

Martin Sikora

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

80
papers

6,201
citations

35
h-index

78
g-index

86
ext. papers

8,046
ext. citations

16.9
avg, IF

4.87
L-index

#	Paper	IF	Citations
80	Population genomics of Bronze Age Eurasia. <i>Nature</i> , 2015 , 522, 167-72	50.4	827
79	Human genetics. The genetics of Mexico recapitulates Native American substructure and affects biomedical traits. <i>Science</i> , 2014 , 344, 1280-5	33.3	331
78	Molecular evidence for a single evolutionary origin of domesticated rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 8351-6	11.5	314
77	New insights into the Tyrolean Iceman's origin and phenotype as inferred by whole-genome sequencing. <i>Nature Communications</i> , 2012 , 3, 698	17.4	301
76	Early divergent strains of <i>Yersinia pestis</i> in Eurasia 5,000 years ago. <i>Cell</i> , 2015 , 163, 571-82	56.2	294
75	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016 , 538, 207-214	50.4	268
74	Paleogenomics. Genomic structure in Europeans dating back at least 36,200 years. <i>Science</i> , 2014 , 346, 1113-8	33.3	232
73	Pulling out the 1%: whole-genome capture for the targeted enrichment of ancient DNA sequencing libraries. <i>American Journal of Human Genetics</i> , 2013 , 93, 852-64	11	221
72	137 ancient human genomes from across the Eurasian steppes. <i>Nature</i> , 2018 , 557, 369-374	50.4	197
71	Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. <i>Nature</i> , 2018 , 553, 203-207	50.4	178
70	The prehistoric peopling of Southeast Asia. <i>Science</i> , 2018 , 361, 88-92	33.3	174
69	A natural history of FUT2 polymorphism in humans. <i>Molecular Biology and Evolution</i> , 2009 , 26, 1993-2003	3.3	169
68	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. <i>Science</i> , 2018 , 360,	33.3	162
67	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , 2017 , 358, 659-662	33.3	160
66	The ancestry and affiliations of Kennewick Man. <i>Nature</i> , 2015 , 523, 455-458	50.4	157
65	Balancing selection is the main force shaping the evolution of innate immunity genes. <i>Journal of Immunology</i> , 2008 , 181, 1315-22	5.3	150
64	The population history of northeastern Siberia since the Pleistocene. <i>Nature</i> , 2019 , 570, 182-188	50.4	137

63	Early human dispersals within the Americas. <i>Science</i> , 2018 , 362,	33.3	118
62	Ancient hepatitis B viruses from the Bronze Age to the Medieval period. <i>Nature</i> , 2018 , 557, 418-423	50.4	112
61	Re-theorising mobility and the formation of culture and language among the Corded Ware Culture in Europe. <i>Antiquity</i> , 2017 , 91, 334-347	1	108
60	A functional ABCA1 gene variant is associated with low HDL-cholesterol levels and shows evidence of positive selection in Native Americans. <i>Human Molecular Genetics</i> , 2010 , 19, 2877-85	5.6	98
59	Type 2 diabetes risk alleles demonstrate extreme directional differentiation among human populations, compared to other diseases. <i>PLoS Genetics</i> , 2012 , 8, e1002621	6	95
58	Melanesian blond hair is caused by an amino acid change in TYRP1. <i>Science</i> , 2012 , 336, 554	33.3	85
57	Physiological and Genetic Adaptations to Diving in Sea Nomads. <i>Cell</i> , 2018 , 173, 569-580.e15	56.2	82
56	Genome-wide ancestry of 17th-century enslaved Africans from the Caribbean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 3669-73	11.5	82
55	Population genomic analysis of ancient and modern genomes yields new insights into the genetic ancestry of the Tyrolean Iceman and the genetic structure of Europe. <i>PLoS Genetics</i> , 2014 , 10, e1004353 ⁶		73
54	Analysis of the genetic basis of disease in the context of worldwide human relationships and migration. <i>PLoS Genetics</i> , 2013 , 9, e1003447	6	58
53	Evidence of human occupation in Mexico around the Last Glacial Maximum. <i>Nature</i> , 2020 , 584, 87-92	50.4	58
52	Unraveling ancestry, kinship, and violence in a Late Neolithic mass grave. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 10705-10710	11.5	56
51	Population genetic analysis of the DARC locus (Duffy) reveals adaptation from standing variation associated with malaria resistance in humans. <i>PLoS Genetics</i> , 2017 , 13, e1006560	6	55
50	Selection in Europeans on Fatty Acid Desaturases Associated with Dietary Changes. <i>Molecular Biology and Evolution</i> , 2017 , 34, 1307-1318	8.3	50
49	Ancient Biomolecules and Evolutionary Inference. <i>Annual Review of Biochemistry</i> , 2018 , 87, 1029-1060	29.1	47
48	Origins and genetic legacies of the Caribbean Taino. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 2341-2346	11.5	45
47	Diverse variola virus (smallpox) strains were widespread in northern Europe in the Viking Age. <i>Science</i> , 2020 , 369,	33.3	42
46	Ancient human parvovirus B19 in Eurasia reveals its long-term association with humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 7557-7562	11.5	39

45	Population genomics of the Viking world. <i>Nature</i> , 2020 , 585, 390-396	50.4	35
44	Human Disease Variation in the Light of Population Genomics. <i>Cell</i> , 2019 , 177, 115-131	56.2	34
43	A 5700 year-old human genome and oral microbiome from chewed birch pitch. <i>Nature Communications</i> , 2019 , 10, 5520	17.4	31
42	Genome-wide Ancestry and Demographic History of African-Descendant Maroon Communities from French Guiana and Suriname. <i>American Journal of Human Genetics</i> , 2017 , 101, 725-736	11	29
41	A genomic analysis identifies a novel component in the genetic structure of sub-Saharan African populations. <i>European Journal of Human Genetics</i> , 2011 , 19, 84-8	5.3	29
40	Network evolution: rewiring and signatures of conservation in signaling. <i>PLoS Computational Biology</i> , 2012 , 8, e1002411	5	27
39	Exome capture from saliva produces high quality genomic and metagenomic data. <i>BMC Genomics</i> , 2014 , 15, 262	4.5	26
38	Genomic Evidence for Local Adaptation of Hunter-Gatherers to the African Rainforest. <i>Current Biology</i> , 2019 , 29, 2926-2935.e4	6.3	25
37	Sequence variation and genetic evolution at the human F12 locus: mapping quantitative trait nucleotides that influence FXII plasma levels. <i>Human Molecular Genetics</i> , 2010 , 19, 517-25	5.6	24
36	Beyond broad strokes: sociocultural insights from the study of ancient genomes. <i>Nature Reviews Genetics</i> , 2020 , 21, 355-366	30.1	23
35	Ancient pathogen DNA in human teeth and petrous bones. <i>Ecology and Evolution</i> , 2018 , 8, 3534-3542	2.8	23
34	Mapping human mobility during the third and second millennia BC in present-day Denmark. <i>PLoS ONE</i> , 2019 , 14, e0219850	3.7	22
33	Reply to Ge and Sang: A single origin of domesticated rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, E756-E756	11.5	22
32	Network-level and population genetics analysis of the insulin/TOR signal transduction pathway across human populations. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1379-92	8.3	22
31	Genetic adaptation of the antibacterial human innate immunity network. <i>BMC Evolutionary Biology</i> , 2011 , 11, 202	3	20
30	Interrogating 11 fast-evolving genes for signatures of recent positive selection in worldwide human populations. <i>Molecular Biology and Evolution</i> , 2009 , 26, 2285-97	8.3	20
29	Ancient Jomon genome sequence analysis sheds light on migration patterns of early East Asian populations. <i>Communications Biology</i> , 2020 , 3, 437	6.7	19
28	Distribution of events of positive selection and population differentiation in a metabolic pathway: the case of asparagine N-glycosylation. <i>BMC Evolutionary Biology</i> , 2012 , 12, 98	3	17

27	Diversity of KIR, HLA Class I, and Their Interactions in Seven Populations of Sub-Saharan Africans. <i>Journal of Immunology</i> , 2019 , 202, 2636-2647	5.3	16
26	The spatiotemporal spread of human migrations during the European Holocene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 8989-9000	11.5	16
25	Isolated populations as treasure troves in genetic epidemiology: the case of the Basques. <i>European Journal of Human Genetics</i> , 2009 , 17, 1490-4	5.3	16
24	Ancient nuclear genomes enable repatriation of Indigenous human remains. <i>Science Advances</i> , 2018 , 4, eaau5064	14.3	16
23	Similarity in recombination rate estimates highly correlates with genetic differentiation in humans. <i>PLoS ONE</i> , 2011 , 6, e17913	3.7	13
22	Human pseudogenes of the ABO family show a complex evolutionary dynamics and loss of function. <i>Glycobiology</i> , 2009 , 19, 583-91	5.8	12
21	Discussion: Are the Origins of Indo-European Languages Explained by the Migration of the Yamnaya Culture to the West?. <i>European Journal of Archaeology</i> , 2018 , 21, 3-17	0.7	10
20	A Genomic View of the Pleistocene Population History of Asia. <i>Current Anthropology</i> , 2017 , 58, S397-S405.1		9
19	A variant in the gene FUT9 is associated with susceptibility to placental malaria infection. <i>Human Molecular Genetics</i> , 2009 , 18, 3136-44	5.6	9
18	High Y-chromosomal Differentiation Among Ethnic Groups of Dir and Swat Districts, Pakistan. <i>Annals of Human Genetics</i> , 2017 , 81, 234-248	2.2	6
17	Long-standing balancing selection in the THBS4 gene: influence on sex-specific brain expression and gray matter volumes in Alzheimer disease. <i>Human Mutation</i> , 2013 , 34, 743-53	4.7	6
16	Evolutionary analysis of genes of two pathways involved in placental malaria infection. <i>Human Genetics</i> , 2008 , 123, 343-57	6.3	6
15	A targeted association study of immunity genes and networks suggests novel associations with placental malaria infection. <i>PLoS ONE</i> , 2011 , 6, e24996	3.7	6
14	Jomon genome sheds light on East Asian population history		6
13	Environmental genomics of Late Pleistocene black bears and giant short-faced bears. <i>Current Biology</i> , 2021 , 31, 2728-2736.e8	6.3	6
12	African signatures of recent positive selection in human FOXI1. <i>BMC Evolutionary Biology</i> , 2010 , 10, 267	3	3
11	Ancient human genomes and environmental DNA from the cement attaching 2,000 year-old head lice nits.. <i>Molecular Biology and Evolution</i> , 2021 ,	8.3	3
10	Ancient Genomics Reveals Four Prehistoric Migration Waves into Southeast Asia		2

9	Population genomics of the Viking world		2
8	Selection on the FADS region in Europeans		2
7	Genomic Steppe ancestry in skeletons from the Neolithic Single Grave Culture in Denmark. <i>PLoS ONE</i> , 2021 , 16, e0244872	3-7	2
6	The population history of northeastern Siberia since the Pleistocene		1
5	A geostatistical approach to modelling human Holocene migrations in Europe using ancient DNA		1
4	Population Genetic Analysis of the DARC Locus (Duffy) Reveals Adaptation from Standing Variation Associated with Malaria Resistance in Humans		1
3	Chiquihuite Cave and America's Hidden Limestone Industries: A Reply to Chatters et al.. <i>PaleoAmerica</i> , 1-12	1-3	0
2	Re-theorising mobility and the formation of culture and language among the Corded Ware Culture in Europe CORRIGENDUM. <i>Antiquity</i> , 2020 , 94, 839-839		1
1	Serious chronic disease of the cervical spine and trauma in a young female from the middle ages (Czech Republic). <i>International Journal of Paleopathology</i> , 2019 , 24, 185-196		1-5