Martin Sikora

List of Publications by Year
in descending order

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		81839	76872
73	9,311	39	74
papers	citations	h-index	g-index

86	86	86	11656
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Population genomics of Bronze Age Eurasia. Nature, 2015, 522, 167-172.	13.7	1,166
2	A genomic history of Aboriginal Australia. Nature, 2016, 538, 207-214.	13.7	439
3	Early Divergent Strains of Yersinia pestis in Eurasia 5,000 Years Ago. Cell, 2015, 163, 571-582.	13.5	425
4	Molecular evidence for a single evolutionary origin of domesticated rice. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 8351-8356.	3.3	422
5	The genetics of Mexico recapitulates Native American substructure and affects biomedical traits. Science, 2014, 344, 1280-1285.	6.0	420
6	New insights into the Tyrolean Iceman's origin and phenotype as inferred by whole-genome sequencing. Nature Communications, 2012, 3, 698.	5.8	382
7	137 ancient human genomes from across the Eurasian steppes. Nature, 2018, 557, 369-374.	13.7	325
8	Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. Nature, 2018, 553, 203-207.	13.7	304
9	The prehistoric peopling of Southeast Asia. Science, 2018, 361, 88-92.	6.0	291
10	Genomic structure in Europeans dating back at least 36,200 years. Science, 2014, 346, 1113-1118.	6.0	287
11	Pulling out the 1%: Whole-Genome Capture for the Targeted Enrichment of Ancient DNA Sequencing Libraries. American Journal of Human Genetics, 2013, 93, 852-864.	2.6	284
12	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. Science, 2017, 358, 659-662.	6.0	263
13	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. Science, 2018, 360, .	6.0	262
14	The population history of northeastern Siberia since the Pleistocene. Nature, 2019, 570, 182-188.	13.7	259
15	The ancestry and affiliations of Kennewick Man. Nature, 2015, 523, 455-458.	13.7	241
16	Early human dispersals within the Americas. Science, 2018, 362, .	6.0	230
17	A Natural History of FUT2 Polymorphism in Humans. Molecular Biology and Evolution, 2009, 26, 1993-2003.	3.5	209
18	Balancing Selection Is the Main Force Shaping the Evolution of Innate Immunity Genes. Journal of Immunology, 2008, 181, 1315-1322.	0.4	173

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19	Re-theorising mobility and the formation of culture and language among the Corded Ware Culture in Europe. Antiquity, 2017, 91, 334-347.	0.5	157
20	Ancient hepatitis B viruses from the Bronze Age to the Medieval period. Nature, 2018, 557, 418-423.	13.7	155
21	Population genomics of the Viking world. Nature, 2020, 585, 390-396.	13.7	143
22	A functional ABCA1 gene variant is associated with low HDL-cholesterol levels and shows evidence of positive selection in Native Americans. Human Molecular Genetics, 2010, 19, 2877-2885.	1.4	133
23	Physiological and Genetic Adaptations to Diving in Sea Nomads. Cell, 2018, 173, 569-580.e15.	13.5	129
24	Unraveling ancestry, kinship, and violence in a Late Neolithic mass grave. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10705-10710.	3.3	119
25	Evidence of human occupation in Mexico around the Last Glacial Maximum. Nature, 2020, 584, 87-92.	13.7	115
26	Genome-wide ancestry of 17th-century enslaved Africans from the Caribbean. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3669-3673.	3.3	110
27	Diverse variola virus (smallpox) strains were widespread in northern Europe in the Viking Age. Science, 2020, 369, .	6.0	108
28	Type 2 Diabetes Risk Alleles Demonstrate Extreme Directional Differentiation among Human Populations, Compared to Other Diseases. PLoS Genetics, 2012, 8, e1002621.	1.5	106
29	Melanesian Blond Hair Is Caused by an Amino Acid Change in TYRP1. Science, 2012, 336, 554-554.	6.0	104
30	Selection in Europeans on Fatty Acid Desaturases Associated with Dietary Changes. Molecular Biology and Evolution, 2017, 34, 1307-1318.	3.5	90
31	Population genetic analysis of the DARC locus (Duffy) reveals adaptation from standing variation associated with malaria resistance in humans. PLoS Genetics, 2017, 13, e1006560.	1.5	87
32	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. PLoS Genetics, 2014, 10, e1004353.	1.5	86
33	Ancient Biomolecules and Evolutionary Inference. Annual Review of Biochemistry, 2018, 87, 1029-1060.	5.0	76
34	Human Disease Variation in the Light of Population Genomics. Cell, 2019, 177, 115-131.	13.5	75
35	Analysis of the Genetic Basis of Disease in the Context of Worldwide Human Relationships and Migration. PLoS Genetics, 2013, 9, e1003447.	1.5	67
36	Origins and genetic legacies of the Caribbean Taino. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 2341-2346.	3.3	64

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37	Ancient human parvovirus B19 in Eurasia reveals its long-term association with humans. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7557-7562.	3.3	64
38	A 5700 year-old human genome and oral microbiome from chewed birch pitch. Nature Communications, 2019, 10, 5520.	5.8	61
39	The spatiotemporal spread of human migrations during the European Holocene. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 8989-9000.	3.3	52
40	Genome-wide Ancestry and Demographic History of African-Descendant Maroon Communities from French Guiana and Suriname. American Journal of Human Genetics, 2017, 101, 725-736.	2.6	50
41	Beyond broad strokes: sociocultural insights from the study of ancient genomes. Nature Reviews Genetics, 2020, 21, 355-366.	7.7	50
42	Mapping human mobility during the third and second millennia BC in present-day Denmark. PLoS ONE, 2019, 14, e0219850.	1.1	44
43	Ancient Jomon genome sequence analysis sheds light on migration patterns of early East Asian populations. Communications Biology, 2020, 3, 437.	2.0	44
44	Environmental genomics of Late Pleistocene black bears and giant short-faced bears. Current Biology, 2021, 31, 2728-2736.e8.	1.8	42
45	Ancient nuclear genomes enable repatriation of Indigenous human remains. Science Advances, 2018, 4, eaau5064.	4.7	41
46	Genomic Evidence for Local Adaptation of Hunter-Gatherers to the African Rainforest. Current Biology, 2019, 29, 2926-2935.e4.	1.8	40
47	Ancient pathogen <scp>DNA</scp> in human teeth and petrous bones. Ecology and Evolution, 2018, 8, 3534-3542.	0.8	38
48	A genomic analysis identifies a novel component in the genetic structure of sub-Saharan African populations. European Journal of Human Genetics, 2011, 19, 84-88.	1.4	35
49	Exome capture from saliva produces high quality genomic and metagenomic data. BMC Genomics, 2014, 15, 262.	1.2	34
50	Reply to Ge and Sang: A single origin of domesticated rice. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, .	3.3	31
51	Network Evolution: Rewiring and Signatures of Conservation in Signaling. PLoS Computational Biology, 2012, 8, e1002411.	1.5	30
52	Sequence variation and genetic evolution at the human F12 locus: mapping quantitative trait nucleotides that influence FXII plasma levels. Human Molecular Genetics, 2010, 19, 517-525.	1.4	28
53	Diversity of KIR, HLA Class I, and Their Interactions in Seven Populations of Sub-Saharan Africans. Journal of Immunology, 2019, 202, 2636-2647.	0.4	26
54	Network-Level and Population Genetics Analysis of the Insulin/TOR Signal Transduction Pathway Across Human Populations. Molecular Biology and Evolution, 2012, 29, 1379-1392.	3.5	24

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55	Genetic adaptation of the antibacterial human innate immunity network. BMC Evolutionary Biology, 2011, 11, 202.	3.2	23
56	Interrogating 11 Fast-Evolving Genes for Signatures of Recent Positive Selection in Worldwide Human Populations. Molecular Biology and Evolution, 2009, 26, 2285-2297.	3.5	20
57	Distribution of events of positive selection and population differentiation in a metabolic pathway: the case of asparagine N-glycosylation. BMC Evolutionary Biology, 2012, 12, 98.	3.2	19
58	Similarity in Recombination Rate Estimates Highly Correlates with Genetic Differentiation in Humans. PLoS ONE, 2011, 6, e17913.	1.1	18
59	Isolated populations as treasure troves in genetic epidemiology: the case of the Basques. European Journal of Human Genetics, 2009, 17, 1490-1494.	1.4	17
60	Discussion: Are the Origins of Indo-European Languages Explained by the Migration of the Yamnaya Culture to the West?. European Journal of Archaeology, 2018, 21, 3-17.	0.3	17
61	Human pseudogenes of the ABO family show a complex evolutionary dynamics and loss of function. Glycobiology, 2009, 19, 583-591.	1.3	12
62	A Genomic View of the Pleistocene Population History of Asia. Current Anthropology, 2017, 58, S397-S405.	0.8	12
63	A variant in the gene FUT9 is associated with susceptibility to placental malaria infection. Human Molecular Genetics, 2009, 18, 3136-3144.	1.4	11
64	Genomic Steppe ancestry in skeletons from the Neolithic Single Grave Culture in Denmark. PLoS ONE, 2021, 16, e0244872.	1.1	11
65	Ancient Human Genomes and Environmental DNA from the Cement Attaching 2,000-Year-Old Head Lice Nits. Molecular Biology and Evolution, 2022, 39, .	3.5	10
66	High Yâ€chromosomal Differentiation Among Ethnic Groups of Dir and Swat Districts, Pakistan. Annals of Human Genetics, 2017, 81, 234-248.	0.3	9
67	Long-Standing Balancing Selection in the<i>THBS</i><i>4</i>Gene: Influence on Sex-Specific Brain Expression and Gray Matter Volumes in Alzheimer Disease. Human Mutation, 2013, 34, 743-753.	1.1	7
68	Evolutionary analysis of genes of two pathways involved in placental malaria infection. Human Genetics, 2008, 123, 343-357.	1.8	6
69	African signatures of recent positive selection in human FOXI1. BMC Evolutionary Biology, 2010, 10, 267.	3.2	6
70	A Targeted Association Study of Immunity Genes and Networks Suggests Novel Associations with Placental Malaria Infection. PLoS ONE, 2011, 6, e24996.	1.1	6
71	Chiquihuite Cave and Americaâ€™s Hidden Limestone Industries: A Reply to Chatters et al.. PaleoAmerica, 2022, 8, 17-28.	0.4	3
72	Serious chronic disease of the cervical spine and trauma in a young female from the middle ages (Czech Republic). International Journal of Paleopathology, 2019, 24, 185-196.	0.8	2

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73	Re-theorising mobility and the formation of culture and language among the Corded Ware Culture in Europeâ€”CORRIGENDUM. Antiquity, 2020, 94, 839-839.	0.5	0