	The place of metropolitan France in the European genomic landscape. <i>Human Genetics</i> , 2020 , 139, 1091	-6.305	О
204	Sex-biased patterns shaped the genetic history of Roma. <i>Scientific Reports</i> , 2020 , 10, 14464	4.9	3
203	European Roma groups show complex West Eurasian admixture footprints and a common South Asian genetic origin. <i>PLoS Genetics</i> , 2019 , 15, e1008417	6	15
202	Patterns of genetic structure and adaptive positive selection in the Lithuanian population from high-density SNP data. <i>Scientific Reports</i> , 2019 , 9, 9163	4.9	5
201	The Parallel Lives of Human Y Chromosome Lineages Across the Strait of Gibraltar 2019 , 217-231		
200	People from Ibiza: an unexpected isolate in the Western Mediterranean. <i>European Journal of Human Genetics</i> , 2019 , 27, 941-951	5-3	12
199	The genetic landscape of Mediterranean North African populations through complete mtDNA sequences. <i>Annals of Human Biology</i> , 2018 , 45, 98-104	1.7	10
198	The black legend on the Spanish presence in the low countries: Verifying shared beliefs on genetic ancestry. <i>American Journal of Physical Anthropology</i> , 2018 , 166, 219-227	2.5	4

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197	Sequence diversity of the Rh blood group system in Basques. <i>European Journal of Human Genetics</i> , 2018 , 26, 1859-1866	5.3	4	
196	Ancient DNA of Phoenician remains indicates discontinuity in the settlement history of Ibiza. <i>Scientific Reports</i> , 2018 , 8, 17567	4.9	14	
195	Y-chromosomal sequences of diverse Indian populations and the ancestry of the Andamanese. <i>Human Genetics</i> , 2017 , 136, 499-510	6.3	11	
194	Length and repeat-sequence variation in 58 STRs and 94 SNPs in two Spanish populations. <i>Forensic Science International: Genetics</i> , 2017 , 30, 66-70	4.3	17	
193	Satisfaction With Methadone and Opioid Receptor Genes Polymorphisms in Treatment-Refractory Heroin-Dependent Patients. <i>Journal of Clinical Psychopharmacology</i> , 2017 , 37, 378-380	1.7	2	
192	Characterization of the Iberian Y chromosome haplogroup R-DF27 in Northern Spain. <i>Forensic Science International: Genetics</i> , 2017 , 27, 142-148	4.3	13	
191	Analysis of the R1b-DF27 haplogroup shows that a large fraction of Iberian Y-chromosome lineages originated recently in situ. <i>Scientific Reports</i> , 2017 , 7, 7341	4.9	21	
190	Whole Y-chromosome sequences reveal an extremely recent origin of the most common North African paternal lineage E-M183 (M81). <i>Scientific Reports</i> , 2017 , 7, 15941	4.9	15	
189	The Y chromosome as the most popular marker in genetic genealogy benefits interdisciplinary research. <i>Human Genetics</i> , 2017 , 136, 559-573	6.3	48	
188	The unexpected co-occurrence of GRN and MAPT p.A152T in Basque families: Clinical and pathological characteristics. <i>PLoS ONE</i> , 2017 , 12, e0178093	3.7	5	
187	Signatures of Evolutionary Adaptation in Quantitative Trait Loci Influencing Trace Element Homeostasis in Liver. <i>Molecular Biology and Evolution</i> , 2016 , 33, 738-54	8.3	16	
186	An assessment of a massively parallel sequencing approach for the identification of individuals from mass graves of the Spanish Civil War (1936-1939). <i>Electrophoresis</i> , 2016 , 37, 2841-2847	3.6	16	
185	Combined epigenetic and intraspecific variation of the DRD4 and SERT genes influence novelty seeking behavior in great tit Parus major. <i>Epigenetics</i> , 2015 , 10, 516-25	5.7	50	
184	No Major Host Genetic Risk Factor Contributed to A(H1N1)2009 Influenza Severity. <i>PLoS ONE</i> , 2015 , 10, e0135983	3.7	12	
183	Genetic Heterogeneity in Algerian Human Populations. <i>PLoS ONE</i> , 2015 , 10, e0138453	3.7	26	
182	Y-chromosome diversity in Catalan surname samples: insights into surname origin and frequency. <i>European Journal of Human Genetics</i> , 2015 , 23, 1549-57	5.3	34	
181	Mendelian genes for Parkinson® disease contribute to the sporadic forms of the disease. <i>Human Molecular Genetics</i> , 2015 , 24, 2023-34	5.6	20	
180	Recent radiation of R-M269 and high Y-STR haplotype resemblance confirmed. <i>Annals of Human Genetics</i> , 2014 , 78, 253-4	2.2	19	

179	Consistency of metagenomic assignment programs in simulated and real data. <i>BMC Bioinformatics</i> , 2014 , 15, 90	3.6	14
178	Predictive factors of severe multilobar pneumonia and shock in patients with influenza. <i>Emergency Medicine Journal</i> , 2014 , 31, 301-7	1.5	3
177	Direct squencing from the minimal number of DNA molecules needed to fill a 454 picotiterplate. <i>PLoS ONE</i> , 2014 , 9, e97379	3.7	10
176	Genetic comparison of the head of Henri IV and the presumptive blood from Louis XVI (both Kings of France). <i>Forensic Science International</i> , 2013 , 226, 38-40	2.6	12
175	A new method for extracting skin microbes allows metagenomic analysis of whole-deep skin. <i>PLoS ONE</i> , 2013 , 8, e74914	3.7	16
174	Effectiveness of hand hygiene and provision of information in preventing influenza cases requiring hospitalization. <i>Preventive Medicine</i> , 2012 , 54, 434-9	4.3	38
173	Staphylococcus prevails in the skin microbiota of long-term immunodeficient mice. <i>Environmental Microbiology</i> , 2012 , 14, 2087-98	5.2	12
172	Recombination gives a new insight in the effective population size and the history of the old world human populations. <i>Molecular Biology and Evolution</i> , 2012 , 29, 25-30	8.3	24
171	Y-chromosome analysis in individuals bearing the Basarab name of the first dynasty of Wallachian kings. <i>PLoS ONE</i> , 2012 , 7, e41803	3.7	9
170	Y-chromosome diversity in Native Mexicans reveals continental transition of genetic structure in the Americas. <i>American Journal of Physical Anthropology</i> , 2012 , 148, 395-405	2.5	19
169	Recombination networks as genetic markers in a human variation study of the Old World. <i>Human Genetics</i> , 2012 , 131, 601-13	6.3	7
168	Surname and Y chromosome in Southern Europe: a case study with Colom/Colombo. <i>European Journal of Human Genetics</i> , 2012 , 20, 211-6	5.3	18
167	Search for genetic association between IgA nephropathy and candidate genes selected by function or by gene mapping at loci IGAN2 and IGAN3. <i>Nephrology Dialysis Transplantation</i> , 2012 , 27, 2328-37	4.3	15
166	Genetic analysis of the presumptive blood from Louis XVI, King of France. <i>Forensic Science International: Genetics</i> , 2011 , 5, 459-63	4.3	12
165	Similarity in recombination rate estimates highly correlates with genetic differentiation in humans. <i>PLoS ONE</i> , 2011 , 6, e17913	3.7	13
164	A genomic analysis identifies a novel component in the genetic structure of sub-Saharan African populations. <i>European Journal of Human Genetics</i> , 2011 , 19, 84-8	5.3	29
163	Genetic adaptation of the antibacterial human innate immunity network. <i>BMC Evolutionary Biology</i> , 2011 , 11, 202	3	20
162	Recent human evolution has shaped geographical differences in susceptibility to disease. <i>BMC Genomics</i> , 2011 , 12, 55	4.5	22

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161	Mitochondrial DNA structure in North Africa reveals a genetic discontinuity in the Nile Valley. <i>American Journal of Physical Anthropology</i> , 2011 , 145, 107-17	2.5	34
160	IRiS: construction of ARG networks at genomic scales. <i>Bioinformatics</i> , 2011 , 27, 2448-50	7.2	13
159	Insights into the demographic history of African Pygmies from complete mitochondrial genomes. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1099-110	8.3	83
158	Reconstructing the Indian origin and dispersal of the European Roma: a maternal genetic perspective. <i>PLoS ONE</i> , 2011 , 6, e15988	3.7	53
157	Fragmentation of contaminant and endogenous DNA in ancient samples determined by shotgun sequencing; prospects for human palaeogenomics. <i>PLoS ONE</i> , 2011 , 6, e24161	3.7	38
156	Sequence variation and genetic evolution at the human F12 locus: mapping quantitative trait nucleotides that influence FXII plasma levels. <i>Human Molecular Genetics</i> , 2010 , 19, 517-25	5.6	24
155	A new method to reconstruct recombination events at a genomic scale. <i>PLoS Computational Biology</i> , 2010 , 6, e1001010	5	13
154	A genome-wide survey does not show the genetic distinctiveness of Basques. <i>Human Genetics</i> , 2010 , 127, 455-8	6.3	40
153	African signatures of recent positive selection in human FOXI1. BMC Evolutionary Biology, 2010, 10, 267	7 3	3
152	Human pseudogenes of the ABO family show a complex evolutionary dynamics and loss of function. <i>Glycobiology</i> , 2009 , 19, 583-91	5.8	12
151	Interrogating 11 fast-evolving genes for signatures of recent positive selection in worldwide human populations. <i>Molecular Biology and Evolution</i> , 2009 , 26, 2285-97	8.3	20
150	A natural history of FUT2 polymorphism in humans. <i>Molecular Biology and Evolution</i> , 2009 , 26, 1993-200	D3 8.3	169
149	Genetic and demographic implications of the Bantu expansion: insights from human paternal lineages. <i>Molecular Biology and Evolution</i> , 2009 , 26, 1581-9	8.3	93
148	On the origins and admixture of Malagasy: new evidence from high-resolution analyses of paternal and maternal lineages. <i>Molecular Biology and Evolution</i> , 2009 , 26, 2109-24	8.3	112
147	Minimizing recombinations in consensus networks for phylogeographic studies. <i>BMC Bioinformatics</i> , 2009 , 10 Suppl 1, S72	3.6	11
146	Decay of linkage disequilibrium within genes across HGDP-CEPH human samples: most population isolates do not show increased LD. <i>BMC Genomics</i> , 2009 , 10, 338	4.5	16
145	Linguistic and maternal genetic diversity are not correlated in Native Mexicans. <i>Human Genetics</i> , 2009 , 126, 521-31	6.3	35
144	Isolated populations as treasure troves in genetic epidemiology: the case of the Basques. <i>European Journal of Human Genetics</i> , 2009 , 17, 1490-4	5.3	16

143	An evolutionary approach to the medical implications of the tumor necrosis factor receptor superfamily member 13B (TNFRSF13B) gene. <i>Genes and Immunity</i> , 2009 , 10, 566-78	4.4	8
142	A perspective on the history of the Iberian gypsies provided by phylogeographic analysis of Y-chromosome lineages. <i>Annals of Human Genetics</i> , 2008 , 72, 215-27	2.2	39
141	Genetic origin, admixture, and asymmetry in maternal and paternal human lineages in Cuba. <i>BMC Evolutionary Biology</i> , 2008 , 8, 213	3	84
140	Statistical power analysis of neutrality tests under demographic expansions, contractions and bottlenecks with recombination. <i>Genetics</i> , 2008 , 179, 555-67	4	208
139	FABSIM: a software for generating FST distributions with various ascertainment biases. <i>Bioinformatics</i> , 2008 , 24, 2790-1	7.2	8
138	Potential Transmission of Human Polyomaviruses through the Gastrointestinal Tract after Exposure to Virions or Viral DNA. <i>Journal of Virology</i> , 2008 , 82, 8244-8244	6.6	78
137	Balancing selection is the main force shaping the evolution of innate immunity genes. <i>Journal of Immunology</i> , 2008 , 181, 1315-22	5.3	150
136	SNP analysis to results (SNPator): a web-based environment oriented to statistical genomics analyses upon SNP data. <i>Bioinformatics</i> , 2008 , 24, 1643-4	7.2	57
135	Estimating the ancestral recombinations graph (ARG) as compatible networks of SNP patterns. Journal of Computational Biology, 2008 , 15, 1133-54	1.7	19
134	The Mediterranean paradox for susceptibility factors in coronary heart disease extends to genetics. <i>Annals of Human Genetics</i> , 2008 , 72, 48-56	2.2	11
133	Evolutionary dynamics of the human ABO gene. <i>Human Genetics</i> , 2008 , 124, 123-35	6.3	75
132	Cis-acting factors promoting the CAG intergenerational instability in Machado-Joseph disease. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2008 , 147B, 439-46	3.5	18
131	Admixture and sexual bias in the population settlement of La Rūnion Island (Indian Ocean). <i>American Journal of Physical Anthropology</i> , 2008 , 136, 100-7	2.5	9
130	The genetic legacy of religious diversity and intolerance: paternal lineages of Christians, Jews, and Muslims in the Iberian Peninsula. <i>American Journal of Human Genetics</i> , 2008 , 83, 725-36	11	151
129	Signatures of selection in the human olfactory receptor OR5I1 gene. <i>Molecular Biology and Evolution</i> , 2008 , 25, 144-54	8.3	24
128	Phylogeography of the human mitochondrial L1c haplogroup: genetic signatures of the prehistory of Central Africa. <i>Molecular Phylogenetics and Evolution</i> , 2007 , 43, 635-44	4.1	43
127	Allelic and genotypic associations of DRD2 TaqI A polymorphism with heroin dependence in Spanish subjects: a case control study. <i>Behavioral and Brain Functions</i> , 2007 , 3, 25	4.1	31
126	Extreme individual marker F(ST)values do not imply population-specific selection in humans: the NRG1 example. <i>Human Genetics</i> , 2007 , 121, 759-62	6.3	20

125	Asian origin for the worldwide-spread mutational event in Machado-Joseph disease. <i>Archives of Neurology</i> , 2007 , 64, 1502-8		50	
124	A highly divergent mtDNA sequence in a Neandertal individual from Italy. <i>Current Biology</i> , 2006 , 16, R63	G -3	71	
123	Mitochondrial DNA of an Iberian Neandertal suggests a population affinity with other European Neandertals. <i>Current Biology</i> , 2006 , 16, R629-30	6.3	63	
122	The portability of tagSNPs across populations: a worldwide survey. <i>Genome Research</i> , 2006 , 16, 323-30	9.7	72	
121	The genetics of pre-Roman Iberian Peninsula: A mtDNA study of ancient Iberians. <i>International Congress Series</i> , 2006 , 1288, 142-144		1	
120	Paternal and maternal lineages in the Balkans show a homogeneous landscape over linguistic barriers, except for the isolated Aromuns. <i>Annals of Human Genetics</i> , 2006 , 70, 459-87	2.2	86	
119	Micro-phylogeographic and demographic history of Portuguese male lineages. <i>Annals of Human Genetics</i> , 2006 , 70, 181-94	2.2	73	
118	Mitochondrial DNA reveals a strong phylogeographic structure in the badger across Eurasia. <i>Molecular Ecology</i> , 2006 , 15, 1007-20	5.7	83	
117	A multistep mutation mechanism drives the evolution of the CAG repeat at MJD/SCA3 locus. <i>European Journal of Human Genetics</i> , 2006 , 14, 932-40	5.3	24	
116	Extreme population differences across Neuregulin 1 gene, with implications for association studies. <i>Molecular Psychiatry</i> , 2006 , 11, 66-75	15.1	79	
115	Human F7 sequence is split into three deep clades that are related to FVII plasma levels. <i>Human Genetics</i> , 2006 , 118, 741-51	6.3	12	
114	The prion protein gene in humans revisited: lessons from a worldwide resequencing study. <i>Genome Research</i> , 2006 , 16, 231-9	9.7	27	
113	Paternal and maternal lineages in the Balkans show a homogeneous landscape over linguistic barriers, except for the isolated Aromuns. <i>Annals of Human Genetics</i> , 2006 , 060721082338047	2.2	1	
112	The genetics of the pre-Roman Iberian Peninsula: a mtDNA study of ancient Iberians. <i>Annals of Human Genetics</i> , 2005 , 69, 535-48	2.2	36	
111	Haplotype tagging efficiency in worldwide populations in CTLA4 gene. <i>Genes and Immunity</i> , 2005 , 6, 646	5 - 44	21	
110	Assessing the signatures of selection in PRNP from polymorphism data: results support Kreitman and Di Rienzoß opinion. <i>Trends in Genetics</i> , 2005 , 21, 389-91	8.5	18	
109	Mutation rates at Y chromosome specific microsatellites. <i>Human Mutation</i> , 2005 , 26, 520-8	4.7	123	
108	Brief communication: mtDNA variation in North Cameroon: lack of Asian lineages and implications for back migration from Asia to sub-Saharan Africa. <i>American Journal of Physical Anthropology</i> , 2005 , 128, 678-81	2.5	39	

107	Neandertal evolutionary genetics: mitochondrial DNA data from the iberian peninsula. <i>Molecular Biology and Evolution</i> , 2005 , 22, 1077-81	8.3	98
106	Identification of a novel founder mutation in the DYSF gene causing clinical variability in the Spanish population. <i>Archives of Neurology</i> , 2005 , 62, 1256-9		49
105	A common haplotype associated with the Basque 2362AG> TCATCT mutation in the muscular calpain-3 gene. <i>Human Biology</i> , 2004 , 76, 731-41	1.2	13
104	Microsatellite variation and evolutionary history of PCDHX/Y gene pair within the Xq21.3/Yp11.2 hominid-specific homology block. <i>Molecular Biology and Evolution</i> , 2004 , 21, 2092-101	8.3	9
103	The analysis of variation of mtDNA hypervariable region 1 suggests that Eastern and Western Pygmies diverged before the Bantu expansion. <i>American Naturalist</i> , 2004 , 163, 212-26	3.7	66
102	Evolution of the O alleles of the human ABO blood group gene. <i>Transfusion</i> , 2004 , 44, 707-15	2.9	42
101	Admixture, migrations, and dispersals in Central Asia: evidence from maternal DNA lineages. <i>European Journal of Human Genetics</i> , 2004 , 12, 495-504	5.3	125
100	Insights into the western Bantu dispersal: mtDNA lineage analysis in Angola. <i>Human Genetics</i> , 2004 , 115, 439-47	6.3	60
99	Comparative genetics of functional trinucleotide tandem repeats in humans and apes. <i>Journal of Molecular Evolution</i> , 2004 , 59, 329-39	3.1	26
98	Alu insertion polymorphisms in the Balkans and the origins of the Aromuns. <i>Annals of Human Genetics</i> , 2004 , 68, 120-7	2.2	30
97	Mitochondrial DNA heterogeneity in Tunisian Berbers. Annals of Human Genetics, 2004, 68, 222-33	2.2	77
96	The west side story: MEFV haplotype in Spanish FMF patients and controls, and evidence of high LD and a recombination "hot-spot" at the MEFV locus. <i>Human Mutation</i> , 2004 , 23, 399	4.7	29
95	Evidence for mutational cis-acting factors affecting mutagenesis in the ornithine transcarbamylase gene. <i>Human Mutation</i> , 2004 , 24, 273	4.7	4
94	Variation of the prion gene in chimpanzees and its implication for prion diseases. <i>Neuroscience Letters</i> , 2004 , 355, 157-60	3.3	6
93	Geographic stratification of linkage disequilibrium: a worldwide population study in a region of chromosome 22. <i>Human Genomics</i> , 2004 , 1, 399-409	6.8	11
92	Advanced glossary on genetic epidemiology. <i>Journal of Epidemiology and Community Health</i> , 2003 , 57, 562-4	5.1	5
91	. Psychiatric Genetics, 2003 , 13, 85-90	2.9	1
90	Joint analysis of candidate genes related to Alzheimerß disease in a Spanish population. <i>Psychiatric Genetics</i> , 2003 , 13, 85-90	2.9	22

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89	A recent shift from polygyny to monogamy in humans is suggested by the analysis of worldwide Y-chromosome diversity. <i>Journal of Molecular Evolution</i> , 2003 , 57, 85-97	3.1	74
88	Association study between Alzheimerß disease and genes involved in Abeta biosynthesis, aggregation and degradation: suggestive results with BACE1. <i>Journal of Neurology</i> , 2003 , 250, 956-61	5.5	38
87	High level of male-biased Scandinavian admixture in Greenlandic Inuit shown by Y-chromosomal analysis. <i>Human Genetics</i> , 2003 , 112, 353-63	6.3	57
86	Dynamics of CAG repeat loci revealed by the analysis of their variability. <i>Human Mutation</i> , 2003 , 21, 61-7	7 4 .7	21
85	Prion susceptibility and protective alleles exhibit marked geographic differences. <i>Human Mutation</i> , 2003 , 22, 104-5	4.7	34
84	Mitochondrial DNA from pre-Columbian Ciboneys from Cuba and the prehistoric colonization of the Caribbean. <i>American Journal of Physical Anthropology</i> , 2003 , 121, 97-108	2.5	57
83	TNFA-TNFB haplotypes modify susceptibility to type I diabetes mellitus independently of HLA class II in a Moroccan population. <i>Tissue Antigens</i> , 2003 , 61, 72-9		21
82	Joining the pillars of Hercules: mtDNA sequences show multidirectional gene flow in the western Mediterranean. <i>Annals of Human Genetics</i> , 2003 , 67, 312-28	2.2	114
81	Spatial patterns of cystic fibrosis mutation spectra in European populations. <i>European Journal of Human Genetics</i> , 2003 , 11, 385-94	5.3	36
8o	Association of the CTLA4 promoter region (-1661G allele) with type 1 diabetes in the South Moroccan population. <i>Genes and Immunity</i> , 2003 , 4, 132-7	4.4	73
79	Understanding the dynamics of Spinocerebellar Ataxia 8 (SCA8) locus through a comparative genetic approach in humans and apes. <i>Neuroscience Letters</i> , 2003 , 336, 143-6	3.3	14
78	Basic glossary on genetic epidemiology. <i>Journal of Epidemiology and Community Health</i> , 2003 , 57, 480-2	5.1	11
77	Basic molecular genetics for epidemiologists. <i>Journal of Epidemiology and Community Health</i> , 2003 , 57, 398-400	5.1	10
76	Structure of linkage disequilibrium in humans: genome factors and population stratification. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2003 , 68, 79-88	3.9	11
75	PKLR- GBA region shows almost complete linkage disequilibrium over 70 kb in a set of worldwide populations. <i>Human Genetics</i> , 2002 , 110, 532-44	6.3	16
74	Haplotype analysis and phylogeny of ornithine transcarbamylase polymorphisms. <i>Annals of Human Genetics</i> , 2002 , 66, 379-85	2.2	5
73	High resolution Y chromosome typing: 19 STRs amplified in three multiplex reactions. <i>Forensic Science International</i> , 2002 , 125, 42-51	2.6	86
72	Why names. <i>Genome Research</i> , 2002 , 12, 219-21	9.7	5

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70	Can a place of origin of the main cystic fibrosis mutations be identified?. <i>American Journal of Human Genetics</i> , 2002 , 70, 257-64	11	33
69	Sequence Variability of a Human Pseudogene. <i>Genome Research</i> , 2001 , 11, 1071-1085	9.7	41
68	Recent insertion of an Alu element within a polymorphic human-specific Alu insertion. <i>Molecular Biology and Evolution</i> , 2001 , 18, 85-8	8.3	15
67	Allele frequencies of markers LDLR, GYPA, D7S8, HBGG, GC, HLA-DQA1 and D1S80 in the general and minority populations of Costa Rica. <i>Forensic Science International</i> , 2001 , 124, 1-4	2.6	8
66	Genetic studies of the Roma (Gypsies): a review. <i>BMC Medical Genetics</i> , 2001 , 2, 5	2.1	100
65	MtDNA from extinct Tainos and the peopling of the Caribbean. <i>Annals of Human Genetics</i> , 2001 , 65, 137	7- <u>15</u> 1	64
64	Profiles of accepted mutation: from neutrality in a pseudogene to disease-causing mutation on its homologous gene. <i>Human Genetics</i> , 2001 , 109, 7-10	6.3	6
63	STR data for 21 loci in northwestern Africa. Forensic Science International, 2001, 116, 41-51	2.6	15
62	Patterns of inter- and intra-group genetic diversity in the Vlax Roma as revealed by Y chromosome and mitochondrial DNA lineages. <i>European Journal of Human Genetics</i> , 2001 , 9, 97-104	5.3	56
61	Blood biochemistry reflects seasonal nutritional and reproductive constraints in the eurasian badger (Meles meles). <i>Physiological and Biochemical Zoology</i> , 2001 , 74, 450-60	2	24
60	Haplotype evolution and linkage disequilibrium: A simulation study. <i>Human Heredity</i> , 2001 , 51, 85-96	1.1	26
59	Human mitochondrial DNA sequence variation in the Moroccan population of the Souss area. <i>Annals of Human Biology</i> , 2001 , 28, 295-307	1.7	68
58	Worldwide genetic analysis of the CFTR region. American Journal of Human Genetics, 2001 , 68, 103-17	11	45
57	High-resolution analysis of human Y-chromosome variation shows a sharp discontinuity and limited gene flow between northwestern Africa and the Iberian Peninsula. <i>American Journal of Human Genetics</i> , 2001 , 68, 1019-29	11	204
56	Origins and divergence of the Roma (gypsies). American Journal of Human Genetics, 2001 , 69, 1314-31	11	156
55	Potential transmission of human polyomaviruses through the gastrointestinal tract after exposure to virions or viral DNA. <i>Journal of Virology</i> , 2001 , 75, 10290-9	6.6	156
54	Sequence variability of a human pseudogene. <i>Genome Research</i> , 2001 , 11, 1071-85	9.7	24

53	Nicaraguan population data on LDLR, GYPA, D7S8, HBGG, GC and HLA-DQA1 loci. <i>Revista De Biologia Tropical</i> , 2001 , 49, 1253-60	1.3	3
52	MtDNA from extinct Tainos and the peopling of the Caribbean. <i>Annals of Human Genetics</i> , 2001 , 65, 13	7-5.½	18
51	Georgian and kurd mtDNA sequence analysis shows a lack of correlation between languages and female genetic lineages. <i>American Journal of Physical Anthropology</i> , 2000 , 112, 5-16	2.5	34
50	Deletion pattern in the dystrophin gene in Turks and a comparison with Europeans and Indians. <i>Annals of Human Genetics</i> , 2000 , 64, 33-40	2.2	15
49	Genetic structure of north-west Africa revealed by STR analysis. <i>European Journal of Human Genetics</i> , 2000 , 8, 360-6	5.3	90
48	mtDNA hypervariable region II (HVII) sequences in human evolution studies. <i>European Journal of Human Genetics</i> , 2000 , 8, 964-74	5.3	23
47	Alu insertion polymorphisms in NW Africa and the Iberian Peninsula: evidence for a strong genetic boundary through the Gibraltar Straits. <i>Human Genetics</i> , 2000 , 107, 312-9	6.3	115
46	Genetic distances and microsatellite diversification in humans. <i>Human Genetics</i> , 2000 , 106, 133-134	6.3	4
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