

Genes mirror geography within Europe

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Citation Report

#	ARTICLE	IF	CITATIONS
1	The Population Reference Sample, POPRES: A Resource for Population, Disease, and Pharmacological Genetics Research. <i>American Journal of Human Genetics</i> , 2008, 83, 347-358.	2.6	289
2	Response: CALHM1 Association with Alzheimer's Disease Risk. <i>Cell</i> , 2008, 135, 994-996.	13.5	25
3	Genome-Wide Analysis of Single Nucleotide Polymorphisms Uncovers Population Structure in Northern Europe. <i>PLoS ONE</i> , 2008, 3, e3519.	1.1	112
4	Genetic Variation and Population Substructure in Outbred CD-1 Mice: Implications for Genome-Wide Association Studies. <i>PLoS ONE</i> , 2009, 4, e4729.	1.1	123
5	Genetic Structure of Europeans: A View from the North-East. <i>PLoS ONE</i> , 2009, 4, e5472.	1.1	279
6	Genetic Variation and Recent Positive Selection in Worldwide Human Populations: Evidence from Nearly 1 Million SNPs. <i>PLoS ONE</i> , 2009, 4, e7888.	1.1	127
7	Mitochondrial DNA Variants of Respiratory Complex I that Uniquely Characterize Haplogroup T2 Are Associated with Increased Risk of Age-Related Macular Degeneration. <i>PLoS ONE</i> , 2009, 4, e5508.	1.1	89
8	European Population Genetic Substructure: Further Definition of Ancestry Informative Markers for Distinguishing among Diverse European Ethnic Groups. <i>Molecular Medicine</i> , 2009, 15, 371-383.	1.9	77
9	Methods for optimizing statistical analyses in pharmacogenomics research. <i>Expert Review of Clinical Pharmacology</i> , 2009, 2, 559-570.	1.3	9
10	Nature's Genetic Gradients and the Clinical Phenotype. <i>Circulation: Cardiovascular Genetics</i> , 2009, 2, 537-539.	5.1	37
11	Inference of locus-specific ancestry in closely related populations. <i>Bioinformatics</i> , 2009, 25, i213-i221.	1.8	122
12	Global distribution of genomic diversity underscores rich complex history of continental human populations. <i>Genome Research</i> , 2009, 19, 795-803.	2.4	155
13	Geographical structure and differential natural selection among North European populations. <i>Genome Research</i> , 2009, 19, 804-814.	2.4	75
14	Approximate Bayesian Computation Without Summary Statistics: The Case of Admixture. <i>Genetics</i> , 2009, 181, 1507-1519.	1.2	56
15	A Strategy for Analyzing Gene-Nutrient Interactions in Type 2 Diabetes. <i>Journal of Diabetes Science and Technology</i> , 2009, 3, 710-721.	1.3	10
16	Many colorectal cancers are clonal expansions. <i>Cell Cycle</i> , 2009, 8, 2187-2193.	1.3	29
17	Physiogenomic analysis of the Puerto Rican population. <i>Pharmacogenomics</i> , 2009, 10, 565-577.	0.6	28
18	Clinical and basic research papers - March 2009. <i>IBMS BoneKEy</i> , 2009, 6, 94-98.	0.1	0

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19	Impact of apolipoprotein A5 variants on statin treatment efficacy. <i>Pharmacogenomics</i> , 2009, 10, 945-950.	0.6	38
20	A Risk Variant in an miR-125b Binding Site in <i>BMPR1B</i> Is Associated with Breast Cancer Pathogenesis. <i>Cancer Research</i> , 2009, 69, 7459-7465.	0.4	131
21	Genetic Association Studies in Drug-Induced Liver Injury. <i>Seminars in Liver Disease</i> , 2009, 29, 400-411.	1.8	98
22	A Genomewide Comparison of Population Structure at STRPs and Nearby SNPs in Humans. <i>Molecular Biology and Evolution</i> , 2009, 26, 1369-1377.	3.5	25
23	A Genealogical Interpretation of Principal Components Analysis. <i>PLoS Genetics</i> , 2009, 5, e1000686.	1.5	462
24	Common Genetic Variation and the Control of HIV-1 in Humans. <i>PLoS Genetics</i> , 2009, 5, e1000791.	1.5	377
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26	The Impact of Divergence Time on the Nature of Population Structure: An Example from Iceland. <i>PLoS Genetics</i> , 2009, 5, e1000505.	1.5	90
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28	Genome-wide Association Study of Alcohol Dependence. <i>Archives of General Psychiatry</i> , 2009, 66, 773.	13.8	354
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34	Discovering genetic ancestry using spectral graph theory. <i>Genetic Epidemiology</i> , 2010, 34, 51-59.	0.6	90
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40	Looking forwards or looking backwards in avian phylogeography? A comment on Zink and Barrowclough 2008. <i>Molecular Ecology</i> , 2009, 18, 2930-2933.	2.0	200
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58	A spectral graph approach to discovering genetic ancestry. <i>Annals of Applied Statistics</i> , 2010, 4, 179-202.	0.5	26
59	Principal Component Analysis under Population Genetic Models of Range Expansion and Admixture. <i>Molecular Biology and Evolution</i> , 2010, 27, 1257-1268.	3.5	125
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61	Inferring Genetic Ancestry: Opportunities, Challenges, and Implications. <i>American Journal of Human Genetics</i> , 2010, 86, 661-673.	2.6	214
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70	A generic coalescent-based framework for the selection of a reference panel for imputation. <i>Genetic Epidemiology</i> , 2010, 34, 773-782.	0.6	22
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87	COMT but not serotonin-related genes modulates the influence of childhood abuse on anger traits. Genes, Brain and Behavior, 2010, 9, 193-202.	1.1	55
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98	Parallel Adaptation: One or Many Waves of Advance of an Advantageous Allele?. <i>Genetics</i> , 2010, 186, 647-668.	1.2	163
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135	Genetic Characterization of Indigenous Peoples from Oaxaca, Mexico, and Its Relation to Linguistic and Geographic Isolation. <i>Human Biology</i> , 2010, 82, 409-432.	0.4	20
136	Interview with Luigi Luca Cavalli-Sforza: Past Research and Directions for Future Investigations in Human Population Genetics. <i>Human Biology</i> , 2010, 82, 245-266.	0.4	14
137	Genome-wide patterns of population structure and admixture in West Africans and African Americans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 786-791.	3.3	430
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146	Genetic Epidemiology. <i>Methods in Molecular Biology</i> , 2011, , .	0.4	3
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150	The Demand for Social Insurance: Does Culture Matter?. <i>SSRN Electronic Journal</i> , 2011, , .	0.4	7

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156	Association between Variants of the Leptin Receptor Gene (LEPR) and Overweight: A Systematic Review and an Analysis of the CoLaus Study. PLoS ONE, 2011, 6, e26157.	1.1	58
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172	Investigating population stratification and admixture using eigenanalysis of dense genotypes. <i>Heredity</i> , 2011, 107, 413-420.	1.2	27
173	Contrasting signals of positive selection in genes involved in human skin-color variation from tests based on SNP scans and resequencing. <i>Investigative Genetics</i> , 2011, 2, 24.	3.3	17
174	Range-wide genetic population structure of common pochard (<i>Aythya ferina</i>): a potentially important vector of highly pathogenic avian influenza viruses. <i>Ecology and Evolution</i> , 2011, 1, 529-545.	0.8	18
175	The use of race, ethnicity and ancestry in human genetic research. <i>The HUGO Journal</i> , 2011, 5, 47-63.	4.1	38
176	Replication of genome-wide discovered breast cancer risk loci in the Cypriot population. <i>Breast Cancer Research and Treatment</i> , 2011, 128, 267-272.	1.1	8
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181	Southeast Asian origins of five Hill Tribe populations and correlation of genetic to linguistic relationships inferred with genome-wide SNP data. <i>American Journal of Physical Anthropology</i> , 2011, 144, 300-308.	2.1	16
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