

Stephan Schiffels

List of Publications by Year in descending order

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Version: 2024-02-01

38
papers

7,056
citations

126708

33
h-index

301761

39
g-index

52
all docs

52
docs citations

52
times ranked

12191
citing authors

#	ARTICLE	IF	CITATIONS
1	The UK10K project identifies rare variants in health and disease. <i>Nature</i> , 2015, 526, 82-90.	13.7	1,014
2	Inferring human population size and separation history from multiple genome sequences. <i>Nature Genetics</i> , 2014, 46, 919-925.	9.4	870
3	The genetic history of Ice Age Europe. <i>Nature</i> , 2016, 534, 200-205.	13.7	729
4	Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015, 349, aab3884.	6.0	449
5	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016, 538, 207-214.	13.7	439
6	Genomic islands of speciation separate cichlid ecomorphs in an East African crater lake. <i>Science</i> , 2015, 350, 1493-1498.	6.0	330
7	Reconstructing the Deep Population History of Central and South America. <i>Cell</i> , 2018, 175, 1185-1197.e22.	13.5	259
8	Genomic insights into the formation of human populations in East Asia. <i>Nature</i> , 2021, 591, 413-419.	13.7	216
9	Kinship-based social inequality in Bronze Age Europe. <i>Science</i> , 2019, 366, 731-734.	6.0	175
10	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
11	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. <i>Cell</i> , 2019, 179, 984-1002.e36.	13.5	152
12	The genetic prehistory of the Baltic Sea region. <i>Nature Communications</i> , 2018, 9, 442.	5.8	151
13	Iron Age and Anglo-Saxon genomes from East England reveal British migration history. <i>Nature Communications</i> , 2016, 7, 10408.	5.8	144
14	Pleistocene North African genomes link Near Eastern and sub-Saharan African human populations. <i>Science</i> , 2018, 360, 548-552.	6.0	142
15	The genetic history of admixture across inner Eurasia. <i>Nature Ecology and Evolution</i> , 2019, 3, 966-976.	3.4	135
16	Ancient Egyptian mummy genomes suggest an increase of Sub-Saharan African ancestry in post-Roman periods. <i>Nature Communications</i> , 2017, 8, 15694.	5.8	131
17	A Dynamic 6,000-Year Genetic History of Eurasia's Eastern Steppe. <i>Cell</i> , 2020, 183, 890-904.e29.	13.5	124
18	Palaeo-Eskimo genetic ancestry and the peopling of Chukotka and North America. <i>Nature</i> , 2019, 570, 236-240.	13.7	118

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19	Current evidence allows multiple models for the peopling of the Americas. <i>Science Advances</i> , 2018, 4, eaat5473.	4.7	114
20	MSMC and MSMC2: The Multiple Sequentially Markovian Coalescent. <i>Methods in Molecular Biology</i> , 2020, 2090, 147-166.	0.4	114
21	Ancient human genome-wide data from a 3000-year interval in the Caucasus corresponds with eco-geographic regions. <i>Nature Communications</i> , 2019, 10, 590.	5.8	113
22	Emergent Neutrality in Adaptive Asexual Evolution. <i>Genetics</i> , 2011, 189, 1361-1375.	1.2	109
23	Ancient genome-wide DNA from France highlights the complexity of interactions between Mesolithic hunter-gatherers and Neolithic farmers. <i>Science Advances</i> , 2020, 6, eaaz5344.	4.7	92
24	Survival of Late Pleistocene Hunter-Gatherer Ancestry in the Iberian Peninsula. <i>Current Biology</i> , 2019, 29, 1169-1177.e7.	1.8	90
25	Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe. <i>Nature Communications</i> , 2018, 9, 5018.	5.8	86
26	Tracking human population structure through time from whole genome sequences. <i>PLoS Genetics</i> , 2020, 16, e1008552.	1.5	71
27	Quantifying Selection Acting on a Complex Trait Using Allele Frequency Time Series Data. <i>Molecular Biology and Evolution</i> , 2012, 29, 1187-1197.	3.5	64
28	Ten millennia of hepatitis B virus evolution. <i>Science</i> , 2021, 374, 182-188.	6.0	64
29	Ancient genomes reveal complex patterns of population movement, interaction, and replacement in sub-Saharan Africa. <i>Science Advances</i> , 2020, 6, eaaz0183.	4.7	56
30	Ancient genomes reveal social and genetic structure of Late Neolithic Switzerland. <i>Nature Communications</i> , 2020, 11, 1915.	5.8	50
31	Ethics of DNA research on human remains: five globally applicable guidelines. <i>Nature</i> , 2021, 599, 41-46.	13.7	49
32	Dynamic changes in genomic and social structures in third millennium BCE central Europe. <i>Science Advances</i> , 2021, 7, .	4.7	46
33	Arrival routes of first Americans uncertain. <i>Science</i> , 2018, 359, 1224-1225.	6.0	42
34	Ancient proteins provide evidence of dairy consumption in eastern Africa. <i>Nature Communications</i> , 2021, 12, 632.	5.8	39
35	Evolution of molecular phenotypes under stabilizing selection. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2013, 2013, P01012.	0.9	23
36	Reconstructing genetic histories and social organisation in Neolithic and Bronze Age Croatia. <i>Scientific Reports</i> , 2021, 11, 16729.	1.6	8

#	ARTICLE	IF	CITATIONS
37	bleiglas: An R package for interpolation and visualisation of spatiotemporal data with 3D tessellation. Journal of Open Source Software, 2021, 6, 3092.	2.0	1
38	Review and Assessment of Performance of Genomic Inference Methods based on the Sequentially Markovian Coalescent. Peer Community in Evolutionary Biology, 0, , .	0.0	0