

Aylwyn Scally

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2781190/publications.pdf>

Version: 2024-02-01

27
papers

9,143
citations

361413

20
h-index

580821

25
g-index

31
all docs

31
docs citations

31
times ranked

16836
citing authors

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

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | Rethinking the dispersal of <i>Homo sapiens</i> out of Africa. <i>Evolutionary Anthropology</i> , 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. <i>American Journal of Human Genetics</i> , 2015, 96, 986-991. | 6.2 | 152 |
| 21 | Mountain gorilla genomes reveal the impact of long-term population decline and inbreeding. <i>Science</i> , 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. <i>PLoS Genetics</i> , 2012, 8, e1003125. | 3.5 | 102 |
| 23 | Revising the human mutation rate: implications for understanding human evolution. <i>Nature Reviews Genetics</i> , 2012, 13, 745-753. | 16.3 | 483 |
| 24 | Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , 2012, 483, 169-175. | 27.8 | 663 |
| 25 | Mapping copy number variation by population-scale genome sequencing. <i>Nature</i> , 2011, 470, 59-65. | 27.8 | 991 |
| 26 | Accurate whole human genome sequencing using reversible terminator chemistry. <i>Nature</i> , 2008, 456, 53-59. | 27.8 | 3,118 |
| 27 | A large genome center's improvements to the Illumina sequencing system. <i>Nature Methods</i> , 2008, 5, 1005-1010. | 19.0 | 656 |