

Thorfinn S Korneliussen

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

13,497
citations

81434

41
h-index

169272

56
g-index

67
all docs

67
docs citations

67
times ranked

20417
citing authors

#	ARTICLE	IF	CITATIONS
1	ANGSD: Analysis of Next Generation Sequencing Data. BMC Bioinformatics, 2014, 15, 356.	1.2	1,935
2	Sequencing of 50 Human Exomes Reveals Adaptation to High Altitude. Science, 2010, 329, 75-78.	6.0	1,339
3	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. Nature, 2013, 499, 74-78.	13.7	717
4	Estimating Individual Admixture Proportions from Next Generation Sequencing Data. Genetics, 2013, 195, 693-702.	1.2	515
5	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. Nature, 2014, 506, 225-229.	13.7	500
6	Genomic evidence for the Pleistocene and recent population history of Native Americans. Science, 2015, 349, aab3884.	6.0	449
7	A genomic history of Aboriginal Australia. Nature, 2016, 538, 207-214.	13.7	439
8	Greenlandic Inuit show genetic signatures of diet and climate adaptation. Science, 2015, 349, 1343-1347.	6.0	397
9	Population Genomics Reveal Recent Speciation and Rapid Evolutionary Adaptation in Polar Bears. Cell, 2014, 157, 785-794.	13.5	363
10	A recent bottleneck of Y chromosome diversity coincides with a global change in culture. Genome Research, 2015, 25, 459-466.	2.4	348
11	A common Greenlandic TBC1D4 variant confers muscle insulin resistance and type 2 diabetes. Nature, 2014, 512, 190-193.	13.7	338
12	SNP Calling, Genotype Calling, and Sample Allele Frequency Estimation from New-Generation Sequencing Data. PLoS ONE, 2012, 7, e37558.	1.1	336
13	On Detecting Incomplete Soft or Hard Selective Sweeps Using Haplotype Structure. Molecular Biology and Evolution, 2014, 31, 1275-1291.	3.5	335
14	137 ancient human genomes from across the Eurasian steppes. Nature, 2018, 557, 369-374.	13.7	325
15	Resequencing of 200 human exomes identifies an excess of low-frequency non-synonymous coding variants. Nature Genetics, 2010, 42, 969-972.	9.4	297
16	The prehistoric peopling of Southeast Asia. Science, 2018, 361, 88-92.	6.0	291
17	Genomic structure in Europeans dating back at least 36,200 years. Science, 2014, 346, 1113-1118.	6.0	287
18	The genetic prehistory of the New World Arctic. Science, 2014, 345, 1255832.	6.0	264

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19	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , 2017, 358, 659-662.	6.0	263
20	Prehistoric genomes reveal the genetic foundation and cost of horse domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5661-9.	3.3	260
21	The ancestry and affiliations of Kennewick Man. <i>Nature</i> , 2015, 523, 455-458.	13.7	241
22	Genome-culture coevolution promotes rapid divergence of killer whale ecotypes. <i>Nature Communications</i> , 2016, 7, 11693.	5.8	222
23	Genomic Analyses from Non-invasive Prenatal Testing Reveal Genetic Associations, Patterns of Viral Infections, and Chinese Population History. <i>Cell</i> , 2018, 175, 347-359.e14.	13.5	213
24	Calculation of Tajima's D and other neutrality test statistics from low depth next-generation sequencing data. <i>BMC Bioinformatics</i> , 2013, 14, 289.	1.2	211
25	Maternal age effect and severe germ-line bottleneck in the inheritance of human mitochondrial DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15474-15479.	3.3	201
26	Quantifying Population Genetic Differentiation from Next-Generation Sequencing Data. <i>Genetics</i> , 2013, 195, 979-992.	1.2	187
27	Speciation with gene flow in equids despite extensive chromosomal plasticity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18655-18660.	3.3	183
28	Estimation of allele frequency and association mapping using next-generation sequencing data. <i>BMC Bioinformatics</i> , 2011, 12, 231.	1.2	170
29	Natural Selection Affects Multiple Aspects of Genetic Variation at Putatively Neutral Sites across the Human Genome. <i>PLoS Genetics</i> , 2011, 7, e1002326.	1.5	146
30	Population genomics of the Viking world. <i>Nature</i> , 2020, 585, 390-396.	13.7	143
31	Ancient genomics. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130387.	1.8	142
32	The origin and evolution of maize in the Southwestern United States. <i>Nature Plants</i> , 2015, 1, 14003.	4.7	138
33	Physiological and Genetic Adaptations to Diving in Sea Nomads. <i>Cell</i> , 2018, 173, 569-580.e15.	13.5	129
34	Whole-Exome Sequencing of 2,000 Danish Individuals and the Role of Rare Coding Variants in Type 2 Diabetes. <i>American Journal of Human Genetics</i> , 2013, 93, 1072-1086.	2.6	124
35	Exome sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. <i>Diabetologia</i> , 2013, 56, 298-310.	2.9	119
36	NgsRelate: a software tool for estimating pairwise relatedness from next-generation sequencing data. <i>Bioinformatics</i> , 2015, 31, 4009-4011.	1.8	109

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37	Improving the estimation of genetic distances from Next-Generation Sequencing data. <i>Biological Journal of the Linnean Society</i> , 2016, 117, 139-149.	0.7	102
38	Relatedness mapping and tracts of relatedness for genome-wide data in the presence of linkage disequilibrium. <i>Genetic Epidemiology</i> , 2009, 33, 266-274.	0.6	99
39	Fast and accurate relatedness estimation from high-throughput sequencing data in the presence of inbreeding. <i>GigaScience</i> , 2019, 8, .	3.3	86
40	Uncovering the Genetic History of the Present-Day Greenlandic Population. <i>American Journal of Human Genetics</i> , 2015, 96, 54-69.	2.6	85
41	Human Disease Variation in the Light of Population Genomics. <i>Cell</i> , 2019, 177, 115-131.	13.5	75
42	Joint Estimates of Heterozygosity and Runs of Homozygosity for Modern and Ancient Samples. <i>Genetics</i> , 2019, 212, 587-614.	1.2	61
43	Extensive Genome-Wide Phylogenetic Discordance Is Due to Incomplete Lineage Sorting and Not Ongoing Introgression in a Rapidly Radiated Bryophyte Genus. <i>Molecular Biology and Evolution</i> , 2021, 38, 2750-2766.	3.5	54
44	Association Testing for Next-Generation Sequencing Data Using Score Statistics. <i>Genetic Epidemiology</i> , 2012, 36, 430-437.	0.6	53
45	Ancient Jomon genome sequence analysis sheds light on migration patterns of early East Asian populations. <i>Communications Biology</i> , 2020, 3, 437.	2.0	44
46	Variation and association to diabetes in 2000 full mtDNA sequences mined from an exome study in a Danish population. <i>European Journal of Human Genetics</i> , 2014, 22, 1040-1045.	1.4	26
47	Ancestry-specific association mapping in admixed populations. <i>Genetic Epidemiology</i> , 2019, 43, 506-521.	0.6	26
48	A likelihood method for estimating present-day human contamination in ancient male samples using low-depth X-chromosome data. <i>Bioinformatics</i> , 2020, 36, 828-841.	1.8	14
49	A reference-free approach to analyse RADseq data using standard next generation sequencing toolkits. <i>Molecular Ecology Resources</i> , 2021, 21, 1085-1097.	2.2	12
50	Targeted conservation genetics of the endangered chimpanzee. <i>Heredity</i> , 2020, 125, 15-27.	1.2	11
51	Identifying a living great-grandson of the Lakota Sioux leader Tatanka Iyotake (Sitting Bull). <i>Science Advances</i> , 2021, 7, eabh2013.	4.7	5
52	LocalNgsRelate: a software tool for inferring IBD sharing along the genome between pairs of individuals from low-depth NGS data. <i>Bioinformatics</i> , 2022, 38, 1159-1161.	1.8	4
53	Fast and accurate estimation of multidimensional site frequency spectra from low-coverage high-throughput sequencing data. <i>GigaScience</i> , 2022, 11, .	3.3	4
54	Archaeology Augments Tibet's Genetic History's Response. <i>Science</i> , 2010, 329, 1467-1468.	6.0	3

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55	Low Pass Genomes of 141,431 Chinese Reveal Patterns of Viral Infection, Novel Phenotypic Associations, and the Genetic History of China. SSRN Electronic Journal, 0, , .	0.4	2