

Jaume Bertranpetit

List of Publications by Year in descending order

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Version: 2024-02-01

244
papers

16,286
citations

13827

67
h-index

20307

116
g-index

259
all docs

259
docs citations

259
times ranked

15849
citing authors

#	ARTICLE	IF	CITATIONS
1	Positive Selection in Human Populations: Practical Aspects and Current Knowledge. <i>Evolutionary Studies</i> , 2021, , 29-65.	0.2	1
2	Genetic origins, singularity, and heterogeneity of Basques. <i>Current Biology</i> , 2021, 31, 2167-2177.e4.	1.8	11
3	Enhancers with tissue-specific activity are enriched in intronic regions. <i>Genome Research</i> , 2021, 31, 1325-1336.	2.4	21
4	Evolution of cytokine production capacity in ancient and modern European populations. <i>ELife</i> , 2021, 10, .	2.8	15
5	Chromosome X-wide Analysis of Positive Selection in Human Populations: Common and Private Signals of Selection and its Impact on Inactivated Genes and Enhancers. <i>Frontiers in Genetics</i> , 2021, 12, 714491.	1.1	2
6	HLA-G genetic diversity and evolutive aspects in worldwide populations. <i>Scientific Reports</i> , 2021, 11, 23070.	1.6	11
7	A fully integrated machine learning scan of selection in the chimpanzee genome. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa061.	1.5	1
8	The shaping of immunological responses through natural selection after the Roma Diaspora. <i>Scientific Reports</i> , 2020, 10, 16134.	1.6	2
9	Adaptive selection drives TRPP3 loss-of-function in an Ethiopian population. <i>Scientific Reports</i> , 2020, 10, 20999.	1.6	2
10	Positive selection in admixed populations from Ethiopia. <i>BMC Genetics</i> , 2020, 21, 108.	2.7	6
11	Recent Common Origin, Reduced Population Size, and Marked Admixture Have Shaped European Roma Genomes. <i>Molecular Biology and Evolution</i> , 2020, 37, 3175-3187.	3.5	16
12	Gene connectivity and enzyme evolution in the human metabolic network. <i>Biology Direct</i> , 2019, 14, 17.	1.9	11
13	Is there adaptation in the human genome for taste perception and phase I biotransformation?. <i>BMC Evolutionary Biology</i> , 2019, 19, 39.	3.2	11
14	Approximate Bayesian computation with deep learning supports a third archaic introgression in Asia and Oceania. <i>Nature Communications</i> , 2019, 10, 246.	5.8	97
15	Selection in the Introgressed Regions of the Chimpanzee Genome. <i>Genome Biology and Evolution</i> , 2018, 10, 1132-1138.	1.1	13
16	Genomes reveal marked differences in the adaptive evolution between orangutan species. <i>Genome Biology</i> , 2018, 19, 193.	3.8	18
17	Reply to "No evidence for unknown archaic ancestry in South Asia"™. <i>Nature Genetics</i> , 2018, 50, 1637-1639.	9.4	4
18	Influence of pathway topology and functional class on the molecular evolution of human metabolic genes. <i>PLoS ONE</i> , 2018, 13, e0208782.	1.1	3

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19	PopHuman: the human population genomics browser. <i>Nucleic Acids Research</i> , 2018, 46, D1003-D1010.	6.5	27
20	Y-chromosomal sequences of diverse Indian populations and the ancestry of the Andamanese. <i>Human Genetics</i> , 2017, 136, 499-510.	1.8	18
21	Morphometric, Behavioral, and Genomic Evidence for a New Orangutan Species. <i>Current Biology</i> , 2017, 27, 3487-3498.e10.	1.8	192
22	Cosmic phylogeny: reconstructing the chemical history of the solar neighbourhood with an evolutionary tree. <i>Monthly Notices of the Royal Astronomical Society</i> , 2017, 467, 1140-1153.	1.6	34
23	Recombination. <i>Evolutionary Studies</i> , 2017, , 131-142.	0.2	0
24	Functional role of positively selected amino acid substitutions in mammalian rhodopsin evolution. <i>Scientific Reports</i> , 2016, 6, 21570.	1.6	10
25	A genome-wide association study identifies <i>SLC8A3</i> as a susceptibility locus for ACPA-positive rheumatoid arthritis. <i>Rheumatology</i> , 2016, 55, 1106-1111.	0.9	14
26	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.	1.3	21
27	Genomic analysis of Andamanese provides insights into ancient human migration into Asia and adaptation. <i>Nature Genetics</i> , 2016, 48, 1066-1070.	9.4	126
28	Natural Selection in the Great Apes. <i>Molecular Biology and Evolution</i> , 2016, 33, 3268-3283.	3.5	70
29	Identification of <i>IRX1</i> as a Risk Locus for Rheumatoid Factor Positivity in Rheumatoid Arthritis in a Genome-Wide Association Study. <i>Arthritis and Rheumatology</i> , 2016, 68, 1384-1391.	2.9	6
30	Genome-Wide Pathway Analysis Identifies Genetic Pathways Associated with Psoriasis. <i>Journal of Investigative Dermatology</i> , 2016, 136, 593-602.	0.3	27
31	Origins, admixture and founder lineages in European Roma. <i>European Journal of Human Genetics</i> , 2016, 24, 937-943.	1.4	45
32	The genetics of East African populations: a Nilo-Saharan component in the African genetic landscape. <i>Scientific Reports</i> , 2015, 5, 9996.	1.6	25
33	Extreme selective sweeps independently targeted the X chromosomes of the great apes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6413-6418.	3.3	75
34	Identification of Risk Loci for Crohn's Disease Phenotypes Using a Genome-Wide Association Study. <i>Gastroenterology</i> , 2015, 148, 794-805.	0.6	46
35	Y-chromosome diversity in Catalan surname samples: insights into surname origin and frequency. <i>European Journal of Human Genetics</i> , 2015, 23, 1549-1557.	1.4	42
36	Recent Positive Selection Has Acted on Genes Encoding Proteins with More Interactions within the Whole Human Interactome. <i>Genome Biology and Evolution</i> , 2015, 7, 1141-1154.	1.1	59

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37	Hierarchical boosting: a machine-learning framework to detect and classify hard selective sweeps in human populations. <i>Bioinformatics</i> , 2015, 31, 3946-3952.	1.8	85
38	Dynamic sensitivity and nonlinear interactions influence the system-level evolutionary patterns of phototransduction proteins. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20152215.	1.2	3
39	VCF2Networks: applying genotype networks to single-nucleotide variants data. <i>Bioinformatics</i> , 2015, 31, 438-439.	1.8	5
40	1000 Genomes Selection Browser 1.0: a genome browser dedicated to signatures of natural selection in modern humans. <i>Nucleic Acids Research</i> , 2014, 42, D903-D909.	6.5	143
41	METABOLIC FLUX IS A DETERMINANT OF THE EVOLUTIONARY RATES OF ENZYME-ENCODING GENES. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 605-613.	1.1	16
42	Convergent evolution in European and Roma populations reveals pressure exerted by plague on Toll-like receptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2668-2673.	3.3	88
43	Recent Radiation of R-M269 and High Y-STR Haplotype Resemblance Confirmed. <i>Annals of Human Genetics</i> , 2014, 78, 253-254.	0.3	21
44	A comprehensive model of the phototransduction cascade in mouse rod cells. <i>Molecular BioSystems</i> , 2014, 10, 1481-1489.	2.9	33
45	A genome-wide association study identifies a novel locus at 6q22.1 associated with ulcerative colitis. <i>Human Molecular Genetics</i> , 2014, 23, 6927-6934.	1.4	39
46	Population and genomic lessons from genetic analysis of two Indian populations. <i>Human Genetics</i> , 2014, 133, 1273-1287.	1.8	27
47	An integrative evolution theory of histo-blood group ABO and related genes. <i>Scientific Reports</i> , 2014, 4, 6601.	1.6	48
48	Human Genome Variation and the Concept of Genotype Networks. <i>PLoS ONE</i> , 2014, 9, e99424.	1.1	18
49	Exploring the rate-limiting steps in visual phototransduction recovery by bottom-up kinetic modeling. <i>Cell Communication and Signaling</i> , 2013, 11, 36.	2.7	20
50	A system-level, molecular evolutionary analysis of mammalian phototransduction. <i>BMC Evolutionary Biology</i> , 2013, 13, 52.	3.2	21
51	The genome sequencing of an albino Western lowland gorilla reveals inbreeding in the wild. <i>BMC Genomics</i> , 2013, 14, 363.	1.2	48
52	Great ape genetic diversity and population history. <i>Nature</i> , 2013, 499, 471-475.	13.7	768
53	A genome-wide association study on a southern European population identifies a new Crohn's disease susceptibility locus at <i>10q26</i> . <i>Gut</i> , 2013, 62, 1440-1445.	6.1	42
54	Genome-Wide Diversity in the Levant Reveals Recent Structuring by Culture. <i>PLoS Genetics</i> , 2013, 9, e1003316.	1.5	77

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55	Gene flow from North Africa contributes to differential human genetic diversity in southern Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11791-11796.	3.3	174
56	Genomic Ancestry of North Africans Supports Back-to-Africa Migrations. <i>PLoS Genetics</i> , 2012, 8, e1002397.	1.5	275
57	Network-Level and Population Genetics Analysis of the Insulin/TOR Signal Transduction Pathway Across Human Populations. <i>Molecular Biology and Evolution</i> , 2012, 29, 1379-1392.	3.5	24
58	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.	3.5	31
59	Human Genetic Variation, Shared and Private. <i>Science</i> , 2012, 337, 39-40.	6.0	29
60	Distribution of events of positive selection and population differentiation in a metabolic pathway: the case of asparagine N-glycosylation. <i>BMC Evolutionary Biology</i> , 2012, 12, 98.	3.2	19
61	Recombination networks as genetic markers in a human variation study of the Old World. <i>Human Genetics</i> , 2012, 131, 601-613.	1.8	7
62	Genomic Affinities of Two 7,000-Year-Old Iberian Hunter-Gatherers. <i>Current Biology</i> , 2012, 22, 1494-1499.	1.8	160
63	Molecular Evolution and Network-Level Analysis of the N-Glycosylation Metabolic Pathway Across Primates. <i>Molecular Biology and Evolution</i> , 2011, 28, 813-823.	3.5	30
64	Similarity in Recombination Rate Estimates Highly Correlates with Genetic Differentiation in Humans. <i>PLoS ONE</i> , 2011, 6, e17913.	1.1	18
65	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, 84-88.	1.4	35
66	Genetic adaptation of the antibacterial human innate immunity network. <i>BMC Evolutionary Biology</i> , 2011, 11, 202.	3.2	23
67	Recent human evolution has shaped geographical differences in susceptibility to disease. <i>BMC Genomics</i> , 2011, 12, 55.	1.2	27
68	IRIS: Construction of ARG networks at genomic scales. <i>Bioinformatics</i> , 2011, 27, 2448-2450.	1.8	14
69	The annotation of the asparagine N-linked glycosylation pathway in the Reactome database. <i>Glycobiology</i> , 2011, 21, 1395-1400.	1.3	7
70	Ten Simple Rules for Getting Help from Online Scientific Communities. <i>PLoS Computational Biology</i> , 2011, 7, e1002202.	1.5	12
71	A Targeted Association Study of Immunity Genes and Networks Suggests Novel Associations with Placental Malaria Infection. <i>PLoS ONE</i> , 2011, 6, e24996.	1.1	6
72	A genome-wide survey does not show the genetic distinctiveness of Basques. <i>Human Genetics</i> , 2010, 127, 455-458.	1.8	43

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73	Nucleotide substitution rates for the full set of mitochondrial protein-coding genes in Coleoptera. <i>Molecular Phylogenetics and Evolution</i> , 2010, 56, 796-807.	1.2	141
74	The annotation and the usage of scientific databases could be improved with public issue tracker software. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2010, baq035.	1.4	5
75	A New Method to Reconstruct Recombination Events at a Genomic Scale. <i>PLoS Computational Biology</i> , 2010, 6, e1001010.	1.5	14
76	Human pseudogenes of the ABO family show a complex evolutionary dynamics and loss of function. <i>Glycobiology</i> , 2009, 19, 583-591.	1.3	12
77	Interrogating 11 Fast-Evolving Genes for Signatures of Recent Positive Selection in Worldwide Human Populations. <i>Molecular Biology and Evolution</i> , 2009, 26, 2285-2297.	3.5	20
78	A variant in the gene FUT9 is associated with susceptibility to placental malaria infection. <i>Human Molecular Genetics</i> , 2009, 18, 3136-3144.	1.4	11
79	Sequences From First Settlers Reveal Rapid Evolution in Icelandic mtDNA Pool. <i>PLoS Genetics</i> , 2009, 5, e1000343.	1.5	71
80	A Natural History of FUT2 Polymorphism in Humans. <i>Molecular Biology and Evolution</i> , 2009, 26, 1993-2003.	3.5	209
81	Minimizing recombinations in consensus networks for phylogeographic studies. <i>BMC Bioinformatics</i> , 2009, 10, S72.	1.2	12
82	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.	1.2	19
83	An evaluation of the genetic-matched pair study design using genome-wide SNP data from the European population. <i>European Journal of Human Genetics</i> , 2009, 17, 967-975.	1.4	8
84	Isolated populations as treasure troves in genetic epidemiology: the case of the Basques. <i>European Journal of Human Genetics</i> , 2009, 17, 1490-1494.	1.4	17
85	From the detection of population structure to the reconstruction of population history: the historical reading of the human genome. <i>Heredity</i> , 2009, 103, 362-363.	1.2	2
86	Paleogenomics in a Temperate Environment: Shotgun Sequencing from an Extinct Mediterranean Caprine. <i>PLoS ONE</i> , 2009, 4, e5670.	1.1	30
87	Is There Selection for the Pace of Successive Inactivation of the arpAT Gene in Primates?. <i>Journal of Molecular Evolution</i> , 2008, 67, 23-28.	0.8	2
88	Evolutionary analysis of genes of two pathways involved in placental malaria infection. <i>Human Genetics</i> , 2008, 123, 343-357.	1.8	6
89	Evolutionary dynamics of the human ABO gene. <i>Human Genetics</i> , 2008, 124, 123-135.	1.8	85
90	Worldwide genetic variation in dopamine and serotonin pathway genes: Implications for association studies. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2008, 147B, 1070-1075.	1.1	16

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91	Y-Chromosomal Diversity in Lebanon Is Structured by Recent Historical Events. <i>American Journal of Human Genetics</i> , 2008, 82, 873-882.	2.6	106
92	Identifying Genetic Traces of Historical Expansions: Phoenician Footprints in the Mediterranean. <i>American Journal of Human Genetics</i> , 2008, 83, 633-642.	2.6	127
93	Genetic characterization of the ABO blood group in Neandertals. <i>BMC Evolutionary Biology</i> , 2008, 8, 342.	3.2	53
94	Correlation between Genetic and Geographic Structure in Europe. <i>Current Biology</i> , 2008, 18, 1241-1248.	1.8	449
95	Gly111Ser mutation in CD8A gene causing CD8 immunodeficiency is found in Spanish Gypsies. <i>Molecular Immunology</i> , 2008, 45, 479-484.	1.0	25
96	The Dawn of Human Matrilineal Diversity. <i>American Journal of Human Genetics</i> , 2008, 82, 1130-1140.	2.6	392
97	Population structure in copy number variation and SNPs in the CCL4L chemokine gene. <i>Genes and Immunity</i> , 2008, 9, 279-288.	2.2	19
98	Neuropathologic Findings in an Aged Albino Gorilla. <i>Veterinary Pathology</i> , 2008, 45, 531-537.	0.8	20
99	Balancing Selection Is the Main Force Shaping the Evolution of Innate Immunity Genes. <i>Journal of Immunology</i> , 2008, 181, 1315-1322.	0.4	173
100	SNP analysis to results (SNPator): a web-based environment oriented to statistical genomics analyses upon SNP data. <i>Bioinformatics</i> , 2008, 24, 1643-1644.	1.8	61
101	Estimating the Ancestral Recombinations Graph (ARG) as Compatible Networks of SNP Patterns. <i>Journal of Computational Biology</i> , 2008, 15, 1133-1153.	0.8	27
102	Heterogeneous Rate of Protein Evolution in Serotonin Genes. <i>Molecular Biology and Evolution</i> , 2007, 24, 2707-2715.	3.5	19
103	Palaeogenetic evidence supports a dual model of Neolithic spreading into Europe. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007, 274, 2161-2167.	1.2	93
104	Age and origin of major Smith-Lemli-Opitz syndrome (SLOS) mutations in European populations. <i>Journal of Medical Genetics</i> , 2007, 45, 200-209.	1.5	47
105	Signatures of Selection in the Human Olfactory Receptor OR511 Gene. <i>Molecular Biology and Evolution</i> , 2007, 25, 144-154.	3.5	26
106	On the association between chromosomal rearrangements and genic evolution in humans and chimpanzees. <i>Genome Biology</i> , 2007, 8, R230.	13.9	24
107	Genetic analysis of the skeletal remains attributed to Francesco Petrarca. <i>Forensic Science International</i> , 2007, 173, 36-40.	1.3	33
108	The Mediterranean Paradox for Susceptibility Factors in Coronary Heart Disease Extends to Genetics. <i>Annals of Human Genetics</i> , 2007, 72, 070807042352002-???.	0.3	15

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109	The Derived FOXP2 Variant of Modern Humans Was Shared with Neandertals. <i>Current Biology</i> , 2007, 17, 1908-1912.	1.8	487
110	A Melanocortin 1 Receptor Allele Suggests Varying Pigmentation Among Neanderthals. <i>Science</i> , 2007, 318, 1453-1455.	6.0	264
111	Extreme individual marker FST values do not imply population-specific selection in humans: the NRG1 example. <i>Human Genetics</i> , 2007, 121, 759-762.	1.8	23
112	Variation in estimated recombination rates across human populations. <i>Human Genetics</i> , 2007, 122, 301-310.	1.8	40
113	Genetic variation in prehistoric Sardinia. <i>Human Genetics</i> , 2007, 122, 327-336.	1.8	34
114	Y-chromosome diversity in Bantu and Pygmy populations from Central Africa. <i>International Congress Series</i> , 2006, 1288, 234-236.	0.2	5
115	Extreme population differences across Neuregulin 1 gene, with implications for association studies. <i>Molecular Psychiatry</i> , 2006, 11, 66-75.	4.1	83
116	Human F7 sequence is split into three deep clades that are related to FVII plasma levels. <i>Human Genetics</i> , 2006, 118, 741-751.	1.8	12
117	A highly divergent mtDNA sequence in a Neandertal individual from Italy. <i>Current Biology</i> , 2006, 16, R630-R632.	1.8	80
118	Mitochondrial DNA of an Iberian Neandertal suggests a population affinity with other European Neandertals. <i>Current Biology</i> , 2006, 16, R629-R630.	1.8	68
119	Comparative analysis of cancer genes in the human and chimpanzee genomes. <i>BMC Genomics</i> , 2006, 7, 15.	1.2	94
120	Highly variable neural involvement in sphingomyelinase-deficient Niemann-Pick disease caused by an ancestral Gypsy mutation. <i>Brain</i> , 2006, 130, 1050-1061.	3.7	35
121	The portability of tagSNPs across populations: A worldwide survey. <i>Genome Research</i> , 2006, 16, 323-330.	2.4	82
122	The origin of European cattle: Evidence from modern and ancient DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8113-8118.	3.3	271
123	Tracking down Human Contamination in Ancient Human Teeth. <i>Molecular Biology and Evolution</i> , 2006, 23, 1801-1807.	3.5	105
124	Nuclear Gene Indicates Coat-Color Polymorphism in Mammoths. <i>Science</i> , 2006, 313, 62-62.	6.0	135
125	The Genetics of the Pre-Roman Iberian Peninsula: A mtDNA Study of Ancient Iberians. <i>Annals of Human Genetics</i> , 2005, 69, 535-548.	0.3	56
126	Haplotype tagging efficiency in worldwide populations in CTLA4 gene. <i>Genes and Immunity</i> , 2005, 6, 646-657.	2.2	21

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127	Assessing the signatures of selection in PRNP from polymorphism data: results support Kreitman and Di Rienzo's opinion. <i>Trends in Genetics</i> , 2005, 21, 389-391.	2.9	18
128	Molecular dating of caprines using ancient DNA sequences of <i>Myotragus balearicus</i> , an extinct endemic Balearic mammal. <i>BMC Evolutionary Biology</i> , 2005, 5, 70.	3.2	66
129	The prion protein gene in humans revisited: Lessons from a worldwide resequencing study. <i>Genome Research</i> , 2005, 16, 231-239.	2.4	29
130	Neandertal Evolutionary Genetics: Mitochondrial DNA Data from the Iberian Peninsula. <i>Molecular Biology and Evolution</i> , 2005, 22, 1077-1081.	3.5	139
131	A novel Gypsy founder mutation, p.Arg1109X in the CMT4C gene, causes variable peripheral neuropathy phenotypes. <i>Journal of Medical Genetics</i> , 2005, 42, e69-e69.	1.5	56
132	Ethiopia: between Sub-Saharan Africa and western Eurasia. <i>Annals of Human Genetics</i> , 2005, 69, 275-87.	0.3	15
133	Unravelling migrations in the steppe: mitochondrial DNA sequences from ancient Central Asians. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2004, 271, 941-947.	1.2	100
134	Evolution of the O alleles of the human ABO blood group gene. <i>Transfusion</i> , 2004, 44, 707-715.	0.8	49
135	Admixture, migrations, and dispersals in Central Asia: evidence from maternal DNA lineages. <i>European Journal of Human Genetics</i> , 2004, 12, 495-504.	1.4	145
136	Chromosomal rearrangements and the genomic distribution of gene-expression divergence in humans and chimpanzees. <i>Trends in Genetics</i> , 2004, 20, 524-529.	2.9	66
137	Insights into the western Bantu dispersal: mtDNA lineage analysis in Angola. <i>Human Genetics</i> , 2004, 115, 439-47.	1.8	70
138	Positive selection in MAOA gene is human exclusive: determination of the putative amino acid change selected in the human lineage. <i>Human Genetics</i> , 2004, 115, 377-86.	1.8	36
139	A prevalent POLG CAG microsatellite length allele in humans and African great apes. <i>Mammalian Genome</i> , 2004, 15, 492-502.	1.0	22
140	Comparative Analysis of Alu Insertion Sequences in the APP 5' Flanking Region in Humans and Other Primates. <i>Journal of Molecular Evolution</i> , 2004, 58, 722-731.	0.8	4
141	Comparative Genetics of Functional Trinucleotide Tandem Repeats in Humans and Apes. <i>Journal of Molecular Evolution</i> , 2004, 59, 329-339.	0.8	33
142	Radiation and phylogeography in the Japanese macaque, <i>Macaca fuscata</i> . <i>Molecular Phylogenetics and Evolution</i> , 2004, 30, 676-685.	1.2	46
143	Alu insertion polymorphisms in the Balkans and the origins of the Aromuns. <i>Annals of Human Genetics</i> , 2004, 68, 120-127.	0.3	35
144	Variation of the prion gene in chimpanzees and its implication for prion diseases. <i>Neuroscience Letters</i> , 2004, 355, 157-160.	1.0	7

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145	Geographic stratification of linkage disequilibrium: a worldwide population study in a region of chromosome 22. <i>Human Genomics</i> , 2004, 1, 399.	1.4	13
146	Association study between Alzheimer's disease and genes involved in A β biosynthesis, aggregation and degradation: suggestive results with BACE1. <i>Journal of Neurology</i> , 2003, 250, 956-961.	1.8	39
147	Possible increased risk for Alzheimer's disease associated with neprilysin gene. <i>Journal of Neural Transmission</i> , 2003, 110, 651-657.	1.4	41
148	Dynamics of CAG repeat loci revealed by the analysis of their variability. <i>Human Mutation</i> , 2003, 21, 61-70.	1.1	30
149	Prion susceptibility and protective alleles exhibit marked geographic differences. <i>Human Mutation</i> , 2003, 22, 104-105.	1.1	43
150	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.	2.1	68
151	Joining the Pillars of Hercules: mtDNA Sequences Show Multidirectional Gene Flow in the Western Mediterranean. <i>Annals of Human Genetics</i> , 2003, 67, 312-328.	0.3	123
152	Spatial patterns of cystic fibrosis mutation spectra in European populations. <i>European Journal of Human Genetics</i> , 2003, 11, 385-394.	1.4	41
153	Association of the CTLA4 promoter region (\sim 1661G allele) with type 1 diabetes in the South Moroccan population. <i>Genes and Immunity</i> , 2003, 4, 132-137.	2.2	81
154	Understanding the dynamics of Spinocerebellar Ataxia 8 (SCA8) locus through a comparative genetic approach in humans and apes. <i>Neuroscience Letters</i> , 2003, 336, 143-146.	1.0	16
155	Evidence for a genetic discontinuity between Neandertals and 24,000-year-old anatomically modern Europeans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 6593-6597.	3.3	324
156	HSP70-2 (HSPA1B) is Associated with Noncognitive Symptoms in Late-Onset Alzheimer's Disease. <i>Journal of Geriatric Psychiatry and Neurology</i> , 2003, 16, 146-150.	1.2	37
157	Title is missing!. <i>Psychiatric Genetics</i> , 2003, 13, 85-90.	0.6	1
158	Joint analysis of candidate genes related to Alzheimer's disease in a Spanish population. <i>Psychiatric Genetics</i> , 2003, 13, 85-90.	0.6	25
159	Structure of Linkage Disequilibrium in Humans: Genome Factors and Population Stratification. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2003, 68, 79-88.	2.0	12
160	Why Names. <i>Genome Research</i> , 2002, 12, 219-221.	2.4	5
161	From genetic variation to population dynamics: insights into the biological understanding of humans. , 2002, , 83-102.		0
162	Determination of Haploid DNA Sequences in Humans: Application to the Glucocerebrosidase Pseudogene. <i>DNA Sequence</i> , 2002, 13, 9-13.	0.7	7

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163	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
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