Aylwyn Scally

List of Publications by Year in descending order

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361413 580821 9,143 27 20 25 citations h-index g-index papers 31 31 31 16836 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Accurate whole human genome sequencing using reversible terminator chemistry. Nature, 2008, 456, 53-59.	27.8	3,118
2	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	27.8	991
3	Insights into hominid evolution from the gorilla genome sequence. Nature, 2012, 483, 169-175.	27.8	663
4	A large genome center's improvements to the Illumina sequencing system. Nature Methods, 2008, 5, 1005-1010.	19.0	656
5	Insights into human genetic variation and population history from 929 diverse genomes. Science, 2020, 367, .	12.6	534
6	BCFtools/RoH: a hidden Markov model approach for detecting autozygosity from next-generation sequencing data. Bioinformatics, 2016, 32, 1749-1751.	4.1	506
7	Revising the human mutation rate: implications for understanding human evolution. Nature Reviews Genetics, 2012, 13, 745-753.	16.3	483
8	Mountain gorilla genomes reveal the impact of long-term population decline and inbreeding. Science, 2015, 348, 242-245.	12.6	326
9	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
10	Rethinking the dispersal of <i>Homo sapiens</i> out of Africa. Evolutionary Anthropology, 2015, 24, 149-164.	3.4	263
11	Chimpanzee genomic diversity reveals ancient admixture with bonobos. Science, 2016, 354, 477-481.	12.6	230
12	Morphometric, Behavioral, and Genomic Evidence for a New Orangutan Species. Current Biology, 2017, 27, 3487-3498.e10.	3.9	192
13	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
14	Ancient human parallel lineages within North America contributed to a coastal expansion. Science, 2018, 360, 1024-1027.	12.6	138
15	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
16	The mutation rate in human evolution and demographic inference. Current Opinion in Genetics and Development, 2016, 41, 36-43.	3.3	100
17	What is ancestry?. PLoS Genetics, 2020, 16, e1008624.	3.5	91
18	Estimating the human mutation rate from autozygous segments reveals population differences in human mutational processes. Nature Communications, 2017, 8, 303.	12.8	81

#	Article	IF	CITATIONS
19	Detecting archaic introgression using an unadmixed outgroup. PLoS Genetics, 2018, 14, e1007641.	3.5	78
20	Mutation rates and the evolution of germline structure. Philosophical Transactions of the Royal Society B: Biological Sciences, 2016, 371, 20150137.	4.0	49
21	Inference of Candidate Germline Mutator Loci in Humans from Genome-Wide Haplotype Data. PLoS Genetics, 2017, 13, e1006549.	3.5	22
22	Genomes reveal marked differences in the adaptive evolution between orangutan species. Genome Biology, 2018, 19, 193.	8.8	18
23	Short-range template switching in great ape genomes explored using pair hidden Markov models. PLoS Genetics, 2021, 17, e1009221.	3.5	11
24	Human origins in Southern African palaeo-wetlands? Strong claims from weak evidence. Journal of Archaeological Science, 2021, 130, 105374.	2.4	9
25	Global clues to the nature of genomic mutations in humans. ELife, 2017, 6, .	6.0	2
26	Reforming social genetics. Nature Ecology and Evolution, 2021, 5, 1563.	7.8	0
27	Complexity in human ancestral demography. Journal of Anthropological Sciences, 2021, 99, .	0.4	0