

# Thorfinn S Korneliussen

## List of Publications by Citations

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61  
papers

9,104  
citations

39  
h-index

67  
g-index

67  
ext. papers

11,805  
ext. citations

19.5  
avg, IF

5.71  
L-index

#	Paper	IF	Citations
61	ANGSD: Analysis of Next Generation Sequencing Data. <i>BMC Bioinformatics</i> , <b>2014</b> , 15, 356	3.6	1087
60	Sequencing of 50 human exomes reveals adaptation to high altitude. <i>Science</i> , <b>2010</b> , 329, 75-8	33.3	1020
59	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , <b>2013</b> , 499, 74-8	50.4	563
58	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , <b>2014</b> , 506, 225-9	50.4	357
57	POPULATION GENETICS. Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , <b>2015</b> , 349, aab3884	33.3	317
56	Greenlandic Inuit show genetic signatures of diet and climate adaptation. <i>Science</i> , <b>2015</b> , 349, 1343-7	33.3	298
55	Estimating individual admixture proportions from next generation sequencing data. <i>Genetics</i> , <b>2013</b> , 195, 693-702	4	270
54	A genomic history of Aboriginal Australia. <i>Nature</i> , <b>2016</b> , 538, 207-214	50.4	268
53	Resequencing of 200 human exomes identifies an excess of low-frequency non-synonymous coding variants. <i>Nature Genetics</i> , <b>2010</b> , 42, 969-72	36.3	264
52	A common Greenlandic TBC1D4 variant confers muscle insulin resistance and type 2 diabetes. <i>Nature</i> , <b>2014</b> , 512, 190-3	50.4	258
51	Population genomics reveal recent speciation and rapid evolutionary adaptation in polar bears. <i>Cell</i> , <b>2014</b> , 157, 785-94	56.2	242
50	SNP calling, genotype calling, and sample allele frequency estimation from New-Generation Sequencing data. <i>PLoS ONE</i> , <b>2012</b> , 7, e37558	3.7	242
49	A recent bottleneck of Y chromosome diversity coincides with a global change in culture. <i>Genome Research</i> , <b>2015</b> , 25, 459-66	9.7	235
48	Paleogenomics. Genomic structure in Europeans dating back at least 36,200 years. <i>Science</i> , <b>2014</b> , 346, 1113-8	33.3	232
47	On detecting incomplete soft or hard selective sweeps using haplotype structure. <i>Molecular Biology and Evolution</i> , <b>2014</b> , 31, 1275-91	8.3	214
46	The genetic prehistory of the New World Arctic. <i>Science</i> , <b>2014</b> , 345, 1255832	33.3	204
45	137 ancient human genomes from across the Eurasian steppes. <i>Nature</i> , <b>2018</b> , 557, 369-374	50.4	197

44	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> , <b>2014</b> , 111, E5661-9	11.5	197
43	The prehistoric peopling of Southeast Asia. <i>Science</i> , <b>2018</b> , 361, 88-92	33.3	174
42	Genome-culture coevolution promotes rapid divergence of killer whale ecotypes. <i>Nature Communications</i> , <b>2016</b> , 7, 11693	17.4	161
41	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , <b>2017</b> , 358, 659-662	33.3	160
40	The ancestry and affiliations of Kennewick Man. <i>Nature</i> , <b>2015</b> , 523, 455-458	50.4	157
39	Quantifying population genetic differentiation from next-generation sequencing data. <i>Genetics</i> , <b>2013</b> , 195, 979-92	4	141
38	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> , <b>2014</b> , 111, 15474-9	11.5	140
37	Calculation of Tajima's D and other neutrality test statistics from low depth next-generation sequencing data. <i>BMC Bioinformatics</i> , <b>2013</b> , 14, 289	3.6	140
36	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> , <b>2014</b> , 111, 18655-60	11.5	133
35	Estimation of allele frequency and association mapping using next-generation sequencing data. <i>BMC Bioinformatics</i> , <b>2011</b> , 12, 231	3.6	126
34	Genomic Analyses from Non-invasive Prenatal Testing Reveal Genetic Associations, Patterns of Viral Infections, and Chinese Population History. <i>Cell</i> , <b>2018</b> , 175, 347-359.e14	56.2	123
33	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> , <b>2013</b> , 93, 1072-86	11	109
32	Ancient genomics. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2015</b> , 370, 20130387	38.7	107
31	Natural selection affects multiple aspects of genetic variation at putatively neutral sites across the human genome. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002326	6	107
30	Exome sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. <i>Diabetologia</i> , <b>2013</b> , 56, 298-310	10.3	102
29	The origin and evolution of maize in the Southwestern United States. <i>Nature Plants</i> , <b>2015</b> , 1, 14003	11.5	99
28	Physiological and Genetic Adaptations to Diving in Sea Nomads. <i>Cell</i> , <b>2018</b> , 173, 569-580.e15	56.2	82
27	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> , <b>2014</b> , 94, 479	11	78

26	Relatedness mapping and tracts of relatedness for genome-wide data in the presence of linkage disequilibrium. <i>Genetic Epidemiology</i> , <b>2009</b> , 33, 266-74	2.6	73
25	Uncovering the genetic history of the present-day Greenlandic population. <i>American Journal of Human Genetics</i> , <b>2015</b> , 96, 54-69	11	61
24	Improving the estimation of genetic distances from Next-Generation Sequencing data. <i>Biological Journal of the Linnean Society</i> , <b>2016</b> , 117, 139-149	1.9	51
23	NgsRelate: a software tool for estimating pairwise relatedness from next-generation sequencing data. <i>Bioinformatics</i> , <b>2015</b> , 31, 4009-11	7.2	39
22	Population genomics of the Viking world. <i>Nature</i> , <b>2020</b> , 585, 390-396	50.4	35
21	Human Disease Variation in the Light of Population Genomics. <i>Cell</i> , <b>2019</b> , 177, 115-131	56.2	34
20	Association testing for next-generation sequencing data using score statistics. <i>Genetic Epidemiology</i> , <b>2012</b> , 36, 430-7	2.6	34
19	Fast and accurate relatedness estimation from high-throughput sequencing data in the presence of inbreeding. <i>GigaScience</i> , <b>2019</b> , 8,	7.6	29
18	Joint Estimates of Heterozygosity and Runs of Homozygosity for Modern and Ancient Samples. <i>Genetics</i> , <b>2019</b> , 212, 587-614	4	26
17	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> , <b>2014</b> , 22, 1040-5	5.3	23
16	Ancestry-specific association mapping in admixed populations. <i>Genetic Epidemiology</i> , <b>2019</b> , 43, 506-521	2.6	19
15	Ancient Jomon genome sequence analysis sheds light on migration patterns of early East Asian populations. <i>Communications Biology</i> , <b>2020</b> , 3, 437	6.7	19
14	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> , <b>2021</b> , 38, 2750-2766	8.3	11
13	A likelihood method for estimating present-day human contamination in ancient male samples using low-depth X-chromosome data. <i>Bioinformatics</i> , <b>2020</b> , 36, 828-841	7.2	7
12	Jomon genome sheds light on East Asian population history		6
11	Targeted conservation genetics of the endangered chimpanzee. <i>Heredity</i> , <b>2020</b> , 125, 15-27	3.6	5
10	Ancestry-specific association mapping in admixed populations		5
9	A reference-free approach to analyse RADseq data using standard next generation sequencing toolkits. <i>Molecular Ecology Resources</i> , <b>2021</b> , 21, 1085-1097	8.4	5

8	Archaeology Augments Tibet's Genetic History--Response. <i>Science</i> , <b>2010</b> , 329, 1467-1468	33.3	3
7	Fast and accurate estimation of multidimensional site frequency spectra from low-coverage high-throughput sequencing data.. <i>GigaScience</i> , <b>2022</b> , 11,	7.6	2
6	Low Pass Genomes of 141,431 Chinese Reveal Patterns of Viral Infection, Novel Phenotypic Associations, and the Genetic History of China. <i>SSRN Electronic Journal</i> ,	1	1
5	Population genomics of the emerging forest pathogen <i>Neonectria neomacrospora</i>		1
4	A likelihood method for estimating present-day human contamination in ancient DNA samples using low-depth haploid chromosome data		1
3	The pangenome of the fungal pathogen <i>Neonectria neomacrospora</i>		1
2	Estimation of site frequency spectra from low-coverage sequencing data using stochastic EM reduces overfitting, runtime, and memory usage		1
1	Identifying a living great-grandson of the Lakota Sioux leader Tatanka Iyotake (Sitting Bull). <i>Science Advances</i> , <b>2021</b> , 7, eabh2013	14.3	0