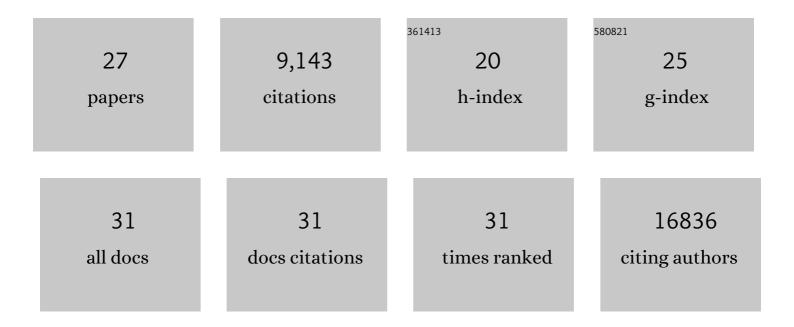
## Aylwyn Scally

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2781190/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Short-range template switching in great ape genomes explored using pair hidden Markov models. PLoS Genetics, 2021, 17, e1009221.	3.5	11
2	Human origins in Southern African palaeo-wetlands? Strong claims from weak evidence. Journal of Archaeological Science, 2021, 130, 105374.	2.4	9
3	Reforming social genetics. Nature Ecology and Evolution, 2021, 5, 1563.	7.8	0
4	Complexity in human ancestral demography. Journal of Anthropological Sciences, 2021, 99, .	0.4	0
5	What is ancestry?. PLoS Genetics, 2020, 16, e1008624.	3.5	91
6	Insights into human genetic variation and population history from 929 diverse genomes. Science, 2020, 367, .	12.6	534
7	Genomes reveal marked differences in the adaptive evolution between orangutan species. Genome Biology, 2018, 19, 193.	8.8	18
8	Detecting archaic introgression using an unadmixed outgroup. PLoS Genetics, 2018, 14, e1007641.	3.5	78
9	Ancient human parallel lineages within North America contributed to a coastal expansion. Science, 2018, 360, 1024-1027.	12.6	138
10	Did Our Species Evolve in Subdivided Populations across Africa, and Why Does It Matter?. Trends in Ecology and Evolution, 2018, 33, 582-594.	8.7	315
11	Morphometric, Behavioral, and Genomic Evidence for a New Orangutan Species. Current Biology, 2017, 27, 3487-3498.e10.	3.9	192
12	Estimating the human mutation rate from autozygous segments reveals population differences in human mutational processes. Nature Communications, 2017, 8, 303.	12.8	81
13	Inference of Candidate Germline Mutator Loci in Humans from Genome-Wide Haplotype Data. PLoS Genetics, 2017, 13, e1006549.	3.5	22
14	Global clues to the nature of genomic mutations in humans. ELife, 2017, 6, .	6.0	2
15	BCFtools/RoH: a hidden Markov model approach for detecting autozygosity from next-generation sequencing data. Bioinformatics, 2016, 32, 1749-1751.	4.1	506
16	The mutation rate in human evolution and demographic inference. Current Opinion in Genetics and Development, 2016, 41, 36-43.	3.3	100
17	Chimpanzee genomic diversity reveals ancient admixture with bonobos. Science, 2016, 354, 477-481.	12.6	230
18	Mutation rates and the evolution of germline structure. Philosophical Transactions of the Royal Society B: Biological Sciences, 2016, 371, 20150137.	4.0	49

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#	Article	IF	CITATION
19	Rethinking the dispersal of <i>Homo sapiens</i> out of Africa. Evolutionary Anthropology, 2015, 24, 149-164.	3.4	263
20	Tracing the Route of Modern Humans out of Africa by Using 225 Human Genome Sequences from Ethiopians and Egyptians. American Journal of Human Genetics, 2015, 96, 986-991.	6.2	152
21	Mountain gorilla genomes reveal the impact of long-term population decline and inbreeding. Science, 2015, 348, 242-245.	12.6	326
22	A New Isolation with Migration Model along Complete Genomes Infers Very Different Divergence Processes among Closely Related Great Ape Species. PLoS Genetics, 2012, 8, e1003125.	3.5	102
23	Revising the human mutation rate: implications for understanding human evolution. Nature Reviews Genetics, 2012, 13, 745-753.	16.3	483
24	Insights into hominid evolution from the gorilla genome sequence. Nature, 2012, 483, 169-175.	27.8	663
25	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	27.8	991
26	Accurate whole human genome sequencing using reversible terminator chemistry. Nature, 2008, 456, 53-59.	27.8	3,118
27	A large genome center's improvements to the Illumina sequencing system. Nature Methods, 2008, 5, 1005-1010.	19.0	656