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Citation Report

#	ARTICLE	IF	CITATIONS
1	The delayed rise of present-day mammals. <i>Nature</i> , 2007, 446, 507-512.	27.8	1,832
2	Structural basis for specific cleavage of Lys <sup>63</sup> -linked polyubiquitin chains. <i>Nature</i> , 2008, 455, 358-362.	27.8	300
3	STING is an endoplasmic reticulum adaptor that facilitates innate immune signalling. <i>Nature</i> , 2008, 455, 674-678.	27.8	2,526
4	Genes mirror geography within Europe. <i>Nature</i> , 2008, 456, 98-101.	27.8	1,287
11	Laplacian Eigenfunctions Learn Population Structure. <i>PLoS ONE</i> , 2009, 4, e7928.	2.5	24
12	Global distribution of genomic diversity underscores rich complex history of continental human populations. <i>Genome Research</i> , 2009, 19, 795-803.	5.5	155
13	Application of principal component analysis to pharmacogenomic studies in Canada. <i>Pharmacogenomics Journal</i> , 2009, 9, 362-372.	2.0	23
14	Fine-scaled human genetic structure revealed by SNP microarrays. <i>Genome Research</i> , 2009, 19, 815-825.	5.5	91
15	Discovering genetic ancestry using spectral graph theory. <i>Genetic Epidemiology</i> , 2010, 34, 51-59.	1.3	90
17	Copy number variation in African Americans. <i>BMC Genetics</i> , 2009, 10, 15.	2.7	29
18	Shared susceptibility variations in autoimmune diseases: a brief perspective on common issues. <i>Genes and Immunity</i> , 2009, 10, 1-4.	4.1	26
19	HLA-B*5701 genotype is a major determinant of drug-induced liver injury due to flucloxacillin. <i>Nature Genetics</i> , 2009, 41, 816-819.	21.4	950
20	Lowering industry firewalls: pre-competitive informatics initiatives in drug discovery. <i>Nature Reviews Drug Discovery</i> , 2009, 8, 701-708.	46.4	79
21	Spatial patterns of variation due to natural selection in humans. <i>Nature Reviews Genetics</i> , 2009, 10, 745-755.	16.3	180
22	Genome-wide Insights into the Patterns and Determinants of Fine-Scale Population Structure in Humans. <i>American Journal of Human Genetics</i> , 2009, 84, 641-650.	6.2	51
23	A spectral graph approach to discovering genetic ancestry. <i>Annals of Applied Statistics</i> , 2010, 4, 179-202.	1.1	26
24	Abraham's Children in the Genome Era: Major Jewish Diaspora Populations Comprise Distinct Genetic Clusters with Shared Middle Eastern Ancestry. <i>American Journal of Human Genetics</i> , 2010, 86, 850-859.	6.2	217
25	Population Genetic Structure of the People of Qatar. <i>American Journal of Human Genetics</i> , 2010, 87, 17-25.	6.2	110

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26	Connecting the Human Variome Project to nutrigenomics. <i>Genes and Nutrition</i> , 2010, 5, 275-283.	2.5	6
27	Meta-analysis of genetic association studies and adjustment for multiple testing of correlated SNPs and traits. <i>Genetic Epidemiology</i> , 2010, 34, 739-746.	1.3	18
28	Using ancestry matching to combine family-based and unrelated samples for genome-wide association studies. <i>Statistics in Medicine</i> , 2010, 29, 2932-2945.	1.6	15
29	Analysis of Population Structure: A Unifying Framework and Novel Methods Based on Sparse Factor Analysis. <i>PLoS Genetics</i> , 2010, 6, e1001117.	3.5	123
30	Ascertainment Biases in SNP Chips Affect Measures of Population Divergence. <i>Molecular Biology and Evolution</i> , 2010, 27, 2534-2547.	8.9	317
31	Genome-wide patterns of population structure and admixture among Hispanic/Latino populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 8954-8961.	7.1	360
32	Genomic and geographic distribution of SNP-defined runs of homozygosity in Europeans. <i>Human Molecular Genetics</i> , 2010, 19, 2927-2935.	2.9	146
33	Population differentiation as a test for selective sweeps. <i>Genome Research</i> , 2010, 20, 393-402.	5.5	600
34	Genetics and Genomics of Human Population Structure. , 2010, , 589-615.		2
35	<i>Genetic Epidemiology</i> . , 2010, , 617-634.		0
36	Ancestry informative markers for fine-scale individual assignment to worldwide populations. <i>Journal of Medical Genetics</i> , 2010, 47, 835-847.	3.2	65
37	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.	7.1	430
38	A Consensus Tree Approach for Reconstructing Human Evolutionary History and Detecting Population Substructure. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 918-928.	3.0	5
39	Susceptibility to Amoxicillin-Clavulanate-Induced Liver Injury Is Influenced by Multiple HLA Class I and II Alleles. <i>Gastroenterology</i> , 2011, 141, 338-347.	1.3	412
40	hzAnalyzer: detection, quantification, and visualization of contiguous homozygosity in high-density genotyping datasets. <i>Genome Biology</i> , 2011, 12, R21.	9.6	3
41	Perspectives on Human Population Structure at the Cusp of the Sequencing Era. <i>Annual Review of Genomics and Human Genetics</i> , 2011, 12, 245-274.	6.2	69
42	Overview: Adverse Drug Reactions. , 0, , 27-37.		0
43	Assessing and managing risk when sharing aggregate genetic variant data. <i>Nature Reviews Genetics</i> , 2011, 12, 730-736.	16.3	48

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44	Genetic variation in the Sorbs of eastern Germany in the context of broader European genetic diversity. <i>European Journal of Human Genetics</i> , 2011, 19, 995-1001.	2.8	59
45	Indian Siddis: African Descendants with Indian Admixture. <i>American Journal of Human Genetics</i> , 2011, 89, 154-161.	6.2	50
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47	Recommendations for genetic variation data capture in developing countries to ensure a comprehensive worldwide data collection. <i>Human Mutation</i> , 2011, 32, 2-9.	2.5	25
48	Phased Whole-Genome Genetic Risk in a Family Quartet Using a Major Allele Reference Sequence. <i>PLoS Genetics</i> , 2011, 7, e1002280.	3.5	137
49	Genetic Association and Gene-Environment Interaction: A New Method for Overcoming the Lack of Exposure Information in Controls. <i>American Journal of Epidemiology</i> , 2011, 173, 225-235.	3.4	23
50	The History of African Gene Flow into Southern Europeans, Levantines, and Jews. <i>PLoS Genetics</i> , 2011, 7, e1001373.	3.5	224
51	A Quantitative Comparison of the Similarity between Genes and Geography in Worldwide Human Populations. <i>PLoS Genetics</i> , 2012, 8, e1002886.	3.5	106
52	Genomewide Pharmacogenetics of Bisphosphonate-Induced Osteonecrosis of the Jaw: The Role of <i>RBMS3</i> . <i>Oncologist</i> , 2012, 17, 279-287.	3.7	100
53	Sequencing human diversity. <i>Science-Business EXchange</i> , 2012, 5, 567-567.	0.0	0
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55	Heterogeneity in Genetic Admixture across Different Regions of Argentina. <i>PLoS ONE</i> , 2012, 7, e34695.	2.5	117
56	Combining Markers into Haplotypes Can Improve Population Structure Inference. <i>Genetics</i> , 2012, 190, 159-174.	2.9	42
57	Limited contribution of common genetic variants to risk for liver injury due to a variety of drugs. <i>Pharmacogenetics and Genomics</i> , 2012, 22, 784-795.	1.5	108
58	Genome resequencing reveals multiscale geographic structure and extensive linkage disequilibrium in the forest tree <i>Populus trichocarpa</i> . <i>New Phytologist</i> , 2012, 196, 713-725.	7.3	173
59	The '3Is' of animal experimentation. <i>Nature Genetics</i> , 2012, 44, 611-611.	21.4	6
60	New insights into the Tyrolean Iceman's origin and phenotype as inferred by whole-genome sequencing. <i>Nature Communications</i> , 2012, 3, 698.	12.8	382
61	Evidence of widespread selection on standing variation in Europe at height-associated SNPs. <i>Nature Genetics</i> , 2012, 44, 1015-1019.	21.4	315

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62	Ancient Admixture in Human History. <i>Genetics</i> , 2012, 192, 1065-1093.	2.9	2,012
63	Dissecting the genetic make-up of North-East Sardinia using a large set of haploid and autosomal markers. <i>European Journal of Human Genetics</i> , 2012, 20, 956-964.	2.8	13
64	Exploring Genomic Structure Differences and Similarities between the Greek and European HapMap Populations: Implications for Association Studies. <i>Annals of Human Genetics</i> , 2012, 76, 472-483.	0.8	6
65	An Abundance of Rare Functional Variants in 202 Drug Target Genes Sequenced in 14,002 People. <i>Science</i> , 2012, 337, 100-104.	12.6	626
66	A model-based approach for analysis of spatial structure in genetic data. <i>Nature Genetics</i> , 2012, 44, 725-731.	21.4	147
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68	Stratificationâ€Score Matching Improves Correction for Confounding by Population Stratification in Caseâ€Control Association Studies. <i>Genetic Epidemiology</i> , 2012, 36, 195-205.	1.3	21
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73	Neurodegenerative Diseases: Integrative PPM Approach as the Medicine of the Future. <i>Advances in Predictive, Preventive and Personalised Medicine</i> , 2013, , .	0.6	3
74	GeneOnEarth: Fitting Genetic PC Plots on the Globe. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 1009-1016.	3.0	2
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76	Genetic ancestry inference using support vector machines, and the active emergence of a unique American population. <i>European Journal of Human Genetics</i> , 2013, 21, 554-562.	2.8	16
77	Separation of the largest eigenvalues in eigenanalysis of genotype data from discrete subpopulations. <i>Theoretical Population Biology</i> , 2013, 89, 34-43.	1.1	22
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79	Enhanced Localization of Genetic Samples through Linkage-Disequilibrium Correction. <i>American Journal of Human Genetics</i> , 2013, 92, 882-894.	6.2	31

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81	Anisotropic Isolation by Distance: The Main Orientations of Human Genetic Differentiation. <i>Molecular Biology and Evolution</i> , 2013, 30, 513-525.	8.9	35
82	Analysis of Latino populations from GALA and MEC studies reveals genomic loci with biased local ancestry estimation. <i>Bioinformatics</i> , 2013, 29, 1407-1415.	4.1	38
83	Reconstructing the Population Genetic History of the Caribbean. <i>PLoS Genetics</i> , 2013, 9, e1003925.	3.5	296
84	Analysis of the Genetic Basis of Disease in the Context of Worldwide Human Relationships and Migration. <i>PLoS Genetics</i> , 2013, 9, e1003447.	3.5	67
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87	The Impact of Computer Science in Molecular Medicine: Enabling High- Throughput Research. <i>Current Topics in Medicinal Chemistry</i> , 2013, 13, 526-575.	2.1	13
88	Genome-Wide Association Study Link Novel Loci to Endometriosis. <i>PLoS ONE</i> , 2013, 8, e58257.	2.5	121
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90	Analyzing Genome-Wide Association Studies with an FDR Controlling Modification of the Bayesian Information Criterion. <i>PLoS ONE</i> , 2014, 9, e103322.	2.5	18
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94	Neutral genomic regions refine models of recent rapid human population growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 757-762.	7.1	106
95	Chip-based direct genotyping of coding variants in genome wide association studies: Utility, issues and prospects. <i>Gene</i> , 2014, 540, 104-109.	2.2	10
96	Ancestry estimation and control of population stratification for sequence-based association studies. <i>Nature Genetics</i> , 2014, 46, 409-415.	21.4	136
97	Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. <i>Nature</i> , 2014, 507, 225-228.	27.8	328

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136	EigenGWAS: finding loci under selection through genome-wide association studies of eigenvectors in structured populations. Heredity, 2016, 117, 51-61.	2.6	69
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154	Reconstructing human population history from dental phenotypes. <i>Scientific Reports</i> , 2017, 7, 12495.	3.3	46
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160	Enlarging the gene-geography of Europe and the Mediterranean area to STR loci of common forensic use: longitudinal and latitudinal frequency gradients. <i>Annals of Human Biology</i> , 2018, 45, 77-85.	1.0	5
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166	The Synthesis of the Tang Dynasty. , 2018, , 108-122.		0
167	Genetic History and Migrations in Western Eurasia, 500–1000. , 2018, , 135-150.		2
168	Northern Invaders. , 2018, , 151-165.		3
169	Chinese and Inner Asian Perspectives on the History of the Northern Dynasties (386–589) in Chinese Historiography. , 2018, , 166-175.		0
170	The Spread of Buddhist Culture to China between the Third and Seventh Centuries. , 2018, , 220-234.		0
171	Infrastructures of Legitimacy in Inner Asia. , 2018, , 302-316.		0
172	The Stateless Nomads of Central Eurasia. , 2018, , 317-332.		1
173	Aspects of Elite Representation among the Sixth- and Seventh-Century Turks. , 2018, , 333-356.		1

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175	Ideological Interweaving in Eastern Eurasia. , 2018, , 386-399.		0
176	Followers and Leaders in Northeastern Eurasia, ca. Seventh to Tenth Centuries. , 2018, , 400-418.		0
181	How the Steppes Became Byzantine. , 2018, , 19-34.		2
182	The Relations between China and the Steppe. , 2018, , 35-53.		1
183	Sasanian Iran and the Projection of Power in Late Antique Eurasia. , 2018, , 54-69.		2
184	“Charismatic” Goods. , 2018, , 96-107.		0
185	Central Asia in the Late Roman Mental Map, Second to Sixth Centuries. , 2018, , 123-132.		0
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188	The Languages of Christianity on the Silk Roads and the Transmission of Mediterranean Culture into Central Asia. , 2018, , 206-219.		0
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191	Byzantium’s Eurasian Policy in the Age of the Turk Empire. , 2018, , 271-286.		2
192	Sasanian Iran and Its Northeastern Frontier. , 2018, , 287-301.		9
193	Patterns of Roman Diplomacy with Iran and the Steppe Peoples. , 2018, , 357-368.		1
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197	Population genomic analysis of elongated skulls reveals extensive female-biased immigration in Early Medieval Bavaria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3494-3499.	7.1	73
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