Anders BergstrÃ¶m

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4357432/publications.pdf

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28 papers	4,684 citations	279798 23 h-index	501196 28 g-index
30 all docs	30 docs citations	30 times ranked	6650 citing authors

#	Article	IF	Citations
1	Genome evolution across 1,011 Saccharomyces cerevisiae isolates. Nature, 2018, 556, 339-344.	27.8	952
2	Insights into human genetic variation and population history from 929 diverse genomes. Science, 2020, 367, .	12.6	534
3	Genomic evidence for the Pleistocene and recent population history of Native Americans. Science, 2015, 349, aab3884.	12.6	449
4	A genomic history of Aboriginal Australia. Nature, 2016, 538, 207-214.	27.8	439
5	Contrasting evolutionary genome dynamics between domesticated and wild yeasts. Nature Genetics, 2017, 49, 913-924.	21.4	340
6	A High-Definition View of Functional Genetic Variation from Natural Yeast Genomes. Molecular Biology and Evolution, 2014, 31, 872-888.	8.9	328
7	Million-year-old DNA sheds light on the genomic history of mammoths. Nature, 2021, 591, 265-269.	27.8	179
8	Origins of modern human ancestry. Nature, 2021, 590, 229-237.	27.8	166
9	High-Resolution Mapping of Complex Traits with a Four-Parent Advanced Intercross Yeast Population. Genetics, 2013, 195, 1141-1155.	2.9	164
10	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. Cell, 2019, 179, 984-1002.e36.	28.9	152
11	Origins and genetic legacy of prehistoric dogs. Science, 2020, 370, 557-564.	12.6	152
12	The Genetic Basis of Natural Variation in Oenological Traits in Saccharomyces cerevisiae. PLoS ONE, 2012, 7, e49640.	2.5	107
13	Y Chromosome Sequences Reveal a Short Beringian Standstill, Rapid Expansion, and early Population structure of Native American Founders. Current Biology, 2019, 29, 149-157.e3.	3.9	94
14	High quality de novo sequencing and assembly of the Saccharomyces arboricolus genome. BMC Genomics, 2013, 14, 69.	2.8	87
15	Population Structure, Stratification, and Introgression of Human Structural Variation. Cell, 2020, 182, 189-199.e15.	28.9	79
16	Clonal Heterogeneity Influences the Fate of New Adaptive Mutations. Cell Reports, 2017, 21, 732-744.	6.4	70
17	Extensive Recombination of a Yeast Diploid Hybrid through Meiotic Reversion. PLoS Genetics, 2016, 12, e1005781.	3.5	60
18	Deep Roots for Aboriginal Australian Y Chromosomes. Current Biology, 2016, 26, 809-813.	3.9	54

#	Article	IF	Citations
19	Grey wolf genomic history reveals a dual ancestry of dogs. Nature, 2022, 607, 313-320.	27.8	48
20	A Neolithic expansion, but strong genetic structure, in the independent history of New Guinea. Science, 2017, 357, 1160-1163.	12.6	45
21	Chad Genetic Diversity Reveals an African History Marked by Multiple Holocene Eurasian Migrations. American Journal of Human Genetics, 2016, 99, 1316-1324.	6.2	37
22	Archaeological Central American maize genomes suggest ancient gene flow from South America. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 33124-33129.	7.1	36
23	Genome-scale sequencing and analysis of human, wolf, and bison DNA from 25,000-year-old sediment. Current Biology, 2021, 31, 3564-3574.e9.	3.9	34
24	Inferring Genome-Wide Recombination Landscapes from Advanced Intercross Lines: Application to Yeast Crosses. PLoS ONE, 2013, 8, e62266.	2.5	29
25	Y-chromosomal sequences of diverse Indian populations and the ancestry of the Andamanese. Human Genetics, 2017, 136, 499-510.	3.8	18
26	Copy number variation arising from gene conversion on the human Y chromosome. Human Genetics, 2018, 137, 73-83.	3.8	9
27	Human Genetics: Busy Subway Networks in Remote Oceania?. Current Biology, 2018, 28, R549-R551.	3.9	2
28	Paleolithic networking. Science, 2017, 358, 586-587.	12.6	1