Thorfinn S Korneliussen

List of Publications by Year in descending order

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THODEINN S KODNELLISSEN

#	Article	IF	CITATIONS
1	ANGSD: Analysis of Next Generation Sequencing Data. BMC Bioinformatics, 2014, 15, 356.	2.6	1,935
2	Sequencing of 50 Human Exomes Reveals Adaptation to High Altitude. Science, 2010, 329, 75-78.	12.6	1,339
3	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. Nature, 2013, 499, 74-78.	27.8	717
4	Estimating Individual Admixture Proportions from Next Generation Sequencing Data. Genetics, 2013, 195, 693-702.	2.9	515
5	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. Nature, 2014, 506, 225-229.	27.8	500
6	Genomic evidence for the Pleistocene and recent population history of Native Americans. Science, 2015, 349, aab3884.	12.6	449
7	A genomic history of Aboriginal Australia. Nature, 2016, 538, 207-214.	27.8	439
8	Greenlandic Inuit show genetic signatures of diet and climate adaptation. Science, 2015, 349, 1343-1347.	12.6	397
9	Population Genomics Reveal Recent Speciation and Rapid Evolutionary Adaptation in Polar Bears. Cell, 2014, 157, 785-794.	28.9	363
10	A recent bottleneck of Y chromosome diversity coincides with a global change in culture. Genome Research, 2015, 25, 459-466.	5.5	348
11	A common Greenlandic TBC1D4 variant confers muscle insulin resistance and type 2 diabetes. Nature, 2014, 512, 190-193.	27.8	338
12	SNP Calling, Genotype Calling, and Sample Allele Frequency Estimation from New-Generation Sequencing Data. PLoS ONE, 2012, 7, e37558.	2.5	336
13	On Detecting Incomplete Soft or Hard Selective Sweeps Using Haplotype Structure. Molecular Biology and Evolution, 2014, 31, 1275-1291.	8.9	335
14	137 ancient human genomes from across the Eurasian steppes. Nature, 2018, 557, 369-374.	27.8	325
15	Resequencing of 200 human exomes identifies an excess of low-frequency non-synonymous coding variants. Nature Genetics, 2010, 42, 969-972.	21.4	297
16	The prehistoric peopling of Southeast Asia. Science, 2018, 361, 88-92.	12.6	291
17	Genomic structure in Europeans dating back at least 36,200 years. Science, 2014, 346, 1113-1118.	12.6	287
18	The genetic prehistory of the New World Arctic. Science, 2014, 345, 1255832.	12.6	264

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19	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. Science, 2017, 358, 659-662.	12.6	263
20	Prehistoric genomes reveal the genetic foundation and cost of horse domestication. Proceedings of the United States of America, 2014, 111, E5661-9.	7.1	260
21	The ancestry and affiliations of Kennewick Man. Nature, 2015, 523, 455-458.	27.8	241
22	Genome-culture coevolution promotes rapid divergence of killer whale ecotypes. Nature Communications, 2016, 7, 11693.	12.8	222
23	Genomic Analyses from Non-invasive Prenatal Testing Reveal Genetic Associations, Patterns of Viral Infections, and Chinese Population History. Cell, 2018, 175, 347-359.e14.	28.9	213
24	Calculation of Tajima's D and other neutrality test statistics from low depth next-generation sequencing data. BMC Bioinformatics, 2013, 14, 289.	2.6	211
25	Maternal age effect and severe germ-line bottleneck in the inheritance of human mitochondrial DNA. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15474-15479.	7.1	201
26	Quantifying Population Genetic Differentiation from Next-Generation Sequencing Data. Genetics, 2013, 195, 979-992.	2.9	187
27	Speciation with gene flow in equids despite extensive chromosomal plasticity. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18655-18660.	7.1	183
28	Estimation of allele frequency and association mapping using next-generation sequencing data. BMC Bioinformatics, 2011, 12, 231.	2.6	170
29	Natural Selection Affects Multiple Aspects of Genetic Variation at Putatively Neutral Sites across the Human Genome. PLoS Genetics, 2011, 7, e1002326.	3.5	146
30	Population genomics of the Viking world. Nature, 2020, 585, 390-396.	27.8	143
31	Ancient genomics. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20130387.	4.0	142
32	The origin and evolution of maize in the Southwestern United States. Nature Plants, 2015, 1, 14003.	9.3	138
33	Physiological and Genetic Adaptations to Diving in Sea Nomads. Cell, 2018, 173, 569-580.e15.	28.9	129
34	Whole-Exome Sequencing of 2,000 Danish Individuals and the Role of Rare Coding Variants in Type 2 Diabetes. American Journal of Human Genetics, 2013, 93, 1072-1086.	6.2	124
35	Exome sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. Diabetologia, 2013, 56, 298-310.	6.3	119
36	NgsRelate: a software tool for estimating pairwise relatedness from next-generation sequencing data. Bioinformatics, 2015, 31, 4009-4011.	4.1	109

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37	Improving the estimation of genetic distances from Next-Generation Sequencing data. Biological Journal of the Linnean Society, 2016, 117, 139-149.	1.6	102
38	Relatedness mapping and tracts of relatedness for genomeâ€wide data in the presence of linkage disequilibrium. Genetic Epidemiology, 2009, 33, 266-274.	1.3	99
39	Fast and accurate relatedness estimation from high-throughput sequencing data in the presence of inbreeding. GigaScience, 2019, 8, .	6.4	86
40	Uncovering the Genetic History of the Present-Day Greenlandic Population. American Journal of Human Genetics, 2015, 96, 54-69.	6.2	85
41	Human Disease Variation in the Light of Population Genomics. Cell, 2019, 177, 115-131.	28.9	75
42	Joint Estimates of Heterozygosity and Runs of Homozygosity for Modern and Ancient Samples. Genetics, 2019, 212, 587-614.	2.9	61
43	Extensive Genome-Wide Phylogenetic Discordance Is Due to Incomplete Lineage Sorting and Not Ongoing Introgression in a Rapidly Radiated Bryophyte Genus. Molecular Biology and Evolution, 2021, 38, 2750-2766.	8.9	54
44	Association Testing for Nextâ€Generation Sequencing Data Using Score Statistics. Genetic Epidemiology, 2012, 36, 430-437.	1.3	53
45	Ancient Jomon genome sequence analysis sheds light on migration patterns of early East Asian populations. Communications Biology, 2020, 3, 437.	4.4	44
46	Variation and association to diabetes in 2000 full mtDNA sequences mined from an exome study in a Danish population. European Journal of Human Genetics, 2014, 22, 1040-1045.	2.8	26
47	Ancestryâ€specific association mapping in admixed populations. Genetic Epidemiology, 2019, 43, 506-521.	1.3	26
48	A likelihood method for estimating present-day human contamination in ancient male samples using low-depth X-chromosome data. Bioinformatics, 2020, 36, 828-841.	4.1	14
49	A referenceâ€free approach to analyse RADseq data using standard next generation sequencing toolkits. Molecular Ecology Resources, 2021, 21, 1085-1097.	4.8	12
50	Targeted conservation genetics of the endangered chimpanzee. Heredity, 2020, 125, 15-27.	2.6	11
51	Identifying a living great-grandson of the Lakota Sioux leader Tatanka Iyotake (Sitting Bull). Science Advances, 2021, 7, eabh2013.	10.3	5
52	LocalNgsRelate: a software tool for inferring IBD sharing along the genome between pairs of individuals from low-depth NGS data. Bioinformatics, 2022, 38, 1159-1161.	4.1	4
53	Fast and accurate estimation of multidimensional site frequency spectra from low-coverage high-throughput sequencing data. GigaScience, 2022, 11, .	6.4	4
54	Archaeology Augments Tibet's Genetic History—Response. Science, 2010, 329, 1467-1468.	12.6	3

#	Article	IF	CITATIONS
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