

# Thorfinn S Korneliussen

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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 | 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         |
| 60 | 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         |
| 59 | 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        |
| 58 | 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         |
| 57 | Targeted conservation genetics of the endangered chimpanzee. <i>Heredity</i> , <b>2020</b> , 125, 15-27   | 3.6  | 5         |
| 56 | 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        |
| 55 | Population genomics of the Viking world. <i>Nature</i> , <b>2020</b> , 585, 390-396   | 50.4 | 35        |
| 54 | 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         |
| 53 | Joint Estimates of Heterozygosity and Runs of Homozygosity for Modern and Ancient Samples. <i>Genetics</i> , <b>2019</b> , 212, 587-614   | 4    | 26        |
| 52 | 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        |
| 51 | Human Disease Variation in the Light of Population Genomics. <i>Cell</i> , <b>2019</b> , 177, 115-131   | 56.2 | 34        |
| 50 | Ancestry-specific association mapping in admixed populations. <i>Genetic Epidemiology</i> , <b>2019</b> , 43, 506-521   | 2.6  | 19        |
| 49 | Physiological and Genetic Adaptations to Diving in Sea Nomads. <i>Cell</i> , <b>2018</b> , 173, 569-580.e15   | 56.2 | 82        |
| 48 | 137 ancient human genomes from across the Eurasian steppes. <i>Nature</i> , <b>2018</b> , 557, 369-374  | 50.4 | 197       |
| 47 | 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       |
| 46 | The prehistoric peopling of Southeast Asia. <i>Science</i> , <b>2018</b> , 361, 88-92   | 33.3 | 174       |
| 45 | Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , <b>2017</b> , 358, 659-662  | 33.3 | 160       |

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|----|---|------|-----|
| 44 | 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  |
| 43 | A genomic history of Aboriginal Australia. <i>Nature</i> , <b>2016</b> , 538, 207-214   | 50.4 | 268 |
| 42 | Genome-culture coevolution promotes rapid divergence of killer whale ecotypes. <i>Nature Communications</i> , <b>2016</b> , 7, 11693  | 17.4 | 161 |
| 41 | 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 |
| 40 | The ancestry and affiliations of Kennewick Man. <i>Nature</i> , <b>2015</b> , 523, 455-458  | 50.4 | 157 |
| 39 | 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 |
| 38 | Greenlandic Inuit show genetic signatures of diet and climate adaptation. <i>Science</i> , <b>2015</b> , 349, 1343-7  | 33.3 | 298 |
| 37 | The origin and evolution of maize in the Southwestern United States. <i>Nature Plants</i> , <b>2015</b> , 1, 14003  | 11.5 | 99  |
| 36 | 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  |
| 35 | 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  |
| 34 | Ancient genomics. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2015</b> , 370, 20130387   | 33.3 | 107 |
| 33 | 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 |
| 32 | 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 |
| 31 | 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  |
| 30 | Population genomics reveal recent speciation and rapid evolutionary adaptation in polar bears. <i>Cell</i> , <b>2014</b> , 157, 785-94  | 56.2 | 242 |
| 29 | Paleogenomics. Genomic structure in Europeans dating back at least 36,200 years. <i>Science</i> , <b>2014</b> , 346, 1113-8   | 33.3 | 232 |
| 28 | The genetic prehistory of the New World Arctic. <i>Science</i> , <b>2014</b> , 345, 1255832   | 33.3 | 204 |
| 27 | 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 |

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|----|--|------|------|
| 26 | 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  |
| 25 | 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  |
| 24 | 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  |
| 23 | 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   |
| 22 | ANGSD: Analysis of Next Generation Sequencing Data. <i>BMC Bioinformatics</i> , <b>2014</b> , 15, 356  | 3.6  | 1087 |
| 21 | Exome sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. <i>Diabetologia</i> , <b>2013</b> , 56, 298-310   | 10.3 | 102  |
| 20 | 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  |
| 19 | 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  |
| 18 | Quantifying population genetic differentiation from next-generation sequencing data. <i>Genetics</i> , <b>2013</b> , 195, 979-92   | 4    | 141  |
| 17 | Estimating individual admixture proportions from next generation sequencing data. <i>Genetics</i> , <b>2013</b> , 195, 693-702   | 4    | 270  |
| 16 | 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  |
| 15 | Association testing for next-generation sequencing data using score statistics. <i>Genetic Epidemiology</i> , <b>2012</b> , 36, 430-7  | 2.6  | 34   |
| 14 | 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  |
| 13 | Estimation of allele frequency and association mapping using next-generation sequencing data. <i>BMC Bioinformatics</i> , <b>2011</b> , 12, 231  | 3.6  | 126  |
| 12 | 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  |
| 11 | 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  |
| 10 | Archaeology Augments Tibet's Genetic History--Response. <i>Science</i> , <b>2010</b> , 329, 1467-1468  | 33.3 | 3    |
| 9  | Sequencing of 50 human exomes reveals adaptation to high altitude. <i>Science</i> , <b>2010</b> , 329, 75-8  | 33.3 | 1020 |

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|---|---|-----|----|
| 8 | 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 |
| 7 | 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  |
| 6 | Population genomics of the emerging forest pathogen <i>Neonectria neomacrospora</i>   |     | 1  |
| 5 | Ancestry-specific association mapping in admixed populations  |     | 5  |
| 4 | Jomon genome sheds light on East Asian population history   |     | 6  |
| 3 | A likelihood method for estimating present-day human contamination in ancient DNA samples using low-depth haploid chromosome data   |     | 1  |
| 2 | The pangenome of the fungal pathogen <i>Neonectria neomacrospora</i>  |     | 1  |
| 1 | Estimation of site frequency spectra from low-coverage sequencing data using stochastic EM reduces overfitting, runtime, and memory usage                                 |     | 1  |