Swapan Mallick

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4565016/publications.pdf

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66 papers

24,686 citations

47006 47 h-index 91884 69 g-index

84 all docs

84 docs citations

times ranked

84

19502 citing authors

#	Article	IF	Citations
1	Large-scale migration into Britain during the Middle to Late Bronze Age. Nature, 2022, 601, 588-594.	27.8	86
2	A unified genealogy of modern and ancient genomes. Science, 2022, 375, eabi8264.	12.6	59
3	A genetic history of the pre-contact Caribbean. Nature, 2021, 590, 103-110.	27.8	67
4	Genomic insights into the formation of human populations in East Asia. Nature, 2021, 591, 413-419.	27.8	216
5	Ancient genomes reveal long-range influence of the pre-Columbian culture and site of Tiwanaku. Science Advances, 2021, 7, eabg7261.	10.3	8
6	Mitochondrial genome diversity on the Central Siberian Plateau with particular reference to the prehistory of northernmost Eurasia. PLoS ONE, 2021, 16, e0244228.	2.5	4
7	Ethics of DNA research on human remains: five globally applicable guidelines. Nature, 2021, 599, 41-46.	27.8	49
8	Social stratification without genetic differentiation at the site of Kulubnarti in Christian Period Nubia. Nature Communications, 2021, 12, 7283.	12.8	13
9	Ancient genomes in South Patagonia reveal population movements associated with technological shifts and geography. Nature Communications, 2020, 11 , 3868 .	12.8	28
10	ContamLD: estimation of ancient nuclear DNA contamination using breakdown of linkage disequilibrium. Genome Biology, 2020, 21, 199.	8.8	29
11	A Paleogenomic Reconstruction of the Deep Population History of the Andes. Cell, 2020, 181, 1131-1145.e21.	28.9	69
12	The Genomic History of the Bronze Age Southern Levant. Cell, 2020, 181, 1146-1157.e11.	28.9	51
13	Insights into human genetic variation and population history from 929 diverse genomes. Science, 2020, 367, .	12.6	534
14	Human auditory ossicles as an alternative optimal source of ancient DNA. Genome Research, 2020, 30, 427-436.	5.5	37
15	The spread of steppe and Iranian-related ancestry in the islands of the western Mediterranean. Nature Ecology and Evolution, 2020, 4, 334-345.	7.8	95
16	Ancient West African foragers in the context of African population history. Nature, 2020, 577, 665-670.	27.8	86
17	Ancient DNA from the skeletons of Roopkund Lake reveals Mediterranean migrants in India. Nature Communications, 2019, 10, 3670.	12.8	19
18	An Ancient Harappan Genome Lacks Ancestry from Steppe Pastoralists or Iranian Farmers. Cell, 2019, 179, 729-735.e10.	28.9	62

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19	The formation of human populations in South and Central Asia. Science, 2019, 365, .	12.6	383
20	Palaeo-Eskimo genetic ancestry and the peopling of Chukotka and North America. Nature, 2019, 570, 236-240.	27.8	118
21	Ancient genomes indicate population replacement in Early Neolithic Britain. Nature Ecology and Evolution, 2019, 3, 765-771.	7.8	156
22	African evolutionary history inferred from whole genome sequence data of 44 indigenous African populations. Genome Biology, 2019, 20, 82.	8.8	84
23	The genomic history of the Iberian Peninsula over the past 8000 years. Science, 2019, 363, 1230-1234.	12.6	340
24	Ancient human genome-wide data from a 3000-year interval in the Caucasus corresponds with eco-geographic regions. Nature Communications, 2019, 10, 590.	12.8	113
25	The Beaker phenomenon and the genomic transformation of northwest Europe. Nature, 2018, 555, 190-196.	27.8	503
26	The genomic history of southeastern Europe. Nature, 2018, 555, 197-203.	27.8	479
27	A comprehensive genomic history of extinct and living elephants. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2566-E2574.	7.1	142
28	Population Turnover in Remote Oceania Shortly after Initial Settlement. Current Biology, 2018, 28, 1157-1165.e7.	3.9	91
29	No evidence for unknown archaic ancestry in South Asia. Nature Genetics, 2018, 50, 632-633.	21.4	7
30	Reconstructing the Deep Population History of Central and South America. Cell, 2018, 175, 1185-1197.e22.	28.9	259
31	Ancient genomes document multiple waves of migration in Southeast Asian prehistory. Science, 2018, 361, 92-95.	12.6	250
32	Paternal origin of Paleo-Indians in Siberia: insights from Y-chromosome sequences. European Journal of Human Genetics, 2018, 26, 1687-1696.	2.8	21
33	Ancient DNA from Chalcolithic Israel reveals the role of population mixture in cultural transformation. Nature Communications, 2018, 9, 3336.	12.8	71
34	Reconstruction of Y-chromosome phylogeny reveals two neolithic expansions of Tibeto-Burman populations. Molecular Genetics and Genomics, 2018, 293, 1293-1300.	2.1	46
35	Archaeogenomic evidence reveals prehistoric matrilineal dynasty. Nature Communications, 2017, 8, 14115.	12.8	210
36	Reconstructing Prehistoric African Population Structure. Cell, 2017, 171, 59-71.e21.	28.9	308

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37	Genetic origins of the Minoans and Mycenaeans. Nature, 2017, 548, 214-218.	27.8	203
38	Parallel palaeogenomic transects reveal complex genetic history of early European farmers. Nature, 2017, 551, 368-372.	27.8	306
39	Palaeogenomes of Eurasian straight-tusked elephants challenge the current view of elephant evolution. ELife, 2017, 6, .	6.0	50
40	Mitochondrial DNA analysis of eneolithic trypillians from Ukraine reveals neolithic farming genetic roots. PLoS ONE, 2017, 12, e0172952.	2.5	19
41	The genetic history of Ice Age Europe. Nature, 2016, 534, 200-205.	27.8	729
42	Genomic insights into the peopling of the Southwest Pacific. Nature, 2016, 538, 510-513.	27.8	262
43	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. Nature, 2016, 538, 201-206.	27.8	1,216
44	Genomic insights into the origin of farming in the ancient Near East. Nature, 2016, 536, 419-424.	27.8	733
45	Ancient mitochondrial DNA provides high-resolution time scale of the peopling of the Americas. Science Advances, 2016, 2, e1501385.	10.3	306
46	Population Structure of UK Biobank and Ancient Eurasians Reveals Adaptation at Genes Influencing Blood Pressure. American Journal of Human Genetics, 2016, 99, 1130-1139.	6.2	53
47	The contribution of rare variation to prostate cancer heritability. Nature Genetics, 2016, 48, 30-35.	21.4	139
48	The Combined Landscape of Denisovan and Neanderthal Ancestry in Present-Day Humans. Current Biology, 2016, 26, 1241-1247.	3.9	377
49	Whole-exome sequencing of over 4100 men of African ancestry and prostate cancer risk. Human Molecular Genetics, 2016, 25, 371-381.	2.9	26
50	Massive migration from the steppe was a source for Indo-European languages in Europe. Nature, 2015, 522, 207-211.	27.8	1,435
51	Global diversity, population stratification, and selection of human copy-number variation. Science, 2015, 349, aab3761.	12.6	293
52	Genetic evidence for two founding populations of the Americas. Nature, 2015, 525, 104-108.	27.8	348
53	An early modern human from Romania with a recent Neanderthal ancestor. Nature, 2015, 524, 216-219.	27.8	633
54	Complete Genomes Reveal Signatures of Demographic and Genetic Declines in the Woolly Mammoth. Current Biology, 2015, 25, 1395-1400.	3.9	263

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55	Genome-wide patterns of selection in 230 ancient Eurasians. Nature, 2015, 528, 499-503.	27.8	1,160
56	Partial uracil–DNA–glycosylase treatment for screening of ancient DNA. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20130624.	4.0	381
57	A Re-Appraisal of the Early Andean Human Remains from Lauricocha in Peru. PLoS ONE, 2015, 10, e0127141.	2.5	41
58	The complete genome sequence of a Neanderthal from the Altai Mountains. Nature, 2014, 505, 43-49.	27.8	1,830
59	The genomic landscape of Neanderthal ancestry in present-day humans. Nature, 2014, 507, 354-357.	27.8	877
60	A framework for the interpretation of de novo mutation in human disease. Nature Genetics, 2014, 46, 944-950.	21.4	943
61	Gibbon genome and the fast karyotype evolution of small apes. Nature, 2014, 513, 195-201.	27.8	320
62	Ancient human genomes suggest three ancestral populations for present-day Europeans. Nature, 2014, 513, 409-413.	27.8	1,179
63	Ancient Admixture in Human History. Genetics, 2012, 192, 1065-1093.	2.9	2,012
64	A High-Coverage Genome Sequence from an Archaic Denisovan Individual. Science, 2012, 338, 222-226.	12.6	1,695
65	Genetic history of an archaic hominin group from Denisova Cave in Siberia. Nature, 2010, 468, 1053-1060.	27.8	1,537
66	The difficulty of avoiding false positives in genome scans for natural selection. Genome Research, 2009, 19, 922-933.	5 . 5	89