

Luca Pagani

List of Publications by Year in descending order

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Version: 2024-02-01

88

papers

5,148

citations

126708

33

h-index

110170

64

g-index

106

all docs

106

docs citations

106

times ranked

8753

citing authors

#	ARTICLE	IF	CITATIONS
1	The African Genome Variation Project shapes medical genetics in Africa. <i>Nature</i> , 2015, 517, 327-332.	13.7	473
2	Genomic analyses inform on migration events during the peopling of Eurasia. <i>Nature</i> , 2016, 538, 238-242.	13.7	360
3	A recent bottleneck of Y chromosome diversity coincides with a global change in culture. <i>Genome Research</i> , 2015, 25, 459-466.	2.4	348
4	Mountain gorilla genomes reveal the impact of long-term population decline and inbreeding. <i>Science</i> , 2015, 348, 242-245.	6.0	326
5	Deeply divergent archaic mitochondrial genome provides lower time boundary for African gene flow into Neanderthals. <i>Nature Communications</i> , 2017, 8, 16046.	5.8	211
6	Evidence for a Common Origin of Blacksmiths and Cultivators in the Ethiopian Ari within the Last 4500 Years: Lessons for Clustering-Based Inference. <i>PLoS Genetics</i> , 2015, 11, e1005397.	1.5	194
7	Multiple Deeply Divergent Denisovan Ancestries in Papuans. <i>Cell</i> , 2019, 177, 1010-1021.e32.	13.5	181
8	Ethiopian Genetic Diversity Reveals Linguistic Stratification and Complex Influences on the Ethiopian Gene Pool. <i>American Journal of Human Genetics</i> , 2012, 91, 83-96.	2.6	177
9	Genetic Signatures Reveal High-Altitude Adaptation in a Set of Ethiopian Populations. <i>Molecular Biology and Evolution</i> , 2013, 30, 1877-1888.	3.5	173
10	Tracing the Route of Modern Humans out of Africa by Using 225 Human Genome Sequences from Ethiopians and Egyptians. <i>American Journal of Human Genetics</i> , 2015, 96, 986-991.	2.6	152
11	Ancient human parallel lineages within North America contributed to a coastal expansion. <i>Science</i> , 2018, 360, 1024-1027.	6.0	138
12	Genome-Wide Analysis of Cold Adaptation in Indigenous Siberian Populations. <i>PLoS ONE</i> , 2014, 9, e98076.	1.1	128
13	A Selective Sweep on a Deleterious Mutation in CPT1A in Arctic Populations. <i>American Journal of Human Genetics</i> , 2014, 95, 584-589.	2.6	119
14	Geographic population structure analysis of worldwide human populations infers their biogeographical origins. <i>Nature Communications</i> , 2014, 5, 3513.	5.8	114
15	Extensive Farming in Estonia Started through a Sex-Biased Migration from the Steppe. <i>Current Biology</i> , 2017, 27, 2185-2193.e6.	1.8	111
16	The Genomic Impact of European Colonization of the Americas. <i>Current Biology</i> , 2019, 29, 3974-3986.e4.	1.8	89
17	Genome-wide evidence of Austronesian-Bantu admixture and cultural reversion in a hunter-gatherer group of Madagascar. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 936-941.	3.3	75
18	Revisiting the Thrifty Gene Hypothesis via 65 Loci Associated with Susceptibility to Type 2 Diabetes. <i>American Journal of Human Genetics</i> , 2014, 94, 176-185.	2.6	72

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19	Human genomic regions with exceptionally high levels of population differentiation identified from 911 whole-genome sequences. <i>Genome Biology</i> , 2014, 15, R88.	13.9	72
20	Global diversity in the TAS2R38 bitter taste receptor: revisiting a classic evolutionary PROPosal. <i>Scientific Reports</i> , 2016, 6, 25506.	1.6	69
21	Selective sweep on human amylase genes postdates the split with Neanderthals. <i>Scientific Reports</i> , 2016, 6, 37198.	1.6	67
22	Evolution of the Pygmy Phenotype: Evidence of Positive Selection from Genome-wide Scans in African, Asian, and Melanesian Pygmies. <i>Human Biology</i> , 2013, 85, 251-284.	0.4	66
23	Ancestry deconvolution and partial polygenic score can improve susceptibility predictions in recently admixed individuals. <i>Nature Communications</i> , 2020, 11, 1628.	5.8	66
24	Disentangling Timing of Admixture, Patterns of Introgression, and Phenotypic Indicators in a Hybridizing Wolf Population. <i>Molecular Biology and Evolution</i> , 2017, 34, 2324-2339.	3.5	62
25	Creating artificial human genomes using generative neural networks. <i>PLoS Genetics</i> , 2021, 17, e1009303.	1.5	62
26	The Andean Adaptive Toolkit to Counteract High Altitude Maladaptation: Genome-Wide and Phenotypic Analysis of the Collas. <i>PLoS ONE</i> , 2014, 9, e93314.	1.1	55
27	The GenoChip: A New Tool for Genetic Anthropology. <i>Genome Biology and Evolution</i> , 2013, 5, 1021-1031.	1.1	54
28	Population structure of modern-day Italians reveals patterns of ancient and archaic ancestries in Southern Europe. <i>Science Advances</i> , 2019, 5, eaaw3492.	4.7	53
29	Ancient and recent admixture layers in Sicily and Southern Italy trace multiple migration routes along the Mediterranean. <i>Scientific Reports</i> , 2017, 7, 1984.	1.6	52
30	Multi-layered population structure in Island Southeast Asians. <i>European Journal of Human Genetics</i> , 2016, 24, 1605-1611.	1.4	50
31	A Cover Story for a Nature cover: genetic signature of human expansions into Eurasia revealed by a panel of worldwide high coverage genomes. <i>Journal of Anthropological Sciences</i> , 2017, 95, 1-5.	0.4	49
32	The Kalash Genetic Isolate: Ancient Divergence, Drift, and Selection. <i>American Journal of Human Genetics</i> , 2015, 96, 775-783.	2.6	46
33	Disentangling Immediate Adaptive Introgression from Selection on Standing Introgressed Variation in Humans. <i>Molecular Biology and Evolution</i> , 2018, 35, 623-630.	3.5	46
34	Shifts in the Genetic Landscape of the Western Eurasian Steppe Associated with the Beginning and End of the Scythian Dominance. <i>Current Biology</i> , 2019, 29, 2430-2441.e10.	1.8	44
35	The Genetic Ancestry of Modern Indus Valley Populations from Northwest India. <i>American Journal of Human Genetics</i> , 2018, 103, 918-929.	2.6	38
36	Ancient genomes reveal structural shifts after the arrival of Steppe-related ancestry in the Italian Peninsula. <i>Current Biology</i> , 2021, 31, 2576-2591.e12.	1.8	38

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37	Inferring patterns of folktale diffusion using genomic data. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 9140-9145.	3.3	37
38	Genomic approaches to identify hybrids and estimate admixture times in European wildcat populations. Scientific Reports, 2019, 9, 11612.	1.6	34
39	Genetic signature of differential sensitivity to stevioside in the Italian population. Genes and Nutrition, 2014, 9, 401.	1.2	33
40	Positive selection of AS3MT to arsenic water in Andean populations. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2015, 780, 97-102.	0.4	32
41	High altitude adaptation in Daghestani populations from the Caucasus. Human Genetics, 2012, 131, 423-433.	1.8	31
42	The genetic legacy of continental scale admixture in Indian Austroasiatic speakers. Scientific Reports, 2019, 9, 3818.	1.6	30
43	Archaeogenomic distinctiveness of the Isthmo-Colombian area. Cell, 2021, 184, 1706-1723.e24.	13.5	30
44	Evidence of Early-Stage Selection on EPAS1 and GPR126 Genes in Andean High Altitude Populations. Scientific Reports, 2017, 7, 13042.	1.6	29
45	Detection of Neanderthal Adaptively Introgressed Genetic Variants That Modulate Reporter Gene Expression in Human Immune Cells. Molecular Biology and Evolution, 2022, 39, .	3.5	24
46	An African-specific haplotype in MRGPRX4 is associated with menthol cigarette smoking. PLoS Genetics, 2019, 15, e1007916.	1.5	23
47	Differences in local population history at the finest level: the case of the Estonian population. European Journal of Human Genetics, 2020, 28, 1580-1591.	1.4	23
48	Mutation Rates and Discriminating Power for 13 Rapidly-Mutating Y-STRs between Related and Unrelated Individuals. PLoS ONE, 2016, 11, e0165678.	1.1	22
49	Ancestry-Specific Analyses Reveal Differential Demographic Histories and Opposite Selective Pressures in Modern South Asian Populations. Molecular Biology and Evolution, 2019, 36, 1628-1642.	3.5	20
50	Partial <i>F8</i> gene duplication (factor VIII Padua) associated with high factor VIII levels and familial thrombophilia. Blood, 2021, 137, 2383-2393.	0.6	20
51	A general linear model-based approach for inferring selection to climate. BMC Genetics, 2013, 14, 87.	2.7	18
52	Genetic and phenotypic differentiation of an Andean intermediate altitude population. Physiological Reports, 2015, 3, e12376.	0.7	18
53	Impact of non-LTR retrotransposons in the differentiation and evolution of anatomically modern humans. Mobile DNA, 2018, 9, 28.	1.3	18
54	Early Alpine occupation backdates westward human migration in Late Glacial Europe. Current Biology, 2021, 31, 2484-2493.e7.	1.8	17

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55	The key role of patrilineal inheritance in shaping the genetic variation of Dagestan highlanders. <i>Journal of Human Genetics</i> , 2009, 54, 689-694.	1.1	16
56	Overcoming the dichotomy between open and isolated populations using genomic data from a large European dataset. <i>Scientific Reports</i> , 2017, 7, 41614.	1.6	15
57	Genetics and Material Culture Support Repeated Expansions into Paleolithic Eurasia from a Population Hub Out of Africa. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	15
58	Three Reportedly Unrelated Families With Liddle Syndrome Inherited From a Common Ancestor. <i>Hypertension</i> , 2018, 71, 273-279.	1.3	14
59	West Asian sources of the Eurasian component in Ethiopians: a reassessment. <i>Scientific Reports</i> , 2019, 9, 18811.	1.6	14
60	The genetic variation in the R1a clade among the Ashkenazi Levitesâ€™ Y chromosome. <i>Scientific Reports</i> , 2017, 7, 14969.	1.6	13
61	Evolution of the Pygmy Phenotype: Evidence of Positive Selection from Genome-wide Scans in African, Asian, and Melanesian Pygmies. <i>Human Biology</i> , 2013, 85, 251.	0.4	12
62	High Levels of Genetic Diversity within Nilo-Saharan Populations: Implications for Human Adaptation. <i>American Journal of Human Genetics</i> , 2020, 107, 473-486.	2.6	12
63	Through 40,000Âyears of human presence in Southern Europe: the Italian case study. <i>Human Genetics</i> , 2021, 140, 1417-1431.	1.8	11
64	Patterns of genetic connectedness between modern and medieval Estonian genomes reveal the origins of a major ancestry component of the Finnish population. <i>American Journal of Human Genetics</i> , 2021, 108, 1792-1806.	2.6	11
65	A world in a grain of sand: human history from genetic data. <i>Genome Biology</i> , 2011, 12, 234.	13.9	9
66	The Genetic Origin of Daunians and the Pan-Mediterranean Southern Italian Iron Age Context. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	9
67	Mitochondrial and Y chromosome haplotype motifs as diagnostic markers of Jewish ancestry: a reconsideration. <i>Frontiers in Genetics</i> , 2014, 5, 384.	1.1	8
68	Human evolutionary history of Eastern Africa. <i>Current Opinion in Genetics and Development</i> , 2018, 53, 134-139.	1.5	8
69	The dual origin of tatiâ€speakers from dagestan as written in the genealogy of uniparental variants. <i>American Journal of Human Biology</i> , 2012, 24, 391-399.	0.8	7
70	Positive selection in admixed populations from Ethiopia. <i>BMC Genetics</i> , 2020, 21, 108.	2.7	6
71	Improving Selection Detection with Population Branch Statistic on Admixed Populations. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
72	Evaluating the Impact of Sex-Biased Genetic Admixture in the Americas through the Analysis of Haplotype Data. <i>Genes</i> , 2021, 12, 1580.	1.0	6

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73	Revisiting the out of Africa event with a deep-learning approach. American Journal of Human Genetics, 2021, 108, 2037-2051.	2.6	6
74	Ancestral genomic contributions to complex traits in contemporary Europeans. Current Biology, 2022, 32, 1412-1419.e3.	1.8	6
75	Genes Regulated by Vitamin D in Bone Cells Are Positively Selected in East Asians. PLoS ONE, 2015, 10, e0146072.	1.1	5
76	Reply to dâ€™Huy et al.: Navigating biases and charting new ground in the cultural diffusion of folktales. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E8556.	3.3	4
77	Response to Wyckelsma et al.: Loss of Î±-actinin-3 during human evolution provides superior cold resilience and muscle heat generation. American Journal of Human Genetics, 2022, 109, 967-972.	2.6	4
78	Inter-individual genomic heterogeneity within European population isolates. PLoS ONE, 2019, 14, e0214564.	1.1	3
79	A Chromosome-Painting-Based Pipeline to Infer Local Ancestry under Limited Source Availability. Genome Biology and Evolution, 2021, 13, .	1.1	3
80	An Ethnolinguistic and Genetic Perspective on the Origins of the Dravidian-Speaking Brahui in Pakistan. Man in India, 2017, 97, 267-278.	2.0	3
81	Application of Graph Theory to the elaboration of personal genomic data for genealogical research. PeerJ Computer Science, 0, 1, e27.	2.7	2
82	Response to Hellenthal et al.: American Journal of Human Genetics, 2016, 98, 398.	2.6	1
83	Phylogenetic history of patrilineages rare in northern and eastern Europe from large-scale re-sequencing of human Y-chromosomes. European Journal of Human Genetics, 2021, 29, 1510-1519.	1.4	1
84	Cross-continental admixture in the Kho population from northwest Pakistan. European Journal of Human Genetics, 2022, , .	1.4	1
85	First Application of a Distance-Based Outlier Approach to Detect Highly Differentiated Genomic Regions Across Human Populations. , 2015, , 133-144.		0
86	Shifts in the Genetic Landscape of the Western Eurasian Steppe Associated with the Beginning and End of the Scythian Dominance. SSRN Electronic Journal, 0, , .	0.4	0
87	Next questions in Molecular Anthropology. Journal of Anthropological Sciences, 2021, 99, .	0.4	0
88	Assessing temporal and geographic contacts across the Adriatic Sea through the analysis of genome-wide data from Southern Italy. Genomics, 2022, 114, 110405.	1.3	0