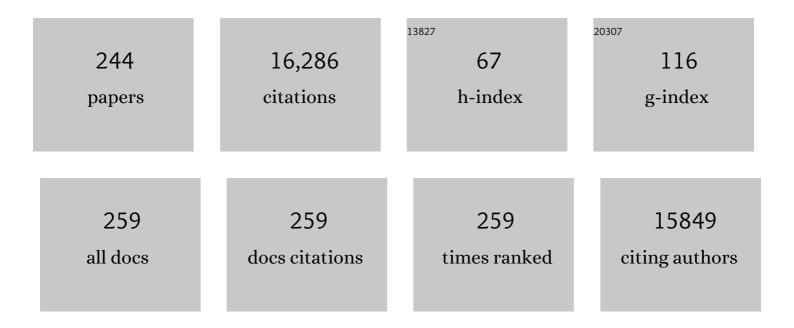
## Jaume Bertranpetit

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Y chromosome sequence variation and the history of human populations. Nature Genetics, 2000, 26, 358-361.	9.4	935
2	Great ape genetic diversity and population history. Nature, 2013, 499, 471-475.	13.7	768
3	Y-Chromosomal Diversity in Europe Is Clinal and Influenced Primarily by Geography, Rather than by Language. American Journal of Human Genetics, 2000, 67, 1526-1543.	2.6	519
4	The Derived FOXP2 Variant of Modern Humans Was Shared with Neandertals. Current Biology, 2007, 17, 1908-1912.	1.8	487
5	Correlation between Genetic and Geographic Structure in Europe. Current Biology, 2008, 18, 1241-1248.	1.8	449
6	The Dawn of Human Matrilineal Diversity. American Journal of Human Genetics, 2008, 82, 1130-1140.	2.6	392
7	Evidence for a genetic discontinuity between Neandertals and 24,000-year-old anatomically modern Europeans. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 6593-6597.	3.3	324
8	The origin of the major cystic fibrosis mutation (ΔF508) in European populations. Nature Genetics, 1994, 7, 169-175.	9.4	323
9	Trading Genes along the Silk Road: mtDNA Sequences and the Origin of Central Asian Populations. American Journal of Human Genetics, 1998, 63, 1824-1838.	2.6	295
10	Genomic Ancestry of North Africans Supports Back-to-Africa Migrations. PLoS Genetics, 2012, 8, e1002397.	1.5	275
11	The origin of European cattle: Evidence from modern and ancient DNA. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 8113-8118.	3.3	271
12	A Melanocortin 1 Receptor Allele Suggests Varying Pigmentation Among Neanderthals. Science, 2007, 318, 1453-1455.	6.0	264
13	A Global Perspective on Genetic Variation at the ADH Genes Reveals Unusual Patterns of Linkage Disequilibrium and Diversity. American Journal of Human Genetics, 2002, 71, 84-99.	2.6	261
14	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.	2.6	234
15	A Natural History of FUT2 Polymorphism in Humans. Molecular Biology and Evolution, 2009, 26, 1993-2003.	3.5	209
16	Genetic diversity in the Iberian Peninsula determined from mitochondrial sequence analysis. Annals of Human Genetics, 1996, 60, 331-350.	0.3	195
17	Geographic Patterns of mtDNA Diversity in Europe. American Journal of Human Genetics, 2000, 66, 262-278.	2.6	194
18	Morphometric, Behavioral, and Genomic Evidence for a New Orangutan Species. Current Biology, 2017, 27, 3487-3498.e10.	1.8	192

#	Article	IF	CITATIONS
19	Human mitochondrial DNA variation and the origin of Basques. Annals of Human Genetics, 1995, 59, 63-81.	0.3	191
20	Gene flow from North Africa contributes to differential human genetic diversity in southern Europe. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11791-11796.	3.3	174
21	Minisatellite diversity supports a recent African origin for modern humans. Nature Genetics, 1996, 13, 154-160.	9.4	173
22	Balancing Selection Is the Main Force Shaping the Evolution of Innate Immunity Genes. Journal of Immunology, 2008, 181, 1315-1322.	0.4	173
23	Genomic Affinities of Two 7,000-Year-Old Iberian Hunter-Gatherers. Current Biology, 2012, 22, 1494-1499.	1.8	160
24	Admixture, migrations, and dispersals in Central Asia: evidence from maternal DNA lineages. European Journal of Human Genetics, 2004, 12, 495-504.	1.4	145
25	1000 Genomes Selection Browser 1.0: a genome browser dedicated to signatures of natural selection in modern humans. Nucleic Acids Research, 2014, 42, D903-D909.	6.5	143
26	mtDNA analysis of the Galician population: a genetic edge of European variation. European Journal of Human Genetics, 1998, 6, 365-375.	1.4	141
27	Nucleotide substitution rates for the full set of mitochondrial protein-coding genes in Coleoptera. Molecular Phylogenetics and Evolution, 2010, 56, 796-807.	1.2	141
28	Neandertal Evolutionary Genetics: Mitochondrial DNA Data from the Iberian Peninsula. Molecular Biology and Evolution, 2005, 22, 1077-1081.	3.5	139
29	Nuclear Gene Indicates Coat-Color Polymorphism in Mammoths. Science, 2006, 313, 62-62.	6.0	135
30	Recent Male-Mediated Gene Flow over a Linguistic Barrier in Iberia, Suggested by Analysis of a Y-Chromosomal DNA Polymorphism. American Journal of Human Genetics, 1999, 65, 1437-1448.	2.6	132
31	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.	3.5	128
32	Identifying Genetic Traces of Historical Expansions: Phoenician Footprints in the Mediterranean. American Journal of Human Genetics, 2008, 83, 633-642.	2.6	127
33	Genomic analysis of Andamanese provides insights into ancient human migration into Asia and adaptation. Nature Genetics, 2016, 48, 1066-1070.	9.4	126
34	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.	1.8	124
35	Joining the Pillars of Hercules: mtDNA Sequences Show Multidirectional Gene Flow in the Western Mediterranean. Annals of Human Genetics, 2003, 67, 312-328.	0.3	123
36	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.	2.6	119

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37	Microsatellite variation and the differentiation of modern humans. Human Genetics, 1996, 99, 1-7.	1.8	115
38	Y-Chromosomal Diversity in Lebanon Is Structured by Recent Historical Events. American Journal of Human Genetics, 2008, 82, 873-882.	2.6	106
39	Principal component analysis of gene frequencies and the origin of Basques. American Journal of Physical Anthropology, 1994, 93, 201-215.	2.1	105
40	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.	2.6	105
41	Tracking down Human Contamination in Ancient Human Teeth. Molecular Biology and Evolution, 2006, 23, 1801-1807.	3.5	105
42	Genetic structure of north-west Africa revealed by STR analysis. European Journal of Human Genetics, 2000, 8, 360-366.	1.4	104
43	Unravelling migrations in the steppe: mitochondrial DNA sequences from ancient Central Asians. Proceedings of the Royal Society B: Biological Sciences, 2004, 271, 941-947.	1.2	100
44	A genetic reconstruction of the history of the population of the Iberian Peninsula. Annals of Human Genetics, 1991, 55, 51-67.	0.3	99
45	Reproductive rates in families of schizophrenic patients in a caseâ€control study. Acta Psychiatrica Scandinavica, 1995, 91, 202-204.	2.2	98
46	Microsatellite haplotypes for cystic fibrosis: mutation frameworks and evolutionary tracers. Human Molecular Genetics, 1993, 2, 1015-1022.	1.4	97
47	Sequence diversity of the control region of mitochondrial DNA in Tuscany and its implications for the peopling of Europe. , 1996, 100, 443-460.		97
48	Microsatellites provide evidence for Y chromosome diversity among the founders of the New World. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 6312-6317.	3.3	97
49	Approximate Bayesian computation with deep learning supports a third archaic introgression in Asia and Oceania. Nature Communications, 2019, 10, 246.	5.8	97
50	Comparative analysis of cancer genes in the human and chimpanzee genomes. BMC Genomics, 2006, 7, 15.	1.2	94
51	Palaeogenetic evidence supports a dual model of Neolithic spreading into Europe. Proceedings of the Royal Society B: Biological Sciences, 2007, 274, 2161-2167.	1.2	93
52	Variability in the serotonin transporter gene and increased risk for major depression with melancholia. Human Genetics, 1998, 103, 319-322.	1.8	92
53	Convergent evolution in European and Rroma populations reveals pressure exerted by plague on Toll-like receptors. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2668-2673.	3.3	88
54	Evolutionary dynamics of the human ABO gene. Human Genetics, 2008, 124, 123-135.	1.8	85

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55	Hierarchical boosting: a machine-learning framework to detect and classify hard selective sweeps in human populations. Bioinformatics, 2015, 31, 3946-3952.	1.8	85
56	Variation in G+C-content and codon choice: differences among synonymous codon groups in vertebrate genes. Nucleic Acids Research, 1989, 17, 6181-6189.	6.5	84
57	Serotonin Transporter Gene and Risk for Bipolar Affective Disorder: An Association Study in a Spanish Population. Biological Psychiatry, 1998, 43, 843-847.	0.7	84
58	Extreme population differences across Neuregulin 1 gene, with implications for association studies. Molecular Psychiatry, 2006, 11, 66-75.	4.1	83
59	Population Genetics of Y-Chromosome Short Tandem Repeats in Humans. Journal of Molecular Evolution, 1997, 45, 265-270.	0.8	82
60	The portability of tagSNPs across populations: A worldwide survey. Genome Research, 2006, 16, 323-330.	2.4	82
61	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.	2.2	81
62	A highly divergent mtDNA sequence in a Neandertal individual from Italy. Current Biology, 2006, 16, R630-R632.	1.8	80
63	Genome-Wide Diversity in the Levant Reveals Recent Structuring by Culture. PLoS Genetics, 2013, 9, e1003316.	1.5	77
64	HLA class I and class II DNA typing and the origin of Basques. Tissue Antigens, 1998, 51, 30-40.	1.0	76
65	Human mitochondrial DNA sequence variation in the Moroccan population of the Souss area. Annals of Human Biology, 2001, 28, 295-307.	0.4	76
66	MtDNA from extinct Tainos and the peopling of the Caribbean. Annals of Human Genetics, 2001, 65, 137-151.	0.3	75
67	Extreme selective sweeps independently targeted the X chromosomes of the great apes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6413-6418.	3.3	75
68	Heteroplasmy in the control region of human mitochondrial DNA Genome Research, 1995, 5, 89-90.	2.4	74
69	Association analysis of the catechol O-methyltransferase gene and bipolar affective disorder. American Journal of Psychiatry, 1997, 154, 113-115.	4.0	74
70	Sequences From First Settlers Reveal Rapid Evolution in Icelandic mtDNA Pool. PLoS Genetics, 2009, 5, e1000343.	1.5	71
71	Insights into the western Bantu dispersal: mtDNA lineage analysis in Angola. Human Genetics, 2004, 115, 439-47.	1.8	70
72	Natural Selection in the Great Apes. Molecular Biology and Evolution, 2016, 33, 3268-3283.	3.5	70

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73	Mitochondrial DNA from pre-Columbian Ciboneys from Cuba and the prehistoric colonization of the Caribbean. American Journal of Physical Anthropology, 2003, 121, 97-108.	2.1	68
74	Mitochondrial DNA of an Iberian Neandertal suggests a population affinity with other European Neandertals. Current Biology, 2006, 16, R629-R630.	1.8	68
75	Chromosomal rearrangements and the genomic distribution of gene-expression divergence in humans and chimpanzees. Trends in Genetics, 2004, 20, 524-529.	2.9	66
76	Molecular dating of caprines using ancient DNA sequences of Myotragus balearicus, an extinct endemic Balearic mammal. BMC Evolutionary Biology, 2005, 5, 70.	3.2	66
77	Mitochondrial DNA variation and the origin of the Europeans. Human Genetics, 1997, 99, 443-449.	1.8	61
78	SNP analysis to results (SNPator): a web-based environment oriented to statistical genomics analyses upon SNP data. Bioinformatics, 2008, 24, 1643-1644.	1.8	61
79	Georgian and Kurd mtDNA sequence analysis shows a lack of correlation between languages and female genetic lineages. , 2000, 112, 5-16.		60
80	Recent Positive Selection Has Acted on Genes Encoding Proteins with More Interactions within the Whole Human Interactome. Genome Biology and Evolution, 2015, 7, 1141-1154.	1.1	59
81	The Genetics of the Pre-Roman Iberian Peninsula: A mtDNA Study of Ancient Iberians. Annals of Human Genetics, 2005, 69, 535-548.	0.3	56
82	A novel Gypsy founder mutation, p.Arg1109X in the CMT4C gene, causes variable peripheral neuropathy phenotypes. Journal of Medical Genetics, 2005, 42, e69-e69.	1.5	56
83	Worldwide Genetic Analysis of the CFTR Region. American Journal of Human Genetics, 2001, 68, 103-117.	2.6	55
84	Genetic characterization of the ABO blood group in Neandertals. BMC Evolutionary Biology, 2008, 8, 342.	3.2	53
85	Evolution of the O alleles of the human ABO blood group gene. Transfusion, 2004, 44, 707-715.	0.8	49
86	The genome sequencing of an albino Western lowland gorilla reveals inbreeding in the wild. BMC Genomics, 2013, 14, 363.	1.2	48
87	An integrative evolution theory of histo-blood group ABO and related genes. Scientific Reports, 2014, 4, 6601.	1.6	48
88	Allele Frequencies for 20 Microsatellites in a Worldwide Population Survey. Human Heredity, 1997, 47, 189-196.	0.4	47
89	Genetic variation of the 5-HT 2A receptor gene and bipolar affective disorder. Human Genetics, 1997, 100, 582-584.	1.8	47
90	Age and origin of major Smith-Lemli-Opitz syndrome (SLOS) mutations in European populations. Journal of Medical Genetics, 2007, 45, 200-209.	1.5	47

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91	Radiation and phylogeography in the Japanese macaque, Macaca fuscata. Molecular Phylogenetics and Evolution, 2004, 30, 676-685.	1.2	46
92	Identification of Risk Loci for Crohn's Disease Phenotypes Using a Genome-Wide Association Study. Gastroenterology, 2015, 148, 794-805.	0.6	46
93	A tale of two islands: population history and mitochondrial DNA sequence variation of Bioko and São Tomé, Gulf of Guinea. Annals of Human Genetics, 1997, 61, 507-518.	0.3	45
94	Sequence Variability of a Human Pseudogene. Genome Research, 2001, 11, 1071-1085.	2.4	45
95	Origins, admixture and founder lineages in European Roma. European Journal of Human Genetics, 2016, 24, 937-943.	1.4	45
96	Prion susceptibility and protective alleles exhibit marked geographic differences. Human Mutation, 2003, 22, 104-105.	1.1	43
97	A genome-wide survey does not show the genetic distinctiveness of Basques. Human Genetics, 2010, 127, 455-458.	1.8	43
98	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.	1.2	42
99	A genome-wide association study on a southern European population identifies a new Crohn's disease susceptibility locus at <i>RBX1-EP300</i> . Gut, 2013, 62, 1440-1445.	6.1	42
100	Y-chromosome diversity in Catalan surname samples: insights into surname origin and frequency. European Journal of Human Genetics, 2015, 23, 1549-1557.	1.4	42
101	Possible increased risk for Alzheimer's disease associated with neprilysin gene. Journal of Neural Transmission, 2003, 110, 651-657.	1.4	41
102	Spatial patterns of cystic fibrosis mutation spectra in European populations. European Journal of Human Genetics, 2003, 11, 385-394.	1.4	41
103	Variation in estimated recombination rates across human populations. Human Genetics, 2007, 122, 301-310.	1.8	40
104	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.	1.8	39
105	A genome-wide association study identifies a novel locus at 6q22.1 associated with ulcerative colitis. Human Molecular Genetics, 2014, 23, 6927-6934.	1.4	39
106	Sequence Variability of a Human Pseudogene. Genome Research, 2001, 11, 1071-1085.	2.4	39
107	Can a Place of Origin of the Main Cystic Fibrosis Mutations Be Identified?. American Journal of Human Genetics, 2002, 70, 257-264.	2.6	37
108	Molecular phylogeny and evolution of the extinct bovid Myotragus balearicus. Molecular Phylogenetics and Evolution, 2002, 25, 501-510.	1.2	37

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109	HSP70-2 (HSPA1B) is Associated with Noncognitive Symptoms in Late-Onset Alzheimer's Disease. Journal of Geriatric Psychiatry and Neurology, 2003, 16, 146-150.	1.2	37
110	Positive selection in MAOA gene is human exclusive: determination of the putative amino acid change selected in the human lineage. Human Genetics, 2004, 115, 377-86.	1.8	36
111	Alu insertion polymorphisms in the Balkans and the origins of the Aromuns. Annals of Human Genetics, 2004, 68, 120-127.	0.3	35
112	Highly variable neural involvement in sphingomyelinase-deficient Niemann-Pick disease caused by an ancestral Gypsy mutation. Brain, 2006, 130, 1050-1061.	3.7	35
113	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.	1.4	35
114	Genetic variation in prehistoric Sardinia. Human Genetics, 2007, 122, 327-336.	1.8	34
115	Cosmic phylogeny: reconstructing the chemical history of the solar neighbourhood with an evolutionary tree. Monthly Notices of the Royal Astronomical Society, 2017, 467, 1140-1153.	1.6	34
116	Y chromosome STR haplotypes in four populations from northwest Africa. International Journal of Legal Medicine, 2000, 114, 36-40.	1.2	33
117	Comparative Genetics of Functional Trinucleotide Tandem Repeats in Humans and Apes. Journal of Molecular Evolution, 2004, 59, 329-339.	0.8	33
118	Genetic analysis of the skeletal remains attributed to Francesco Petrarca. Forensic Science International, 2007, 173, 36-40.	1.3	33
119	A comprehensive model of the phototransduction cascade in mouse rod cells. Molecular BioSystems, 2014, 10, 1481-1489.	2.9	33
120	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.	3.5	31
121	Dynamics of CAG repeat loci revealed by the analysis of their variability. Human Mutation, 2003, 21, 61-70.	1.1	30
122	Molecular Evolution and Network-Level Analysis of the N-Glycosylation Metabolic Pathway Across Primates. Molecular Biology and Evolution, 2011, 28, 813-823.	3.5	30
123	Paleogenomics in a Temperate Environment: Shotgun Sequencing from an Extinct Mediterranean Caprine. PLoS ONE, 2009, 4, e5670.	1.1	30
124	The prion protein gene in humans revisited: Lessons from a worldwide resequencing study. Genome Research, 2005, 16, 231-239.	2.4	29
125	Human Genetic Variation, Shared and Private. Science, 2012, 337, 39-40.	6.0	29
126	Do Basque- and Caucasian- Speaking Populations Share Non-Indo-European Ancestors?. European Journal of Human Genetics, 1995, 3, 256-263.	1.4	28

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127	mtDNA hypervariable region II (HVII) sequences in human evolution studies. European Journal of Human Genetics, 2000, 8, 964-974.	1.4	27
128	Genome, diversity, and origins: The Y chromosome as a storyteller. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 6927-6929.	3.3	27
129	Estimating the Ancestral Recombinations Graph (ARG) as Compatible Networks of SNP Patterns. Journal of Computational Biology, 2008, 15, 1133-1153.	0.8	27
130	Recent human evolution has shaped geographical differences in susceptibility to disease. BMC Genomics, 2011, 12, 55.	1.2	27
131	Population and genomic lessons from genetic analysis of two Indian populations. Human Genetics, 2014, 133, 1273-1287.	1.8	27
132	Genome-Wide Pathway Analysis Identifies Genetic Pathways Associated with Psoriasis. Journal of Investigative Dermatology, 2016, 136, 593-602.	0.3	27
133	PopHuman: the human population genomics browser. Nucleic Acids Research, 2018, 46, D1003-D1010.	6.5	27
134	Genetic and Geographical Variability in Cystic Fibrosis: Evolutionary Considerations. Novartis Foundation Symposium, 1996, 197, 97-118.	1.2	27
135	Signatures of Selection in the Human Olfactory Receptor OR511 Gene. Molecular Biology and Evolution, 2007, 25, 144-154.	3.5	26
136	Reply to — Age of the ΔF508 cystic fibrosis mutation. Nature Genetics, 1994, 8, 216-218.	9.4	25
137	Joint analysis of candidate genes related to Alzheimer's disease in a Spanish population. Psychiatric Genetics, 2003, 13, 85-90.	0.6	25
138	Gly111Ser mutation in CD8A gene causing CD8 immunodeficiency is found in Spanish Gypsies. Molecular Immunology, 2008, 45, 479-484.	1.0	25
139	The genetics of East African populations: a Nilo-Saharan component in the African genetic landscape. Scientific Reports, 2015, 5, 9996.	1.6	25
140	On the association between chromosomal rearrangements and genic evolution in humans and chimpanzees. Genome Biology, 2007, 8, R230.	13.9	24
141	Network-Level and Population Genetics Analysis of the Insulin/TOR Signal Transduction Pathway Across Human Populations. Molecular Biology and Evolution, 2012, 29, 1379-1392.	3.5	24
142	Extreme individual marker FST values do not imply population-specific selection in humans: the NRG1 example. Human Genetics, 2007, 121, 759-762.	1.8	23
143	Genetic adaptation of the antibacterial human innate immunity network. BMC Evolutionary Biology, 2011, 11, 202.	3.2	23
144	Complement Genetic Markers in Schizophrenia: C3, BF and C6 Polymorphisms. Human Heredity, 1992, 42, 162-167.	0.4	22

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145	A prevalent POLG CAG microsatellite length allele in humans and African great apes. Mammalian Genome, 2004, 15, 492-502.	1.0	22
146	HLA evidence for the lack of genetic heterogeneity in Basques. Annals of Human Genetics, 1998, 62, 123-132.	0.3	21
147	Mitochondrial DNA fromMyotragus balearicus, an extinct bovid from the Balearic Islands>. , 2000, 288, 56-62.		21
148	Haplotype tagging efficiency in worldwide populations in CTLA4 gene. Genes and Immunity, 2005, 6, 646-657.	2.2	21
149	A system-level, molecular evolutionary analysis of mammalian phototransduction. BMC Evolutionary Biology, 2013, 13, 52.	3.2	21
150	Recent Radiation of R-M269 and High Y-STR Haplotype Resemblance Confirmed. Annals of Human Genetics, 2014, 78, 253-254.	0.3	21
151	An assessment of a massively parallel sequencing approach for the identification of individuals from mass graves of the Spanish Civil War (1936–1939). Electrophoresis, 2016, 37, 2841-2847.	1.3	21
152	Enhancers with tissue-specific activity are enriched in intronic regions. Genome Research, 2021, 31, 1325-1336.	2.4	21
153	Neuropathologic Findings in an Aged Albino Gorilla. Veterinary Pathology, 2008, 45, 531-537.	0.8	20
154	Interrogating 11 Fast-Evolving Genes for Signatures of Recent Positive Selection in Worldwide Human Populations. Molecular Biology and Evolution, 2009, 26, 2285-2297.	3.5	20
155	Exploring the rate-limiting steps in visual phototransduction recovery by bottom-up kinetic modeling. Cell Communication and Signaling, 2013, 11, 36.	2.7	20
156	Population history of Corsica: a linguistic and genetic analysis. Annals of Human Biology, 1996, 23, 237-251.	0.4	19
157	Recent Insertion of an Alu Element Within a Polymorphic Human-Specific Alu Insertion. Molecular Biology and Evolution, 2001, 18, 85-88.	3.5	19
158	Glucocerebrosidase pseudogene variation and Gaucher disease: Recognizing pseudogene tracts in GBA alleles. Human Mutation, 2001, 17, 191-198.	1.1	19
159	Heterogeneous Rate of Protein Evolution in Serotonin Genes. Molecular Biology and Evolution, 2007, 24, 2707-2715.	3.5	19
160	Population structure in copy number variation and SNPs in the CCL4L chemokine gene. Genes and Immunity, 2008, 9, 279-288.	2.2	19
161	Decay of linkage disequilibrium within genes across HGDP-CEPH human samples: most population isolates do not show increased LD. BMC Genomics, 2009, 10, 338.	1.2	19
162	Distribution of events of positive selection and population differentiation in a metabolic pathway: the case of asparagine N-glycosylation. BMC Evolutionary Biology, 2012, 12, 98.	3.2	19

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163	The Genetic History of the Iberian Peninsula: A Simulation. Current Anthropology, 1993, 34, 735-745.	0.8	19
164	Parental age in schizophrenia in a case-controlled study. British Journal of Psychiatry, 1993, 162, 574-574.	1.7	18
165	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.	2.9	18
166	Similarity in Recombination Rate Estimates Highly Correlates with Genetic Differentiation in Humans. PLoS ONE, 2011, 6, e17913.	1.1	18
167	Y-chromosomal sequences of diverse Indian populations and the ancestry of the Andamanese. Human Genetics, 2017, 136, 499-510.	1.8	18
168	Genomes reveal marked differences in the adaptive evolution between orangutan species. Genome Biology, 2018, 19, 193.	3.8	18
169	Human Genome Variation and the Concept of Genotype Networks. PLoS ONE, 2014, 9, e99424.	1.1	18
170	Isolated populations as treasure troves in genetic epidemiology: the case of the Basques. European Journal of Human Genetics, 2009, 17, 1490-1494.	1.4	17
171	PKLR-GBA region shows almost complete linkage disequilibrium over 70Âkb in a set of worldwide populations. Human Genetics, 2002, 110, 532-544.	1.8	16
172	Understanding the dynamics of Spinocerebellar Ataxia 8 (SCA8) locus through a comparative genetic approach in humans and apes. Neuroscience Letters, 2003, 336, 143-146.	1.0	16
173	Worldwide genetic variation in dopamine and serotonin pathway genes: Implications for association studies. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 1070-1075.	1.1	16
174	METABOLIC FLUX IS A DETERMINANT OF THE EVOLUTIONARY RATES OF ENZYME-ENCODING GENES. Evolution; International Journal of Organic Evolution, 2014, 68, 605-613.	1.1	16
175	Recent Common Origin, Reduced Population Size, and Marked Admixture Have Shaped European Roma Genomes. Molecular Biology and Evolution, 2020, 37, 3175-3187.	3.5	16
176	The Mediterranean Paradox for Susceptibility Factors in Coronary Heart Disease Extends to Genetics. Annals of Human Genetics, 2007, 72, 070807042352002-???.	0.3	15
177	Evolution of cytokine production capacity in ancient and modern European populations. ELife, 2021, 10,	2.8	15
178	Ethiopia: between Sub-Saharan Africa and western Eurasia. Annals of Human Genetics, 2005, 69, 275-87.	0.3	15
179	A New Method to Reconstruct Recombination Events at a Genomic Scale. PLoS Computational Biology, 2010, 6, e1001010.	1.5	14
180	IRiS: Construction of ARG networks at genomic scales. Bioinformatics, 2011, 27, 2448-2450.	1.8	14

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181	A genome-wide association study identifies <i>SLC8A3</i> as a susceptibility locus for ACPA-positive rheumatoid arthritis. Rheumatology, 2016, 55, 1106-1111.	0.9	14
182	Allele Frequencies in a Worldwide Survey of a CA Repeat in the First Intron of the CFTR Gene. Human Heredity, 1999, 49, 15-20.	0.4	13
183	Geographic stratification of linkage disequilibrium: a worldwide population study in a region of chromosome 22. Human Genomics, 2004, 1, 399.	1.4	13
184	Selection in the Introgressed Regions of the Chimpanzee Genome. Genome Biology and Evolution, 2018, 10, 1132-1138.	1.1	13
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