

Oscar Lao

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

5,444
citations

126907

33
h-index

133252

59
g-index

66
all docs

66
docs citations

66
times ranked

7871
citing authors

#	ARTICLE	IF	CITATIONS
1	Correlation between Genetic and Geographic Structure in Europe. <i>Current Biology</i> , 2008, 18, 1241-1248.	3.9	449
2	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016, 538, 207-214.	27.8	439
3	Mutability of Y-Chromosomal Microsatellites: Rates, Characteristics, Molecular Bases, and Forensic Implications. <i>American Journal of Human Genetics</i> , 2010, 87, 341-353.	6.2	324
4	IrisPlex: A sensitive DNA tool for accurate prediction of blue and brown eye colour in the absence of ancestry information. <i>Forensic Science International: Genetics</i> , 2011, 5, 170-180.	3.1	275
5	A Genome-Wide Association Study Identifies Five Loci Influencing Facial Morphology in Europeans. <i>PLoS Genetics</i> , 2012, 8, e1002932.	3.5	274
6	Chimpanzee genomic diversity reveals ancient admixture with bonobos. <i>Science</i> , 2016, 354, 477-481.	12.6	230
7	Three Genome-wide Association Studies and a Linkage Analysis Identify HERC2 as a Human Iris Color Gene. <i>American Journal of Human Genetics</i> , 2008, 82, 411-423.	6.2	220
8	Melanesian and Asian Origins of Polynesians: mtDNA and Y Chromosome Gradients Across the Pacific. <i>Molecular Biology and Evolution</i> , 2006, 23, 2234-2244.	8.9	216
9	Proportioning Whole-Genome Single-Nucleotide Polymorphism Diversity for the Identification of Geographic Population Structure and Genetic Ancestry. <i>American Journal of Human Genetics</i> , 2006, 78, 680-690.	6.2	164
10	Digital Quantification of Human Eye Color Highlights Genetic Association of Three New Loci. <i>PLoS Genetics</i> , 2010, 6, e1000934.	3.5	161
11	Demographic History of Oceania Inferred from Genome-wide Data. <i>Current Biology</i> , 2010, 20, 1983-1992.	3.9	158
12	Inferring Continental Ancestry of Argentineans from Autosomal, Y-Chromosomal and Mitochondrial DNA. <i>Annals of Human Genetics</i> , 2010, 74, 65-76.	0.8	155
13	Admixture, migrations, and dispersals in Central Asia: evidence from maternal DNA lineages. <i>European Journal of Human Genetics</i> , 2004, 12, 495-504.	2.8	145
14	Genetics of skin color variation in Europeans: genome-wide association studies with functional follow-up. <i>Human Genetics</i> , 2015, 134, 823-835.	3.8	133
15	Significant genetic differentiation between Poland and Germany follows present-day political borders, as revealed by Y-chromosome analysis. <i>Human Genetics</i> , 2005, 117, 428-443.	3.8	123
16	Comprehensive mutation analysis of 17 Y-chromosomal short tandem repeat polymorphisms included in the AmpFISTRÂ® YfilerÂ® PCR amplification kit. <i>International Journal of Legal Medicine</i> , 2009, 123, 471-482.	2.2	121
17	Genome-wide Analysis Indicates More Asian than Melanesian Ancestry of Polynesians. <i>American Journal of Human Genetics</i> , 2008, 82, 194-198.	6.2	114
18	Tracking down Human Contamination in Ancient Human Teeth. <i>Molecular Biology and Evolution</i> , 2006, 23, 1801-1807.	8.9	105

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19	Reconstructing the Population History of European Romani from Genome-wide Data. <i>Current Biology</i> , 2012, 22, 2342-2349.	3.9	101
20	Approximate Bayesian computation with deep learning supports a third archaic introgression in Asia and Oceania. <i>Nature Communications</i> , 2019, 10, 246.	12.8	97
21	Diurnal Rhythms in Blood Cell Populations and the Effect of Acute Sleep Deprivation in Healthy Young Men. <i>Sleep</i> , 2012, 35, 933-940.	1.1	96
22	Effect of sleep deprivation on rhythms of clock gene expression and melatonin in humans. <i>Chronobiology International</i> , 2013, 30, 901-909.	2.0	90
23	Improving global and regional resolution of male lineage differentiation by simple single-copy Y-chromosomal short tandem repeat polymorphisms. <i>Forensic Science International: Genetics</i> , 2009, 3, 205-213.	3.1	87
24	Evaluating self-declared ancestry of U.S. Americans with autosomal, Y-chromosomal and mitochondrial DNA. <i>Human Mutation</i> , 2010, 31, E1875-E1893.	2.5	86
25	Comprehensive candidate gene study highlights UGT1A and BNC2 as new genes determining continuous skin color variation in Europeans. <i>Human Genetics</i> , 2013, 132, 147-158.	3.8	86
26	The portability of tagSNPs across populations: A worldwide survey. <i>Genome Research</i> , 2006, 16, 323-330.	5.5	82
27	The Y-chromosome landscape of the Philippines: extensive heterogeneity and varying genetic affinities of Negrito and non-Negrito groups. <i>European Journal of Human Genetics</i> , 2011, 19, 224-230.	2.8	78
28	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , 2014, 24, R1035-R1037.	3.9	73
29	Postnatal parental smoking: an important risk factor for SIDS. <i>European Journal of Pediatrics</i> , 2011, 170, 1281-1291.	2.7	59
30	Worldwide Genetic Analysis of the CFTR Region. <i>American Journal of Human Genetics</i> , 2001, 68, 103-117.	6.2	55
31	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.	8.8	50
32	The genomic history of the Aegean palatial civilizations. <i>Cell</i> , 2021, 184, 2565-2586.e21.	28.9	43
33	Spatial patterns of cystic fibrosis mutation spectra in European populations. <i>European Journal of Human Genetics</i> , 2003, 11, 385-394.	2.8	41
34	Evaluation of mRNA markers for estimating blood deposition time: Towards alibi testing from human forensic stains with rhythmic biomarkers. <i>Forensic Science International: Genetics</i> , 2016, 21, 119-125.	3.1	37
35	Novel taxonomy-independent deep learning microbiome approach allows for accurate classification of different forensically relevant human epithelial materials. <i>Forensic Science International: Genetics</i> , 2019, 41, 72-82.	3.1	34
36	Comparative Genetics of Functional Trinucleotide Tandem Repeats in Humans and Apes. <i>Journal of Molecular Evolution</i> , 2004, 59, 329-339.	1.8	33

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37	Identification of a candidate genetic variant for the high prevalence of type II diabetes in Polynesians. <i>European Journal of Human Genetics</i> , 2007, 15, 584-589.	2.8	33
38	Dynamics of CAG repeat loci revealed by the analysis of their variability. <i>Human Mutation</i> , 2003, 21, 61-70.	2.5	30
39	Unexpected Island Effects at an Extreme: Reduced Y Chromosome and Mitochondrial DNA Diversity in Nias. <i>Molecular Biology and Evolution</i> , 2011, 28, 1349-1361.	8.9	29
40	BMD Loci Contribute to Ethnic and Developmental Differences in Skeletal Fragility across Populations: Assessment of Evolutionary Selection Pressures. <i>Molecular Biology and Evolution</i> , 2015, 32, 2961-2972.	8.9	29
41	Evolutionary and Medical Consequences of Archaic Introgression into Modern Human Genomes. <i>Genes</i> , 2018, 9, 358.	2.4	28
42	Recent human evolution has shaped geographical differences in susceptibility to disease. <i>BMC Genomics</i> , 2011, 12, 55.	2.8	27
43	Adaptive evolution of loci covarying with the human African Pygmy phenotype. <i>Human Genetics</i> , 2012, 131, 1305-1317.	3.8	27
44	Dissecting Daily and Circadian Expression Rhythms of Clock-Controlled Genes in Human Blood. <i>Journal of Biological Rhythms</i> , 2016, 31, 68-81.	2.6	27
45	Mutation analysis at 17 Y-STR loci (Yfiler) in father-son pairs of male pedigrees from Pakistan. <i>Forensic Science International: Genetics</i> , 2018, 36, e17-e18.	3.1	21
46	PHOX2B polyalanine repeat length is associated with sudden infant death syndrome and unclassified sudden infant death in the Dutch population. <i>International Journal of Legal Medicine</i> , 2014, 128, 621-9.	2.2	20
47	Detecting individual ancestry in the human genome. <i>Investigative Genetics</i> , 2015, 6, 7.	3.3	19
48	Clinal distribution of human genomic diversity across the Netherlands despite archaeological evidence for genetic discontinuities in Dutch population history. <i>Investigative Genetics</i> , 2013, 4, 9.	3.3	18
49	Genomic analysis of the natural history of attention-deficit/hyperactivity disorder using Neanderthal and ancient Homo sapiens samples. <i>Scientific Reports</i> , 2020, 10, 8622.	3.3	18
50	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
51	The Mediterranean Paradox for Susceptibility Factors in Coronary Heart Disease Extends to Genetics. <i>Annals of Human Genetics</i> , 2007, 72, 070807042352002-???	0.8	15
52	The Dutch Y-chromosomal landscape. <i>European Journal of Human Genetics</i> , 2020, 28, 287-299.	2.8	15
53	Implications of Population History of European Romani on Genetic Susceptibility to Disease. <i>Human Heredity</i> , 2013, 76, 194-200.	0.8	12
54	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.	2.8	8

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55	GAGA: A New Algorithm for Genomic Inference of Geographic Ancestry Reveals Fine Level Population Substructure in Europeans. PLoS Computational Biology, 2014, 10, e1003480.	3.2	7
56	Fine-scale population structure in five rural populations from the Spanish Eastern Pyrenees using high-coverage whole-genome sequence data. European Journal of Human Genetics, 2021, 29, 1557-1565.	2.8	4
57	Medicine in the Light of Evolution. Genes, 2019, 10, 3.	2.4	3
58	Reply to Hedrick. American Journal of Human Genetics, 2008, 83, 140-142.	6.2	2
59	Analysis of the Batch Effect Due to Sequencing Center in Population Statistics Quantifying Rare Events in the 1000 Genomes Project. Genes, 2022, 13, 44.	2.4	1
60	Genetic Admixture. , 2015, , 887-897.		0
61	Human Population Movements. , 2015, , 219-233.		0
62	Evolution of Complex Traits in Human Populations. , 2017, , 165-186.		0
63	Selection still shapes our genome. Nature Human Behaviour, 2021, , .	12.0	0