

D Comas

List of Publications by Year in descending order

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200
papers

15,376
citations

22099

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22764

112
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210
docs citations

210
times ranked

14826
citing authors

#	ARTICLE	IF	CITATIONS
1	Population Histories and Genomic Diversity of South American Natives. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	10
2	Evidence of Selection in the Ectodysplasin Pathway among Endangered Aquatic Mammals. <i>Integrative Organismal Biology</i> , 2022, 4, .	0.9	2
3	Population history of North Africa based on modern and ancient genomes. <i>Human Molecular Genetics</i> , 2021, 30, R17-R23.	1.4	11
4	The Counteracting Effects of Demography on Functional Genomic Variation: The Roma Paradigm. <i>Molecular Biology and Evolution</i> , 2021, 38, 2804-2817.	3.5	14
5	Deep genetic affinity between coastal Pacific and Amazonian natives evidenced by Australasian ancestry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	21
6	Ancient and modern mitogenomes from Central Argentina: new insights into population continuity, temporal depth and migration in South America. <i>Human Molecular Genetics</i> , 2021, 30, 1200-1217.	1.4	10
7	Genetic origins, singularity, and heterogeneity of Basques. <i>Current Biology</i> , 2021, 31, 2167-2177.e4.	1.8	11
8	Admixture Has Shaped Romani Genetic Diversity in Clinically Relevant Variants. <i>Frontiers in Genetics</i> , 2021, 12, 683880.	1.1	6
9	The Y Chromosome. <i>Evolutionary Studies</i> , 2021, , 121-136.	0.2	0
10	Whole-exome analysis in Tunisian Imazighen and Arabs shows the impact of demography in functional variation. <i>Scientific Reports</i> , 2021, 11, 21125.	1.6	4
11	The genetic scenario of Mercheros: an under-represented group within the Iberian Peninsula. <i>BMC Genomics</i> , 2021, 22, 897.	1.2	1
12	The shaping of immunological responses through natural selection after the Roma Diaspora. <i>Scientific Reports</i> , 2020, 10, 16134.	1.6	2
13	Sex-biased patterns shaped the genetic history of Roma. <i>Scientific Reports</i> , 2020, 10, 14464.	1.6	7
14	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
15	Genomic insight into the origins and dispersal of the Brazilian coastal natives. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 2372-2377.	3.3	27
16	The place of metropolitan France in the European genomic landscape. <i>Human Genetics</i> , 2020, 139, 1091-1105.	1.8	1
17	Heterogeneity in Palaeolithic Population Continuity and Neolithic Expansion in North Africa. <i>Current Biology</i> , 2019, 29, 3953-3959.e4.	1.8	26
18	Reconstructed lost Native American populations from Eastern Brazil are shaped by differential J _A ³ /Tupi ancestry. <i>Genome Biology and Evolution</i> , 2019, 11, 2593-2604.	1.1	8

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19	Distribution of local ancestry and evidence of adaptation in admixed populations. <i>Scientific Reports</i> , 2019, 9, 13900.	1.6	24
20	European Roma groups show complex West Eurasian admixture footprints and a common South Asian genetic origin. <i>PLoS Genetics</i> , 2019, 15, e1008417.	1.5	28
21	Spatially explicit analysis reveals complex human genetic gradients in the Iberian Peninsula. <i>Scientific Reports</i> , 2019, 9, 7825.	1.6	5
22	Patterns of genetic structure and adaptive positive selection in the Lithuanian population from high-density SNP data. <i>Scientific Reports</i> , 2019, 9, 9163.	1.6	13
23	Dissecting human North African gene-flow into its western coastal surroundings. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190471.	1.2	13
24	Whole-genome sequence analysis of a Pan African set of samples reveals archaic gene flow from an extinct basal population of modern humans into sub-Saharan populations. <i>Genome Biology</i> , 2019, 20, 77.	3.8	50
25	Biallelic loss-of-function LACC1/FAMIN Mutations Presenting as Rheumatoid Factor-Negative Polyarticular Juvenile Idiopathic Arthritis. <i>Scientific Reports</i> , 2019, 9, 4579.	1.6	20
26	People from Ibiza: an unexpected isolate in the Western Mediterranean. <i>European Journal of Human Genetics</i> , 2019, 27, 941-951.	1.4	25
27	The genetic landscape of Mediterranean North African populations through complete mtDNA sequences. <i>Annals of Human Biology</i> , 2018, 45, 98-104.	0.4	16
28	Human population genetics of the Mediterranean. <i>Annals of Human Biology</i> , 2018, 45, 1-4.	0.4	3
29	Searching for ancient balanced polymorphisms shared between Neanderthals and Modern Humans. <i>Genetics and Molecular Biology</i> , 2018, 41, 67-81.	0.6	9
30	A Roma founder <i>BIN1</i> mutation causes a novel phenotype of centronuclear myopathy with rigid spine. <i>Neurology</i> , 2018, 91, e339-e348.	1.5	18
31	Sequence diversity of the Rh blood group system in Basques. <i>European Journal of Human Genetics</i> , 2018, 26, 1859-1866.	1.4	5
32	Recent historical migrations have shaped the gene pool of Arabs and Berbers in North Africa. <i>Molecular Biology and Evolution</i> , 2017, 34, msw218.	3.5	56
33	Genetic signature of natural selection in first Americans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 2195-2199.	3.3	76
34	A tale of agriculturalists and hunter-gatherers: Exploring the thrifty genotype hypothesis in native South Americans. <i>American Journal of Physical Anthropology</i> , 2017, 163, 591-601.	2.1	9
35	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.	1.6	28
36	Complement factor 5 (C5) p.A252T mutation is prevalent in, but not restricted to, sub-Saharan Africa: implications for the susceptibility to meningococcal disease. <i>Clinical and Experimental Immunology</i> , 2017, 189, 226-231.	1.1	8

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37	Evaluating the Neolithic Expansion at Both Shores of the Mediterranean Sea. <i>Molecular Biology and Evolution</i> , 2017, 34, 3232-3242.	3.5	13
38	Comparison of Y-chromosomal haplogroup predictors. <i>Forensic Science International: Genetics Supplement Series</i> , 2017, 6, e145-e147.	0.1	13
39	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.	1.6	24
40	Complement factor 5 (C5) p.A252T mutation is prevalent in, but not restricted to, Sub-Saharan Africa: Implications for the susceptibility to meningococcal disease. <i>Molecular Immunology</i> , 2017, 89, 158-159.	1.0	0
41	BIN1 founder mutation in the Spanish gypsy population is the most frequent cause of adult onset centronuclear myopathies in the south of Spain. <i>Neuromuscular Disorders</i> , 2017, 27, S172-S173.	0.3	0
42	Novel Mutations Causing C5 Deficiency in Three North-African Families. <i>Journal of Clinical Immunology</i> , 2016, 36, 388-396.	2.0	13
43	Demographic History of the Genus <i>Pan</i> Inferred from Whole Mitochondrial Genome Reconstructions. <i>Genome Biology and Evolution</i> , 2016, 8, 2020-2030.	1.1	19
44	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. <i>Nature</i> , 2016, 538, 201-206.	13.7	1,216
45	Genomic insights into the origin of farming in the ancient Near East. <i>Nature</i> , 2016, 536, 419-424.	13.7	733
46	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
47	Genetic evidence for an origin of the Armenians from Bronze Age mixing of multiple populations. <i>European Journal of Human Genetics</i> , 2016, 24, 931-936.	1.4	44
48	Origins, admixture and founder lineages in European Roma. <i>European Journal of Human Genetics</i> , 2016, 24, 937-943.	1.4	45
49	The AQP1 del601G mutation in different European Romani (Gypsy) populations. <i>Blood Transfusion</i> , 2016, 14, 580-581.	0.3	1
50	Reassessing the Evolutionary History of the 17q21 Inversion Polymorphism. <i>Genome Biology and Evolution</i> , 2015, 7, 3239-3248.	1.1	11
51	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
52	A family carrying a homozygous LACC1 truncated mutation expands the clinical phenotype of this disease beyond systemic-onset juvenile idiopathic arthritis. <i>Pediatric Rheumatology</i> , 2015, 13, .	0.9	8
53	Genetic Heterogeneity in Algerian Human Populations. <i>PLoS ONE</i> , 2015, 10, e0138453.	1.1	33
54	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

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55	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
56	Evolutionary pattern in the OXT-OXTR system in primates: Coevolution and positive selection footprints. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 88-93.	3.3	61
57	Global diversity, population stratification, and selection of human copy-number variation. <i>Science</i> , 2015, 349, aab3761.	6.0	293
58	Tandem repeat variation in human and great ape populations and its impact on gene expression divergence. <i>Genome Research</i> , 2015, 25, 1591-1599.	2.4	69
59	Genetics and the Reconstruction of African Population History. , 2015, , 379-400.		0
60	Extreme Population Differences in the Human Zinc Transporter ZIP4 (SLC39A4) Are Explained by Positive Selection in Sub-Saharan Africa. <i>PLoS Genetics</i> , 2014, 10, e1004128.	1.5	34
61	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
62	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , 2014, 513, 409-413.	13.7	1,179
63	Geographic population structure analysis of worldwide human populations infers their biogeographical origins. <i>Nature Communications</i> , 2014, 5, 3513.	5.8	114
64	Toward Male Individualization with Rapidly Mutating Y-Chromosomal Short Tandem Repeats. <i>Human Mutation</i> , 2014, 35, 1021-1032.	1.1	151
65	La genÀtica de les migracions humanes: Seguint el rastre de les migracions a travÃ©s del nostre genoma. <i>Metode</i> , 2014, .	0.0	0
66	The influence of habitats on female mobility in Central and Western Africa inferred from human mitochondrial variation. <i>BMC Evolutionary Biology</i> , 2013, 13, 24.	3.2	9
67	GHEP-ISFG proficiency test 2011: Paper challenge on evaluation of mitochondrial DNA results. <i>Forensic Science International: Genetics</i> , 2013, 7, 10-15.	1.6	7
68	Ancient DNA Reveals Prehistoric Gene-Flow from Siberia in the Complex Human Population History of North East Europe. <i>PLoS Genetics</i> , 2013, 9, e1003296.	1.5	78
69	Neolithic mitochondrial haplogroup H genomes and the genetic origins of Europeans. <i>Nature Communications</i> , 2013, 4, 1764.	5.8	180
70	Great ape genetic diversity and population history. <i>Nature</i> , 2013, 499, 471-475.	13.7	768
71	Implications of Population History of European Romani on Genetic Susceptibility to Disease. <i>Human Heredity</i> , 2013, 76, 194-200.	0.4	12
72	Contemporary paternal genetic landscape of Polish and German populations: from early medieval Slavic expansion to post-World War II resettlements. <i>European Journal of Human Genetics</i> , 2013, 21, 415-422.	1.4	41

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73	Genome-Wide Diversity in the Levant Reveals Recent Structuring by Culture. <i>PLoS Genetics</i> , 2013, 9, e1003316.	1.5	77
74	The GenoChip: A New Tool for Genetic Anthropology. <i>Genome Biology and Evolution</i> , 2013, 5, 1021-1031.	1.1	54
75	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
76	Y-Chromosome and mtDNA Genetics Reveal Significant Contrasts in Affinities of Modern Middle Eastern Populations with European and African Populations. <i>PLoS ONE</i> , 2013, 8, e54616.	1.1	49
77	Uniparental Markers in Italy Reveal a Sex-Biased Genetic Structure and Different Historical Strata. <i>PLoS ONE</i> , 2013, 8, e65441.	1.1	61
78	Genome-Wide and Paternal Diversity Reveal a Recent Origin of Human Populations in North Africa. <i>PLoS ONE</i> , 2013, 8, e80293.	1.1	39
79	Genomic Ancestry of North Africans Supports Back-to-Africa Migrations. <i>PLoS Genetics</i> , 2012, 8, e1002397.	1.5	275
80	Similarity in recombination rate and linkage disequilibrium at CYP2C and CYP2D cytochrome P450 gene regions among Europeans indicates signs of selection and no advantage of using tagSNPs in population isolates. <i>Pharmacogenetics and Genomics</i> , 2012, 22, 846-857.	0.7	12
81	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
82	Mitochondrial origin of the matrilineal Mosuo people in China. <i>Mitochondrial DNA</i> , 2012, 23, 13-19.	0.6	11
83	Evidence of Pre-Roman Tribal Genetic Structure in Basques from Uniparentally Inherited Markers. <i>Molecular Biology and Evolution</i> , 2012, 29, 2211-2222.	3.5	37
84	Reconstructing the Population History of European Romani from Genome-wide Data. <i>Current Biology</i> , 2012, 22, 2342-2349.	1.8	101
85	Using the Neandertal and Denisova Genetic Data to Understand the Common MAPT 17q21 Inversion in Modern Humans. <i>Human Biology</i> , 2012, 84, 633-640.	0.4	4
86	Y-chromosome analysis reveals genetic divergence and new founding native lineages in Athapaskan- and Eskimoan-speaking populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8471-8476.	3.3	54
87	Y-Chromosome Analysis in Individuals Bearing the Basarab Name of the First Dynasty of Wallachian Kings. <i>PLoS ONE</i> , 2012, 7, e41803.	1.1	11
88	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.	2.1	26
89	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
90	North African Jewish and non-Jewish populations form distinctive, orthogonal clusters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13865-13870.	3.3	49

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91	Adaptive evolution of loci covarying with the human African Pygmy phenotype. <i>Human Genetics</i> , 2012, 131, 1305-1317.	1.8	27
92	The Basque Paradigm: Genetic Evidence of a Maternal Continuity in the Franco-Cantabrian Region since Pre-Neolithic Times. <i>American Journal of Human Genetics</i> , 2012, 90, 486-493.	2.6	58
93	The Basque Paradigm: Genetic Evidence of a Maternal Continuity in the Franco-Cantabrian Region since Pre-Neolithic Times. <i>American Journal of Human Genetics</i> , 2012, 90, 936.	2.6	0
94	Afghanistan's Ethnic Groups Share a Y-Chromosomal Heritage Structured by Historical Events. <i>PLoS ONE</i> , 2012, 7, e34288.	1.1	46
95	North African Populations Carry the Signature of Admixture with Neandertals. <i>PLoS ONE</i> , 2012, 7, e47765.	1.1	67
96	Population Differentiation of Southern Indian Male Lineages Correlates with Agricultural Expansions Predating the Caste System. <i>PLoS ONE</i> , 2012, 7, e50269.	1.1	40
97	Signatures of the Preagricultural Peopling Processes in Sub-Saharan Africa as Revealed by the Phylogeography of Early Y Chromosome Lineages. <i>Molecular Biology and Evolution</i> , 2011, 28, 2603-2613.	3.5	52
98	GHEP-ISFG Proficiency Test 2011: Paper challenge on evaluation of mitochondrial DNA results. <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e545-e547.	0.1	0
99	Similarity in Recombination Rate Estimates Highly Correlates with Genetic Differentiation in Humans. <i>PLoS ONE</i> , 2011, 6, e17913.	1.1	18
100	Human Migration through Bottlenecks from Southeast Asia into East Asia during Last Glacial Maximum Revealed by Y Chromosomes. <i>PLoS ONE</i> , 2011, 6, e24282.	1.1	75
101	The Bantu expansion revisited: a new analysis of Y chromosome variation in Central Western Africa. <i>Molecular Ecology</i> , 2011, 20, 2693-2708.	2.0	47
102	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
103	Influences of history, geography, and religion on genetic structure: the Maronites in Lebanon. <i>European Journal of Human Genetics</i> , 2011, 19, 334-340.	1.4	40
104	An updated tree of Y-chromosome Haplogroup O and revised phylogenetic positions of mutations P164 and PK4. <i>European Journal of Human Genetics</i> , 2011, 19, 1013-1015.	1.4	74
105	Multiplex single-nucleotide polymorphism typing of the human Y chromosome using TaqMan probes. <i>Investigative Genetics</i> , 2011, 2, 13.	3.3	15
106	Mitochondrial DNA structure in North Africa reveals a genetic discontinuity in the Nile Valley. <i>American Journal of Physical Anthropology</i> , 2011, 145, 107-117.	2.1	40
107	Genetic structure of Tunisian ethnic groups revealed by paternal lineages. <i>American Journal of Physical Anthropology</i> , 2011, 146, 271-280.	2.1	43
108	Novel polymorphic AluYb8 insertion in the WNK1 gene is associated with blood pressure variation in Europeans. <i>Human Mutation</i> , 2011, 32, 806-814.	1.1	23

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109	Insights into the Demographic History of African Pygmies from Complete Mitochondrial Genomes. <i>Molecular Biology and Evolution</i> , 2011, 28, 1099-1110.	3.5	105
110	Hunter-gatherer genomic diversity suggests a southern African origin for modern humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5154-5162.	3.3	394
111	Positive selection on mitochondrial M7 lineages among the Gelong people in Hainan. <i>Journal of Human Genetics</i> , 2011, 56, 253-256.	1.1	6
112	Reconstructing the Indian Origin and Dispersal of the European Roma: A Maternal Genetic Perspective. <i>PLoS ONE</i> , 2011, 6, e15988.	1.1	61
113	The Distribution and Most Recent Common Ancestor of the 17q21 Inversion in Humans. <i>American Journal of Human Genetics</i> , 2010, 86, 161-171.	2.6	59
114	The genome-wide structure of the Jewish people. <i>Nature</i> , 2010, 466, 238-242.	13.7	369
115	A New Method to Reconstruct Recombination Events at a Genomic Scale. <i>PLoS Computational Biology</i> , 2010, 6, e1001010.	1.5	14
116	Ancient DNA from European Early Neolithic Farmers Reveals Their Near Eastern Affinities. <i>PLoS Biology</i> , 2010, 8, e1000536.	2.6	339
117	Baseline Brain Perfusion and the Serotonin Transporter Promoter Polymorphism. <i>Biological Psychiatry</i> , 2010, 67, 317-322.	0.7	33
118	Genetic and Demographic Implications of the Bantu Expansion: Insights from Human Paternal Lineages. <i>Molecular Biology and Evolution</i> , 2009, 26, 1581-1589.	3.5	114
119	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
120	Linguistic and maternal genetic diversity are not correlated in Native Mexicans. <i>Human Genetics</i> , 2009, 126, 521-531.	1.8	40
121	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
122	Linguistic, cultural and genetic perspectives on human diversity in west-central Africa. , 2009, , 93-122.		0
123	A novel 154-bp deletion in the human mitochondrial DNA control region in healthy individuals. <i>Human Mutation</i> , 2008, 29, 1387-1391.	1.1	11
124	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
125	Admixture and sexual bias in the population settlement of La Réunion Island (Indian Ocean). <i>American Journal of Physical Anthropology</i> , 2008, 136, 100-107.	2.1	11
126	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

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127	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
128	Northwest Siberian Khanty and Mansi in the junction of West and East Eurasian gene pools as revealed by uniparental markers. <i>European Journal of Human Genetics</i> , 2008, 16, 1254-1264.	1.4	53
129	Genetic origin, admixture, and asymmetry in maternal and paternal human lineages in Cuba. <i>BMC Evolutionary Biology</i> , 2008, 8, 213.	3.2	101
130	Correlation between Genetic and Geographic Structure in Europe. <i>Current Biology</i> , 2008, 18, 1241-1248.	1.8	449
131	Genomic regulation of CTLA4 and Multiple Sclerosis. <i>Journal of Neuroimmunology</i> , 2008, 203, 108-115.	1.1	29
132	CEREBRAL PERFUSION UNDER BASELINE AND COGNITIVE LOAD CONDITIONS AND VARIABILITY IN THE SEROTONIN TRANSPORTER (SERT) GENE: AN ARTERIAL SPIN LABELLING STUDY. <i>Schizophrenia Research</i> , 2008, 102, 199.	1.1	0
133	Independent Introduction of Two Lactase-Persistence Alleles into Human Populations Reflects Different History of Adaptation to Milk Culture. <i>American Journal of Human Genetics</i> , 2008, 82, 57-72.	2.6	301
134	The Dawn of Human Matrilineal Diversity. <i>American Journal of Human Genetics</i> , 2008, 82, 1130-1140.	2.6	392
135	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
136	2006 GEP-ISFG collaborative exercise on mtDNA: reflections about interpretation, artefacts, and DNA mixtures. <i>Forensic Science International: Genetics</i> , 2008, 2, 126-133.	1.6	21
137	Results of the GEP-ISFG collaborative study on an X-STR Decaplex. <i>Forensic Science International: Genetics Supplement Series</i> , 2008, 1, 677-679.	0.1	20
138	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
139	Maternal traces of deep common ancestry and asymmetric gene flow between Pygmy hunter-gatherers and Bantu-speaking farmers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 1596-1601.	3.3	157
140	The Genographic Project Public Participation Mitochondrial DNA Database. <i>PLoS Genetics</i> , 2007, 3, e104.	1.5	99
141	Evidence of Still-Ongoing Convergence Evolution of the Lactase Persistence T-13910 Alleles in Humans. <i>American Journal of Human Genetics</i> , 2007, 81, 615-625.	2.6	135
142	Family-based association study of neuregulin-1 gene and psychosis in a Spanish sample. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2007, 144B, 954-957.	1.1	23
143	SNPlexing the human Y-chromosome: A single-assay system for major haplogroup screening. <i>Electrophoresis</i> , 2007, 28, 3201-3206.	1.3	10
144	Phylogeography of the human mitochondrial L1c haplogroup: Genetic signatures of the prehistory of Central Africa. <i>Molecular Phylogenetics and Evolution</i> , 2007, 43, 635-644.	1.2	56

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145	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
146	The genetics of pre-Roman Iberian Peninsula: A mtDNA study of ancient Iberians. <i>International Congress Series</i> , 2006, 1288, 142-144.	0.2	1
147	Y-chromosome diversity in Bantu and Pygmy populations from Central Africa. <i>International Congress Series</i> , 2006, 1288, 234-236.	0.2	5
148	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, 459-487.	0.3	97
149	Extreme population differences across Neuregulin 1 gene, with implications for association studies. <i>Molecular Psychiatry</i> , 2006, 11, 66-75.	4.1	83
150	The portability of tagSNPs across populations: A worldwide survey. <i>Genome Research</i> , 2006, 16, 323-330.	2.4	82
151	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, .	0.3	2
152	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
153	Haplotype tagging efficiency in worldwide populations in CTLA4 gene. <i>Genes and Immunity</i> , 2005, 6, 646-657.	2.2	21
154	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, 678-681.	2.1	43
155	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
156	Insights into the western Bantu dispersal: mtDNA lineage analysis in Angola. <i>Human Genetics</i> , 2004, 115, 439-47.	1.8	70
157	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
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