

# Anders Albrechtsen

## 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.

132  
papers

13,120  
citations

53  
h-index

114  
g-index

149  
ext. papers

16,630  
ext. citations

12  
avg, IF

6.22  
L-index

#	Paper	IF	Citations
132	Physical activity attenuates postprandial hyperglycaemia in homozygous TBC1D4 loss-of-function mutation carriers. <i>Diabetologia</i> , <b>2021</b> , 64, 1795-1804	10.3	3
131	A large-scale genome-wide gene expression analysis in peripheral blood identifies very few differentially expressed genes related to antidepressant treatment and response in patients with major depressive disorder. <i>Neuropsychopharmacology</i> , <b>2021</b> , 46, 1324-1332	8.7	0
130	The genetic history of Greenlandic-European contact. <i>Current Biology</i> , <b>2021</b> , 31, 2214-2219.e4	6.3	1
129	High genetic diversity and low differentiation reflect the ecological versatility of the African leopard. <i>Current Biology</i> , <b>2021</b> , 31, 1862-1871.e5	6.3	6
128	Vicariance followed by secondary gene flow in a young gazelle species complex. <i>Molecular Ecology</i> , <b>2021</b> , 30, 528-544	5.7	2
127	Large-scale Inference of Population Structure in Presence of Missingness using PCA. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	1
126	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
125	Predictors and trajectories of treatment response to SSRIs in patients suffering from PTSD. <i>Psychiatry Research</i> , <b>2021</b> , 301, 113964	9.9	2
124	Detecting selection in low-coverage high-throughput sequencing data using principal component analysis. <i>BMC Bioinformatics</i> , <b>2021</b> , 22, 470	3.6	
123	Joint identification of sex and sex-linked scaffolds in non-model organisms using low depth sequencing data. <i>Molecular Ecology Resources</i> , <b>2021</b> ,	8.4	3
122	Genetic study of the Arctic CPT1A variant suggests that its effect on fatty acid levels is modulated by traditional Inuit diet. <i>European Journal of Human Genetics</i> , <b>2020</b> , 28, 1592-1601	5.3	6
121	The derived allele of a novel intergenic variant at chromosome 11 associates with lower body mass index and a favorable metabolic phenotype in Greenlanders. <i>PLoS Genetics</i> , <b>2020</b> , 16, e1008544	6	1
120	Estimating narrow-sense heritability using family data from admixed populations. <i>Heredity</i> , <b>2020</b> , 124, 751-762	3.6	1
119	246-OR: A Loss-of-Function Mutation in the Sucrase-Isomaltase Gene Is Linked to a Markedly Healthier Metabolic Profile in Greenlanders. <i>Diabetes</i> , <b>2020</b> , 69, 246-OR	0.9	
118	Omega-3 fatty acids and risk of cardiovascular disease in Inuit: First prospective cohort study. <i>Atherosclerosis</i> , <b>2020</b> , 312, 28-34	3.1	2
117	Population genomics of the Viking world. <i>Nature</i> , <b>2020</b> , 585, 390-396	50.4	35
116	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

115	Evaluation of model fit of inferred admixture proportions. <i>Molecular Ecology Resources</i> , <b>2020</b> , 20, 936-949	9.4	9
114	Detection of internal N7-methylguanosine (m7G) RNA modifications by mutational profiling sequencing. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, e126	20.1	57
113	DamMet: ancient methylome mapping accounting for errors, true variants, and post-mortem DNA damage. <i>GigaScience</i> , <b>2019</b> , 8,	7.6	7
112	Ancestry-specific association mapping in admixed populations. <i>Genetic Epidemiology</i> , <b>2019</b> , 43, 506-521	2.6	19
111	Testing for Hardy-Weinberg equilibrium in structured populations using genotype or low-depth next generation sequencing data. <i>Molecular Ecology Resources</i> , <b>2019</b> , 19, 1144-1152	8.4	12
110	Genomic diversity and novel genome-wide association with fruit morphology in Capsicum, from 746k polymorphic sites. <i>Scientific Reports</i> , <b>2019</b> , 9, 10067	4.9	25
109	Allele frequency-free inference of close familial relationships from genotypes or low-depth sequencing data. <i>Molecular Ecology</i> , <b>2019</b> , 28, 35-48	5.7	28
108	Ancient genomes revisit the ancestry of domestic and Przewalski's horses. <i>Science</i> , <b>2018</b> , 360, 111-114	33.3	153
107	Genetic architecture of obesity and related metabolic traits-recent insights from isolated populations. <i>Current Opinion in Genetics and Development</i> , <b>2018</b> , 50, 74-78	4.9	3
106	Genetic determinants of glycosylated hemoglobin levels in the Greenlandic Inuit population. <i>European Journal of Human Genetics</i> , <b>2018</b> , 26, 868-875	5.3	3
105	Powerful Inference with the D-Statistic on Low-Coverage Whole-Genome Data. <i>G3: Genes, Genomes, Genetics</i> , <b>2018</b> , 8, 551-566	3.2	38
104	A southern African origin and cryptic structure in the highly mobile plains zebra. <i>Nature Ecology and Evolution</i> , <b>2018</b> , 2, 491-498	12.3	21
103	Loss-of-function variants in ADCY3 increase risk of obesity and type 2 diabetes. <i>Nature Genetics</i> , <b>2018</b> , 50, 172-174	36.3	97
102	Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. <i>Nature</i> , <b>2018</b> , 553, 203-207	50.4	178
101	Identification of novel high-impact recessively inherited type 2 diabetes risk variants in the Greenlandic population. <i>Diabetologia</i> , <b>2018</b> , 61, 2005-2015	10.3	11
100	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
99	Inferring Population Structure and Admixture Proportions in Low-Depth NGS Data. <i>Genetics</i> , <b>2018</b> , 210, 719-731	4	139
98	Ancient genomic changes associated with domestication of the horse. <i>Science</i> , <b>2017</b> , 356, 442-445	33.3	149

97	The Effect of an Extreme and Prolonged Population Bottleneck on Patterns of Deleterious Variation: Insights from the Greenlandic Inuit. <i>Genetics</i> , <b>2017</b> , 205, 787-801	4	31
96	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , <b>2017</b> , 358, 659-662	33.3	160
95	Founder Effect of the RET Mutation in Multiple Endocrine Neoplasia 2A in Denmark: A Nationwide Study. <i>Thyroid</i> , <b>2017</b> , 27, 1505-1510	6.2	14
94	fastNGSadmix: admixture proportions and principal component analysis of a single NGS sample. <i>Bioinformatics</i> , <b>2017</b> , 33, 3148-3150	7.2	16
93	Genetic screening of the FLCN gene identify six novel variants and a Danish founder mutation. <i>Journal of Human Genetics</i> , <b>2017</b> , 62, 151-157	4.3	12
92	Archaic Adaptive Introgression in TBX15/WARS2. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 509-524	8.3	63
91	A genomic history of Aboriginal Australia. <i>Nature</i> , <b>2016</b> , 538, 207-214	50.4	268
90	Weighting sequence variants based on their annotation increases power of whole-genome association studies. <i>Nature Genetics</i> , <b>2016</b> , 48, 314-7	36.3	123
89	Identification of Novel Genetic Determinants of Erythrocyte Membrane Fatty Acid Composition among Greenlanders. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1006119	6	16
88	Next-generation biology: Sequencing and data analysis approaches for non-model organisms. <i>Marine Genomics</i> , <b>2016</b> , 30, 3-13	1.9	97
87	Genetics of Type 2 Diabetes: the Power of Isolated Populations. <i>Current Diabetes Reports</i> , <b>2016</b> , 16, 65	5.6	17
86	Estimating IBD tracts from low coverage NGS data. <i>Bioinformatics</i> , <b>2016</b> , 32, 2096-102	7.2	23
85	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
84	The ancestry and affiliations of Kennewick Man. <i>Nature</i> , <b>2015</b> , 523, 455-458	50.4	157
83	Partial USH2A deletions contribute to Usher syndrome in Denmark. <i>European Journal of Human Genetics</i> , <b>2015</b> , 23, 1646-51	5.3	5
82	Evolutionary Genomics and Conservation of the Endangered Przewalski's Horse. <i>Current Biology</i> , <b>2015</b> , 25, 2577-83	6.3	115
81	Greenlandic Inuit show genetic signatures of diet and climate adaptation. <i>Science</i> , <b>2015</b> , 349, 1343-7	33.3	298
80	Tracking the origins of Yakutian horses and the genetic basis for their fast adaptation to subarctic environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, E6889-97	11.5	89

79	The origin and evolution of maize in the Southwestern United States. <i>Nature Plants</i> , <b>2015</b> , 1, 14003	11.5	99
78	Genetic and environmental determinants of 25-hydroxyvitamin D levels in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , <b>2015</b> , 21, 1414-22	5	17
77	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
76	Diabetes in Population Isolates: Lessons from Greenland. <i>Review of Diabetic Studies</i> , <b>2015</b> , 12, 320-9	3.6	4
75	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
74	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , <b>2014</b> , 505, 87-91	50.4	581
73	Paleogenomics. Genomic structure in Europeans dating back at least 36,200 years. <i>Science</i> , <b>2014</b> , 346, 1113-8	33.3	232
72	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , <b>2014</b> , 24, R1035-7	6.3	62
71	The genetic prehistory of the New World Arctic. <i>Science</i> , <b>2014</b> , 345, 1255832	33.3	204
70	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
69	RelateAdmix: a software tool for estimating relatedness between admixed individuals. <i>Bioinformatics</i> , <b>2014</b> , 30, 1027-8	7.2	41
68	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
67	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
66	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
65	ANGSD: Analysis of Next Generation Sequencing Data. <i>BMC Bioinformatics</i> , <b>2014</b> , 15, 356	3.6	1087
64	Exome sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. <i>Diabetologia</i> , <b>2013</b> , 56, 298-310	10.3	102
63	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
62	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

61	Quantifying population genetic differentiation from next-generation sequencing data. <i>Genetics</i> , <b>2013</b> , 195, 979-92	4	141
60	Genetic architecture of vitamin B12 and folate levels uncovered applying deeply sequenced large datasets. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003530	6	72
59	Estimating individual admixture proportions from next generation sequencing data. <i>Genetics</i> , <b>2013</b> , 195, 693-702	4	270
58	Estimating inbreeding coefficients from NGS data: Impact on genotype calling and allele frequency estimation. <i>Genome Research</i> , <b>2013</b> , 23, 1852-61	9.7	59
57	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
56	Genome-Wide Association Study of Genetic Variants in LPS-Stimulated IL-6, IL-8, IL-10, IL-1ra and TNF- $\alpha$ Cytokine Response in a Danish Cohort. <i>PLoS ONE</i> , <b>2013</b> , 8, e66262	3.7	8
55	Association testing for next-generation sequencing data using score statistics. <i>Genetic Epidemiology</i> , <b>2012</b> , 36, 430-7	2.6	34
54	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
53	Genotype and SNP calling from next-generation sequencing data. <i>Nature Reviews Genetics</i> , <b>2011</b> , 12, 443-51	30.1	959
52	An Aboriginal Australian genome reveals separate human dispersals into Asia. <i>Science</i> , <b>2011</b> , 334, 94-8	33.3	528
51	Estimation of allele frequency and association mapping using next-generation sequencing data. <i>BMC Bioinformatics</i> , <b>2011</b> , 12, 231	3.6	126
50	A method for detecting IBD regions simultaneously in multiple individuals--with applications to disease genetics. <i>Genome Research</i> , <b>2011</b> , 21, 1168-80	9.7	38
49	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
48	Segregation distortion in chicken and the evolutionary consequences of female meiotic drive in birds. <i>Heredity</i> , <b>2010</b> , 105, 290-8	3.6	25
47	Ancient human genome sequence of an extinct Palaeo-Eskimo. <i>Nature</i> , <b>2010</b> , 463, 757-62	50.4	567
46	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
45	Identification of a novel locus for a USH3 like syndrome combined with congenital cataract. <i>Clinical Genetics</i> , <b>2010</b> , 78, 388-97	4	5
44	Family and population-based studies of variation within the ghrelin receptor locus in relation to measures of obesity. <i>PLoS ONE</i> , <b>2010</b> , 5, e10084	3.7	12

43	Interleukin-6 autoantibodies are involved in the pathogenesis of a subset of type 2 diabetes. <i>Journal of Endocrinology</i> , <b>2010</b> , 204, 265-73	4.7	21
42	Natural selection and the distribution of identity-by-descent in the human genome. <i>Genetics</i> , <b>2010</b> , 186, 295-308	4	75
41	Ascertainment biases in SNP chips affect measures of population divergence. <i>Molecular Biology and Evolution</i> , <b>2010</b> , 27, 2534-47	8.3	232
40	Combined analyses of 20 common obesity susceptibility variants. <i>Diabetes</i> , <b>2010</b> , 59, 1667-73	0.9	51
39	Identification of a novel BRCA1 nucleotide 4803delCC/c.4684delCC mutation and a nucleotide 249T>A/c.130T>A (p.Cys44Ser) mutation in two Greenlandic Inuit families: implications for genetic screening of Greenlandic Inuit families with high risk for breast and/or ovarian cancer. <i>Breast Cancer Research and Treatment</i> , <b>2010</b> , 124, 259-64	4.4	8
38	Darwinian and demographic forces affecting human protein coding genes. <i>Genome Research</i> , <b>2009</b> , 19, 838-49	9.7	122
37	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
36	A common Greenlandic Inuit BRCA1 RING domain founder mutation. <i>Breast Cancer Research and Treatment</i> , <b>2009</b> , 115, 69-76	4.4	17
35	Large BRCA1 and BRCA2 genomic rearrangements in Danish high risk breast-ovarian cancer families. <i>Breast Cancer Research and Treatment</i> , <b>2009</b> , 115, 315-23	4.4	53
34	Combined analysis of 19 common validated type 2 diabetes susceptibility gene variants shows moderate discriminative value and no evidence of gene-gene interaction. <i>Diabetologia</i> , <b>2009</b> , 52, 1308-14	10.3	51
33	A variant in the G6PC2/ABCB11 locus is associated with increased fasting plasma glucose, increased basal hepatic glucose production and increased insulin release after oral and intravenous glucose loads. <i>Diabetologia</i> , <b>2009</b> , 52, 2122-9	10.3	28
32	Genetic variant near IRS1 is associated with type 2 diabetes, insulin resistance and hyperinsulinemia. <i>Nature Genetics</i> , <b>2009</b> , 41, 1110-5	36.3	356
31	Functional SOCS1 polymorphisms are associated with variation in obesity in whites. <i>Diabetes, Obesity and Metabolism</i> , <b>2009</b> , 11, 196-203	6.7	20
30	The validation and assessment of machine learning: a game of prediction from high-dimensional data. <i>PLoS ONE</i> , <b>2009</b> , 4, e6287	3.7	18
29	Low physical activity accentuates the effect of the FTO rs9939609 polymorphism on body fat accumulation. <i>Diabetes</i> , <b>2008</b> , 57, 95-101	0.9	386
28	The -250G>A promoter variant in hepatic lipase associates with elevated fasting serum high-density lipoprotein cholesterol modulated by interaction with physical activity in a study of 16,156 Danish subjects. <i>Journal of Clinical Endocrinology and Metabolism</i> , <b>2008</b> , 93, 2294-9	5.6	27
27	Association testing of novel type 2 diabetes risk alleles in the JAZF1, CDC123/CAMK1D, TSPAN8, THADA, ADAMTS9, and NOTCH2 loci with insulin release, insulin sensitivity, and obesity in a population-based sample of 4,516 glucose-tolerant middle-aged Danes. <i>Diabetes</i> , <b>2008</b> , 57, 2534-40	0.9	116
26	The GCKR rs780094 polymorphism is associated with elevated fasting serum triacylglycerol, reduced fasting and OGTT-related insulinaemia, and reduced risk of type 2 diabetes. <i>Diabetologia</i> , <b>2008</b> , 51, 70-5	10.3	137

25	Impact of polymorphisms in WFS1 on prediabetic phenotypes in a population-based sample of middle-aged people with normal and abnormal glucose regulation. <i>Diabetologia</i> , <b>2008</b> , 51, 1646-52	10.3	40
24	Novel de novo BRCA2 mutation in a patient with a family history of breast cancer. <i>BMC Medical Genetics</i> , <b>2008</b> , 9, 58	2.1	32
23	Genetic analysis of the estrogen-related receptor alpha and studies of association with obesity and type 2 diabetes. <i>International Journal of Obesity</i> , <b>2007</b> , 31, 365-70	5.5	12
22	Studies of associations between the Arg389Gly polymorphism of the beta1-adrenergic receptor gene (ADRB1) and hypertension and obesity in 7677 Danish white subjects. <i>Diabetic Medicine</i> , <b>2007</b> , 24, 392-7	3.5	35
21	A -243A->G polymorphism upstream of the gene encoding GAD65 associates with lower levels of body mass index and glycaemia in a population-based sample of 5857 middle-aged White subjects. <i>Diabetic Medicine</i> , <b>2007</b> , 24, 702-6	3.5	8
20	Variation in the peroxisome proliferator-activated receptor delta gene in relation to common metabolic traits in 7,495 middle-aged white people. <i>Diabetologia</i> , <b>2007</b> , 50, 1201-8	10.3	37
19	Studies of the common DIO2 Thr92Ala polymorphism and metabolic phenotypes in 7342 Danish white subjects. <i>Journal of Clinical Endocrinology and Metabolism</i> , <b>2007</b> , 92, 363-6	5.6	51
18	Studies of association of variants near the HHEX, CDKN2A/B, and IGF2BP2 genes with type 2 diabetes and impaired insulin release in 10,705 Danish subjects: validation and extension of genome-wide association studies. <i>Diabetes</i> , <b>2007</b> , 56, 3105-11	0.9	207
17	A Bayesian multilocus association method: allowing for higher-order interaction in association studies. <i>Genetics</i> , <b>2007</b> , 176, 1197-208	4	8
16	Studies of the association of the GNB3 825C>T polymorphism with components of the metabolic syndrome in white Danes. <i>Diabetologia</i> , <b>2006</b> , 49, 75-82	10.3	41
15	Studies of the relationship between the ENPP1 K121Q polymorphism and type 2 diabetes, insulin resistance and obesity in 7,333 Danish white subjects. <i>Diabetologia</i> , <b>2006</b> , 49, 2097-104	10.3	91
14	Variants in the 5Rregion of the neuropeptide Y receptor Y2 gene (NPY2R) are associated with obesity in 5,971 white subjects. <i>Diabetologia</i> , <b>2006</b> , 49, 2653-8	10.3	27
13	A novel -192c/g mutation in the proximal P2 promoter of the hepatocyte nuclear factor-4 alpha gene (HNF4A) associates with late-onset diabetes. <i>Diabetes</i> , <b>2006</b> , 55, 1869-73	0.9	9
12	Large-scale study of the -232C > G polymorphism of PCK1 in Type 2 diabetes. <i>Diabetic Medicine</i> , <b>2006</b> , 23, 1140-4	3.5	7
11	How robust are cross-population signatures of polygenic adaptation in humans?1,		2
10	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
9	Ancestry-specific association mapping in admixed populations		5
8	Archaic adaptive introgression in TBX15/WARS2		3



7	Powerful Inference with the D-statistic on Low-Coverage Whole-Genome Data	1
6	How robust are cross-population signatures of polygenic adaptation in humans?	4
5	Inferring Population Structure and Admixture Proportions in Low Depth NGS Data	3
4	A likelihood method for estimating present-day human contamination in ancient DNA samples using low-depth haploid chromosome data	1
3	Evaluation of Model Fit of Inferred Admixture Proportions	1
2	Efficient approaches for large scale GWAS studies with genotype uncertainty	1
1	Estimation of site frequency spectra from low-coverage sequencing data using stochastic EM reduces overfitting, runtime, and memory usage	1