

# Martin Sikora

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/8530763/martin-sikora-publications-by-year.pdf>

**Version:** 2024-04-26

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Environmental genomics of Late Pleistocene black bears and giant short-faced bears. <i>Current Biology</i> , <b>2021</b> , 31, 2728-2736.e8	6.3	6
79	Genomic Steppe ancestry in skeletons from the Neolithic Single Grave Culture in Denmark. <i>PLoS ONE</i> , <b>2021</b> , 16, e0244872	3.7	2
78	Ancient human genomes and environmental DNA from the cement attaching 2,000 year-old head lice nits.. <i>Molecular Biology and Evolution</i> , <b>2021</b> ,	8.3	3
77	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> , <b>2020</b> , 117, 8989-9000	11.5	16
76	Re-theorising mobility and the formation of culture and language among the Corded Ware Culture in Europe. CORRIGENDUM. <i>Antiquity</i> , <b>2020</b> , 94, 839-839	1	
75	Beyond broad strokes: sociocultural insights from the study of ancient genomes. <i>Nature Reviews Genetics</i> , <b>2020</b> , 21, 355-366	30.1	23
74	Evidence of human occupation in Mexico around the Last Glacial Maximum. <i>Nature</i> , <b>2020</b> , 584, 87-92	50.4	58
73	Diverse variola virus (smallpox) strains were widespread in northern Europe in the Viking Age. <i>Science</i> , <b>2020</b> , 369,	33.3	42
72	Ancient Jomon genome sequence analysis sheds light on migration patterns of early East Asian populations. <i>Communications Biology</i> , <b>2020</b> , 3, 437	6.7	19
71	Population genomics of the Viking world. <i>Nature</i> , <b>2020</b> , 585, 390-396	50.4	35
70	Genomic Evidence for Local Adaptation of Hunter-Gatherers to the African Rainforest. <i>Current Biology</i> , <b>2019</b> , 29, 2926-2935.e4	6.3	25
69	The population history of northeastern Siberia since the Pleistocene. <i>Nature</i> , <b>2019</b> , 570, 182-188	50.4	137
68	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> , <b>2019</b> , 116, 10705-10710	11.5	56
67	Human Disease Variation in the Light of Population Genomics. <i>Cell</i> , <b>2019</b> , 177, 115-131	56.2	34
66	Diversity of KIR, HLA Class I, and Their Interactions in Seven Populations of Sub-Saharan Africans. <i>Journal of Immunology</i> , <b>2019</b> , 202, 2636-2647	5.3	16
65	Mapping human mobility during the third and second millennia BC in present-day Denmark. <i>PLoS ONE</i> , <b>2019</b> , 14, e0219850	3.7	22
64	A 5700 year-old human genome and oral microbiome from chewed birch pitch. <i>Nature Communications</i> , <b>2019</b> , 10, 5520	17.4	31

63	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> , <b>2019</b> , 24, 185-196	1.5	
62	Origins and genetic legacies of the Caribbean Taino. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, 2341-2346	11.5	45
61	Ancient pathogen DNA in human teeth and petrous bones. <i>Ecology and Evolution</i> , <b>2018</b> , 8, 3534-3542	2.8	23
60	Physiological and Genetic Adaptations to Diving in Sea Nomads. <i>Cell</i> , <b>2018</b> , 173, 569-580.e15	56.2	82
59	Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. <i>Nature</i> , <b>2018</b> , 553, 203-207	50.4	178
58	Ancient Biomolecules and Evolutionary Inference. <i>Annual Review of Biochemistry</i> , <b>2018</b> , 87, 1029-1060	29.1	47
57	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> , <b>2018</b> , 21, 3-17	0.7	10
56	137 ancient human genomes from across the Eurasian steppes. <i>Nature</i> , <b>2018</b> , 557, 369-374	50.4	197
55	Ancient hepatitis B viruses from the Bronze Age to the Medieval period. <i>Nature</i> , <b>2018</b> , 557, 418-423	50.4	112
54	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. <i>Science</i> , <b>2018</b> , 360,	33.3	162
53	Early human dispersals within the Americas. <i>Science</i> , <b>2018</b> , 362,	33.3	118
52	Ancient nuclear genomes enable repatriation of Indigenous human remains. <i>Science Advances</i> , <b>2018</b> , 4, eaau5064	14.3	16
51	The prehistoric peopling of Southeast Asia. <i>Science</i> , <b>2018</b> , 361, 88-92	33.3	174
50	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> , <b>2018</b> , 115, 7557-7562	11.5	39
49	Selection in Europeans on Fatty Acid Desaturases Associated with Dietary Changes. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 1307-1318	8.3	50
48	Re-theorising mobility and the formation of culture and language among the Corded Ware Culture in Europe. <i>Antiquity</i> , <b>2017</b> , 91, 334-347	1	108
47	Genome-wide Ancestry and Demographic History of African-Descendant Maroon Communities from French Guiana and Suriname. <i>American Journal of Human Genetics</i> , <b>2017</b> , 101, 725-736	11	29
46	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , <b>2017</b> , 358, 659-662	33.3	160

45	High Y-chromosomal Differentiation Among Ethnic Groups of Dir and Swat Districts, Pakistan. <i>Annals of Human Genetics</i> , <b>2017</b> , 81, 234-248	2.2	6
44	A Genomic View of the Pleistocene Population History of Asia. <i>Current Anthropology</i> , <b>2017</b> , 58, S397-S405.1		9
43	Population genetic analysis of the DARC locus (Duffy) reveals adaptation from standing variation associated with malaria resistance in humans. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006560	6	55
42	A genomic history of Aboriginal Australia. <i>Nature</i> , <b>2016</b> , 538, 207-214	50.4	268
41	The ancestry and affiliations of Kennewick Man. <i>Nature</i> , <b>2015</b> , 523, 455-458	50.4	157
40	Early divergent strains of <i>Yersinia pestis</i> in Eurasia 5,000 years ago. <i>Cell</i> , <b>2015</b> , 163, 571-82	56.2	294
39	Population genomics of Bronze Age Eurasia. <i>Nature</i> , <b>2015</b> , 522, 167-72	50.4	827
38	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> , <b>2015</b> , 112, 3669-73	11.5	82
37	Paleogenomics. Genomic structure in Europeans dating back at least 36,200 years. <i>Science</i> , <b>2014</b> , 346, 1113-8	33.3	232
36	Exome capture from saliva produces high quality genomic and metagenomic data. <i>BMC Genomics</i> , <b>2014</b> , 15, 262	4.5	26
35	Human genetics. The genetics of Mexico recapitulates Native American substructure and affects biomedical traits. <i>Science</i> , <b>2014</b> , 344, 1280-5	33.3	331
34	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> , <b>2014</b> , 10, e1004353 <sup>6</sup>		73
33	Pulling out the 1%: whole-genome capture for the targeted enrichment of ancient DNA sequencing libraries. <i>American Journal of Human Genetics</i> , <b>2013</b> , 93, 852-64	11	221
32	Analysis of the genetic basis of disease in the context of worldwide human relationships and migration. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003447	6	58
31	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> , <b>2013</b> , 34, 743-53	4.7	6
30	New insights into the Tyrolean Iceman's origin and phenotype as inferred by whole-genome sequencing. <i>Nature Communications</i> , <b>2012</b> , 3, 698	17.4	301
29	Distribution of events of positive selection and population differentiation in a metabolic pathway: the case of asparagine N-glycosylation. <i>BMC Evolutionary Biology</i> , <b>2012</b> , 12, 98	3	17
28	Melanesian blond hair is caused by an amino acid change in TYRP1. <i>Science</i> , <b>2012</b> , 336, 554	33.3	85

27	Network evolution: rewiring and signatures of conservation in signaling. <i>PLoS Computational Biology</i> , <b>2012</b> , 8, e1002411	5	27
26	Type 2 diabetes risk alleles demonstrate extreme directional differentiation among human populations, compared to other diseases. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002621	6	95
25	Network-level and population genetics analysis of the insulin/TOR signal transduction pathway across human populations. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 1379-92	8.3	22
24	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> , <b>2011</b> , 108, E756-E756	11.5	22
23	Similarity in recombination rate estimates highly correlates with genetic differentiation in humans. <i>PLoS ONE</i> , <b>2011</b> , 6, e17913	3.7	13
22	A genomic analysis identifies a novel component in the genetic structure of sub-Saharan African populations. <i>European Journal of Human Genetics</i> , <b>2011</b> , 19, 84-8	5.3	29
21	Genetic adaptation of the antibacterial human innate immunity network. <i>BMC Evolutionary Biology</i> , <b>2011</b> , 11, 202	3	20
20	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> , <b>2011</b> , 108, 8351-6	11.5	314
19	A targeted association study of immunity genes and networks suggests novel associations with placental malaria infection. <i>PLoS ONE</i> , <b>2011</b> , 6, e24996	3.7	6
18	Sequence variation and genetic evolution at the human F12 locus: mapping quantitative trait nucleotides that influence FXII plasma levels. <i>Human Molecular Genetics</i> , <b>2010</b> , 19, 517-25	5.6	24
17	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> , <b>2010</b> , 19, 2877-85	5.6	98
16	African signatures of recent positive selection in human FOXI1. <i>BMC Evolutionary Biology</i> , <b>2010</b> , 10, 267	3	3
15	Human pseudogenes of the ABO family show a complex evolutionary dynamics and loss of function. <i>Glycobiology</i> , <b>2009</b> , 19, 583-91	5.8	12
14	Interrogating 11 fast-evolving genes for signatures of recent positive selection in worldwide human populations. <i>Molecular Biology and Evolution</i> , <b>2009</b> , 26, 2285-97	8.3	20
13	A variant in the gene FUT9 is associated with susceptibility to placental malaria infection. <i>Human Molecular Genetics</i> , <b>2009</b> , 18, 3136-44	5.6	9
12	A natural history of FUT2 polymorphism in humans. <i>Molecular Biology and Evolution</i> , <b>2009</b> , 26, 1993-2003	3.3	169
11	Isolated populations as treasure troves in genetic epidemiology: the case of the Basques. <i>European Journal of Human Genetics</i> , <b>2009</b> , 17, 1490-4	5.3	16
10	Balancing selection is the main force shaping the evolution of innate immunity genes. <i>Journal of Immunology</i> , <b>2008</b> , 181, 1315-22	5.3	150

9	Evolutionary analysis of genes of two pathways involved in placental malaria infection. <i>Human Genetics</i> , <b>2008</b> , 123, 343-57	6.3	6
8	Chiquihuite Cave and America's Hidden Limestone Industries: A Reply to Chatters et al.. <i>PaleoAmerica</i> , 1-12	1.3	0
7	Ancient Genomics Reveals Four Prehistoric Migration Waves into Southeast Asia		2
6	The population history of northeastern Siberia since the Pleistocene		1
5	Jomon genome sheds light on East Asian population history		6
4	Population genomics of the Viking world		2
3	A geostatistical approach to modelling human Holocene migrations in Europe using ancient DNA		1
2	Population Genetic Analysis of the DARC Locus (Duffy) Reveals Adaptation from Standing Variation Associated with Malaria Resistance in Humans		1
1	Selection on the FADS region in Europeans		2