

# Luca Pagani

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5573144/publications.pdf>

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	Detection of Neanderthal Adaptively Introgressed Genetic Variants That Modulate Reporter Gene Expression in Human Immune Cells. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	24
2	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
3	Ancestral genomic contributions to complex traits in contemporary Europeans. <i>Current Biology</i> , 2022, 32, 1412-1419.e3.	1.8	6
4	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
5	Cross-continental admixture in the Kho population from northwest Pakistan. <i>European Journal of Human Genetics</i> , 2022, , .	1.4	1
6	Response to Wyckelsma et al.: Loss of $\beta$ -actinin-3 during human evolution provides superior cold resilience and muscle heat generation. <i>American Journal of Human Genetics</i> , 2022, 109, 967-972.	2.6	4
7	Assessing temporal and geographic contacts across the Adriatic Sea through the analysis of genome-wide data from Southern Italy. <i>Genomics</i> , 2022, 114, 110405.	1.3	0
8	Partial <i>F8</i> gene duplication (factor VIII Padua) associated with high factor VIII levels and familial thrombophilia. <i>Blood</i> , 2021, 137, 2383-2393.	0.6	20
9	Creating artificial human genomes using generative neural networks. <i>PLoS Genetics</i> , 2021, 17, e1009303.	1.5	62
10	Improving Selection Detection with Population Branch Statistic on Admixed Populations. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
11	A Chromosome-Painting-Based Pipeline to Infer Local Ancestry under Limited Source Availability. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	3
12	Archaeogenomic distinctiveness of the Isthmo-Colombian area. <i>Cell</i> , 2021, 184, 1706-1723.e24.	13.5	30
13	Phylogenetic history of patrilineages rare in northern and eastern Europe from large-scale re-sequencing of human Y-chromosomes. <i>European Journal of Human Genetics</i> , 2021, 29, 1510-1519.	1.4	1
14	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
15	Early Alpine occupation backdates westward human migration in Late Glacial Europe. <i>Current Biology</i> , 2021, 31, 2484-2493.e7.	1.8	17
16	Through 40,000 years of human presence in Southern Europe: the Italian case study. <i>Human Genetics</i> , 2021, 140, 1417-1431.	1.8	11
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	Revisiting the out of Africa event with a deep-learning approach. <i>American Journal of Human Genetics</i> , 2021, 108, 2037-2051.	2.6	6
20	Next questions in Molecular Anthropology. <i>Journal of Anthropological Sciences</i> , 2021, 99, .	0.4	0
21	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
22	Differences in local population history at the finest level: the case of the Estonian population. <i>European Journal of Human Genetics</i> , 2020, 28, 1580-1591.	1.4	23
23	Positive selection in admixed populations from Ethiopia. <i>BMC Genetics</i> , 2020, 21, 108.	2.7	6
24	Ancestry deconvolution and partial polygenic score can improve susceptibility predictions in recently admixed individuals. <i>Nature Communications</i> , 2020, 11, 1628.	5.8	66
25	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
26	Inter-individual genomic heterogeneity within European population isolates. <i>PLoS ONE</i> , 2019, 14, e0214564.	1.1	3
27	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
28	Genomic approaches to identify hybrids and estimate admixture times in European wildcat populations. <i>Scientific Reports</i> , 2019, 9, 11612.	1.6	34
29	The genetic legacy of continental scale admixture in Indian Austroasiatic speakers. <i>Scientific Reports</i> , 2019, 9, 3818.	1.6	30
30	Multiple Deeply Divergent Denisovan Ancestries in Papuans. <i>Cell</i> , 2019, 177, 1010-1021.e32.	13.5	181
31	Ancestry-Specific Analyses Reveal Differential Demographic Histories and Opposite Selective Pressures in Modern South Asian Populations. <i>Molecular Biology and Evolution</i> , 2019, 36, 1628-1642.	3.5	20
32	An African-specific haplotype in MRGPRX4 is associated with menthol cigarette smoking. <i>PLoS Genetics</i> , 2019, 15, e1007916.	1.5	23
33	West Asian sources of the Eurasian component in Ethiopians: a reassessment. <i>Scientific Reports</i> , 2019, 9, 18811.	1.6	14
34	The Genomic Impact of European Colonization of the Americas. <i>Current Biology</i> , 2019, 29, 3974-3986.e4.	1.8	89
35	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
36	Three Reportedly Unrelated Families With Liddle Syndrome Inherited From a Common Ancestor. <i>Hypertension</i> , 2018, 71, 273-279.	1.3	14

#	ARTICLE	IF	CITATIONS
37	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
38	Human evolutionary history of Eastern Africa. <i>Current Opinion in Genetics and Development</i> , 2018, 53, 134-139.	1.5	8
39	Impact of non-LTR retrotransposons in the differentiation and evolution of anatomically modern humans. <i>Mobile DNA</i> , 2018, 9, 28.	1.3	18
40	Ancient human parallel lineages within North America contributed to a coastal expansion. <i>Science</i> , 2018, 360, 1024-1027.	6.0	138
41	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
42	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
43	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
44	The genetic variation in the R1a clade among the Ashkenazi Levitesâ€™ Y chromosome. <i>Scientific Reports</i> , 2017, 7, 14969.	1.6	13
45	Reply to Huy et al.: Navigating biases and charting new ground in the cultural diffusion of folktales. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E8556.	3.3	4
46	Evidence of Early-Stage Selection on EPAS1 and GPR126 Genes in Andean High Altitude Populations. <i>Scientific Reports</i> , 2017, 7, 13042.	1.6	29
47	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
48	Inferring patterns of folktale diffusion using genomic data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 9140-9145.	3.3	37
49	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
50	An Ethnolinguistic and Genetic Perspective on the Origins of the Dravidian-Speaking Brahui in Pakistan. <i>Man in India</i> , 2017, 97, 267-278.	2.0	3
51	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
52	Mutation Rates and Discriminating Power for 13 Rapidly-Mutating Y-STRs between Related and Unrelated Individuals. <i>PLoS ONE</i> , 2016, 11, e0165678.	1.1	22
53	Global diversity in the TAS2R38 bitter taste receptor: revisiting a classic evolutionary PROPosal. <i>Scientific Reports</i> , 2016, 6, 25506.	1.6	69
54	Genomic analyses inform on migration events during the peopling of Eurasia. <i>Nature</i> , 2016, 538, 238-242.	13.7	360

#	ARTICLE	IF	CITATIONS
55	Selective sweep on human amylase genes postdates the split with Neanderthals. <i>Scientific Reports</i> , 2016, 6, 37198.	1.6	67
56	Multi-layered population structure in Island Southeast Asians. <i>European Journal of Human Genetics</i> , 2016, 24, 1605-1611.	1.4	50
57	Response to Hellenthal et al.: American Journal of Human Genetics, 2016, 98, 398.	2.6	1
58	Genetic and phenotypic differentiation of an Andean intermediate altitude population. <i>Physiological Reports</i> , 2015, 3, e12376.	0.7	18
59	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
60	Genes Regulated by Vitamin D in Bone Cells Are Positively Selected in East Asians. <i>PLoS ONE</i> , 2015, 10, e0146072.	1.1	5
61	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
62	The Kalash Genetic Isolate: Ancient Divergence, Drift, and Selection. <i>American Journal of Human Genetics</i> , 2015, 96, 775-783.	2.6	46
63	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
64	Mountain gorilla genomes reveal the impact of long-term population decline and inbreeding. <i>Science</i> , 2015, 348, 242-245.	6.0	326
65	Positive selection of AS3MT to arsenic water in Andean populations. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2015, 780, 97-102.	0.4	32
66	The African Genome Variation Project shapes medical genetics in Africa. <i>Nature</i> , 2015, 517, 327-332.	13.7	473
67	First Application of a Distance-Based Outlier Approach to Detect Highly Differentiated Genomic Regions Across Human Populations. , 2015, , 133-144.		0
68	Genome-Wide Analysis of Cold Adaptation in Indigenous Siberian Populations. <i>PLoS ONE</i> , 2014, 9, e98076.	1.1	128
69	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
70	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
71	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
72	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

#	ARTICLE	IF	CITATIONS
73	Geographic population structure analysis of worldwide human populations infers their biogeographical origins. <i>Nature Communications</i> , 2014, 5, 3513.	5.8	114
74	Genetic signature of differential sensitivity to stevioside in the Italian population. <i>Genes and Nutrition</i> , 2014, 9, 401.	1.2	33
75	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
76	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
77	A general linear model-based approach for inferring selection to climate. <i>BMC Genetics</i> , 2013, 14, 87.	2.7	18
78	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
79	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
80	The GenoChip: A New Tool for Genetic Anthropology. <i>Genome Biology and Evolution</i> , 2013, 5, 1021-1031.	1.1	54
81	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
82	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
83	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
84	High altitude adaptation in Daghestani populations from the Caucasus. <i>Human Genetics</i> , 2012, 131, 423-433.	1.8	31
85	A world in a grain of sand: human history from genetic data. <i>Genome Biology</i> , 2011, 12, 234.	13.9	9
86	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
87	Application of Graph Theory to the elaboration of personal genomic data for genealogical research. <i>PeerJ Computer Science</i> , 0, 1, e27.	2.7	2
88	Shifts in the Genetic Landscape of the Western Eurasian Steppe Associated with the Beginning and End of the Scythian Dominance. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0