

# Anders Albrechtsen

## List of Publications by Year in descending order

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Version: 2024-02-01

129  
papers

18,916  
citations

26567

56  
h-index

15218

126  
g-index

149  
all docs

149  
docs citations

149  
times ranked

23868  
citing authors

#	ARTICLE	IF	CITATIONS
1	Joint identification of sex and sex-linked scaffolds in non-model organisms using low depth sequencing data. <i>Molecular Ecology Resources</i> , 2022, 22, 458-467.	2.2	19
2	Loss of Sucrase-Isomaltase Function Increases Acetate Levels and Improves Metabolic Health in Greenlandic Cohorts. <i>Gastroenterology</i> , 2022, 162, 1171-1182.e3.	0.6	9
3	Efficient approaches for large-scale GWAS with genotype uncertainty. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	5
4	Life-threatening viral disease in a novel form of autosomal recessive <i>IFNAR2</i> deficiency in the Arctic. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	33
5	An LDLR missense variant poses high risk of familial hypercholesterolemia in 30% of Greenlanders and offers potential of early cardiovascular disease intervention. <i>Human Genetics and Genomics Advances</i> , 2022, 3, 100118.	1.0	4
6	Warthog Genomes Resolve an Evolutionary Conundrum and Reveal Introgression of Disease Resistance Genes. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	11
7	Vicariance followed by secondary gene flow in a young gazelle species complex. <i>Molecular Ecology</i> , 2021, 30, 528-544.	2.0	11
8	Large-scale inference of population structure in presence of missingness using PCA. <i>Bioinformatics</i> , 2021, 37, 1868-1875.	1.8	17
9	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
10	Physical activity attenuates postprandial hyperglycaemia in homozygous <i>TBC1D4</i> loss-of-function mutation carriers. <i>Diabetologia</i> , 2021, 64, 1795-1804.	2.9	6
11	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> , 2021, 46, 1324-1332.	2.8	9
12	The genetic history of Greenlandic-European contact. <i>Current Biology</i> , 2021, 31, 2214-2219.e4.	1.8	9
13	High genetic diversity and low differentiation reflect the ecological versatility of the African leopard. <i>Current Biology</i> , 2021, 31, 1862-1871.e5.	1.8	41
14	NGSremix: a software tool for estimating pairwise relatedness between admixed individuals from next-generation sequencing data. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	12
15	Predictors and trajectories of treatment response to SSRIs in patients suffering from PTSD. <i>Psychiatry Research</i> , 2021, 301, 113964.	1.7	10
16	Detecting selection in low-coverage high-throughput sequencing data using principal component analysis. <i>BMC Bioinformatics</i> , 2021, 22, 470.	1.2	4
17	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
18	Omega-3 fatty acids and risk of cardiovascular disease in Inuit: First prospective cohort study. <i>Atherosclerosis</i> , 2020, 312, 28-34.	0.4	6

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19	Population genomics of the Viking world. <i>Nature</i> , 2020, 585, 390-396.	13.7	143
20	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> , 2020, 28, 1592-1601.	1.4	10
21	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> , 2020, 16, e1008544.	1.5	4
22	Estimating narrow-sense heritability using family data from admixed populations. <i>Heredity</i> , 2020, 124, 751-762.	1.2	6
23	Evaluation of model fit of inferred admixture proportions. <i>Molecular Ecology Resources</i> , 2020, 20, 936-949.	2.2	43
24	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> , 2020, 69, .	0.3	0
25	Genomic diversity and novel genome-wide association with fruit morphology in Capsicum, from 746k polymorphic sites. <i>Scientific Reports</i> , 2019, 9, 10067.	1.6	53
26	Detection of internal N7-methylguanosine (m7G) RNA modifications by mutational profiling sequencing. <i>Nucleic Acids Research</i> , 2019, 47, e126-e126.	6.5	124
27	DamMet: ancient methylome mapping accounting for errors, true variants, and post-mortem DNA damage. <i>GigaScience</i> , 2019, 8, .	3.3	20
28	Ancestry-specific association mapping in admixed populations. <i>Genetic Epidemiology</i> , 2019, 43, 506-521.	0.6	26
29	Testing for Hardy-Weinberg equilibrium in structured populations using genotype or low-depth next generation sequencing data. <i>Molecular Ecology Resources</i> , 2019, 19, 1144-1152.	2.2	26
30	Allele frequency-free inference of close familial relationships from genotypes or low-depth sequencing data. <i>Molecular Ecology</i> , 2019, 28, 35-48.	2.0	73
31	Ancient genomes revisit the ancestry of domestic and Przewalski's horses. <i>Science</i> , 2018, 360, 111-114.	6.0	241
32	Genetic architecture of obesity and related metabolic traits – recent insights from isolated populations. <i>Current Opinion in Genetics and Development</i> , 2018, 50, 74-78.	1.5	3
33	Genetic determinants of glycosylated hemoglobin levels in the Greenlandic Inuit population. <i>European Journal of Human Genetics</i> , 2018, 26, 868-875.	1.4	6
34	Powerful Inference with the D-Statistic on Low-Coverage Whole-Genome Data. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 551-566.	0.8	71
35	A southern African origin and cryptic structure in the highly mobile plains zebra. <i>Nature Ecology and Evolution</i> , 2018, 2, 491-498.	3.4	32
36	Loss-of-function variants in ADCY3 increase risk of obesity and type 2 diabetes. <i>Nature Genetics</i> , 2018, 50, 172-174.	9.4	156

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37	Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. <i>Nature</i> , 2018, 553, 203-207.	13.7	304
38	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
39	Inferring Population Structure and Admixture Proportions in Low-Depth NGS Data. <i>Genetics</i> , 2018, 210, 719-731.	1.2	426
40	Identification of novel high-impact recessively inherited type 2 diabetes risk variants in the Greenlandic population. <i>Diabetologia</i> , 2018, 61, 2005-2015.	2.9	14
41	Archaic adaptive introgression in <i>TBX15/WARS2</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, msw283.	3.5	101
42	Ancient genomic changes associated with domestication of the horse. <i>Science</i> , 2017, 356, 442-445.	6.0	185
43	The Effect of an Extreme and Prolonged Population Bottleneck on Patterns of Deleterious Variation: Insights from the Greenlandic Inuit. <i>Genetics</i> , 2017, 205, 787-801.	1.2	54
44	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , 2017, 358, 659-662.	6.0	263
45	Founder Effect of the <i>RET</i> <sup>C611Y</sup> Mutation in Multiple Endocrine Neoplasia 2A in Denmark: A Nationwide Study. <i>Thyroid</i> , 2017, 27, 1505-1510.	2.4	16
46	fastNGSadmix: admixture proportions and principal component analysis of a single NGS sample. <i>Bioinformatics</i> , 2017, 33, 3148-3150.	1.8	31
47	Genetic screening of the <i>FLCN</i> gene identify six novel variants and a Danish founder mutation. <i>Journal of Human Genetics</i> , 2017, 62, 151-157.	1.1	19
48	Next-generation biology: Sequencing and data analysis approaches for non-model organisms. <i>Marine Genomics</i> , 2016, 30, 3-13.	0.4	164
49	Genetics of Type 2 Diabetes: the Power of Isolated Populations. <i>Current Diabetes Reports</i> , 2016, 16, 65.	1.7	25
50	Estimating IBD tracts from low coverage NGS data. <i>Bioinformatics</i> , 2016, 32, 2096-2102.	1.8	36
51	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016, 538, 207-214.	13.7	439
52	Weighting sequence variants based on their annotation increases power of whole-genome association studies. <i>Nature Genetics</i> , 2016, 48, 314-317.	9.4	178
53	Identification of Novel Genetic Determinants of Erythrocyte Membrane Fatty Acid Composition among Greenlanders. <i>PLoS Genetics</i> , 2016, 12, e1006119.	1.5	20
54	The origin and evolution of maize in the Southwestern United States. <i>Nature Plants</i> , 2015, 1, 14003.	4.7	138

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55	Genetic and environmental determinants of 25-hydroxyvitamin D levels in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2015, 21, 1414-1422.	1.4	18
56	Uncovering the Genetic History of the Present-Day Greenlandic Population. <i>American Journal of Human Genetics</i> , 2015, 96, 54-69.	2.6	85
57	Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015, 349, aab3884.	6.0	449
58	The ancestry and affiliations of Kennewick Man. <i>Nature</i> , 2015, 523, 455-458.	13.7	241
59	Partial USH2A deletions contribute to Usher syndrome in Denmark. <i>European Journal of Human Genetics</i> , 2015, 23, 1646-1651.	1.4	8
60	Evolutionary Genomics and Conservation of the Endangered Przewalski's Horse. <i>Current Biology</i> , 2015, 25, 2577-2583.	1.8	161
61	Greenlandic Inuit show genetic signatures of diet and climate adaptation. <i>Science</i> , 2015, 349, 1343-1347.	6.0	397
62	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> , 2015, 112, E6889-97.	3.3	139
63	Diabetes in Population Isolates: Lessons from Greenland. <i>Review of Diabetic Studies</i> , 2015, 12, 320-329.	0.5	11
64	RelateAdmix: a software tool for estimating relatedness between admixed individuals. <i>Bioinformatics</i> , 2014, 30, 1027-1028.	1.8	61
65	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
66	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
67	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
68	ANGSD: Analysis of Next Generation Sequencing Data. <i>BMC Bioinformatics</i> , 2014, 15, 356.	1.2	1,935
69	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , 2014, 506, 225-229.	13.7	500
70	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , 2014, 505, 87-91.	13.7	821
71	Genomic structure in Europeans dating back at least 36,200 years. <i>Science</i> , 2014, 346, 1113-1118.	6.0	287
72	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , 2014, 24, R1035-R1037.	1.8	73

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73	The genetic prehistory of the New World Arctic. <i>Science</i> , 2014, 345, 1255832.	6.0	264
74	A common Greenlandic TBC1D4 variant confers muscle insulin resistance and type 2 diabetes. <i>Nature</i> , 2014, 512, 190-193.	13.7	338
75	Exome sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. <i>Diabetologia</i> , 2013, 56, 298-310.	2.9	119
76	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
77	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013, 499, 74-78.	13.7	717
78	Quantifying Population Genetic Differentiation from Next-Generation Sequencing Data. <i>Genetics</i> , 2013, 195, 979-992.	1.2	187
79	Genetic Architecture of Vitamin B12 and Folate Levels Uncovered Applying Deeply Sequenced Large Datasets. <i>PLoS Genetics</i> , 2013, 9, e1003530.	1.5	112
80	Estimating Individual Admixture Proportions from Next Generation Sequencing Data. <i>Genetics</i> , 2013, 195, 693-702.	1.2	515
81	Estimating inbreeding coefficients from NGS data: Impact on genotype calling and allele frequency estimation. <i>Genome Research</i> , 2013, 23, 1852-1861.	2.4	89
82	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
83	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> , 2013, 8, e66262.	1.1	10
84	Association Testing for Next-Generation Sequencing Data Using Score Statistics. <i>Genetic Epidemiology</i> , 2012, 36, 430-437.	0.6	53
85	SNP Calling, Genotype Calling, and Sample Allele Frequency Estimation from New-Generation Sequencing Data. <i>PLoS ONE</i> , 2012, 7, e37558.	1.1	336
86	Genotype and SNP calling from next-generation sequencing data. <i>Nature Reviews Genetics</i> , 2011, 12, 443-451.	7.7	1,238
87	An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. <i>Science</i> , 2011, 334, 94-98.	6.0	675
88	Estimation of allele frequency and association mapping using next-generation sequencing data. <i>BMC Bioinformatics</i> , 2011, 12, 231.	1.2	170
89	A method for detecting IBD regions simultaneously in multiple individuals with applications to disease genetics. <i>Genome Research</i> , 2011, 21, 1168-1180.	2.4	42
90	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

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91	Identification of a novel BRCA1 nucleotide 4803delCC/c.4684delCC mutation and a nucleotide 249T&gt;A/c.130T&gt;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> , 2010, 124, 259-264.	1.1	10
92	Segregation distortion in chicken and the evolutionary consequences of female meiotic drive in birds. <i>Heredity</i> , 2010, 105, 290-298.	1.2	33
93	Ancient human genome sequence of an extinct Palaeo-Eskimo. <i>Nature</i> , 2010, 463, 757-762.	13.7	750
94	Resequencing of 200 human exomes identifies an excess of low-frequency non-synonymous coding variants. <i>Nature Genetics</i> , 2010, 42, 969-972.	9.4	297
95	Identification of a novel locus for a USH3 like syndrome combined with congenital cataract. <i>Clinical Genetics</i> , 2010, 78, 388-397.	1.0	6
96	Family and Population-Based Studies of Variation within the Ghrelin Receptor Locus in Relation to Measures of Obesity. <i>PLoS ONE</i> , 2010, 5, e10084.	1.1	18
97	Interleukin-6 autoantibodies are involved in the pathogenesis of a subset of type 2 diabetes. <i>Journal of Endocrinology</i> , 2010, 204, 265-273.	1.2	25
98	Natural Selection and the Distribution of Identity-by-Descent in the Human Genome. <i>Genetics</i> , 2010, 186, 295-308.	1.2	119
99	Ascertainment Biases in SNP Chips Affect Measures of Population Divergence. <i>Molecular Biology and Evolution</i> , 2010, 27, 2534-2547.	3.5	317
100	Combined Analyses of 20 Common Obesity Susceptibility Variants. <i>Diabetes</i> , 2010, 59, 1667-1673.	0.3	55
101	Darwinian and demographic forces affecting human protein coding genes. <i>Genome Research</i> , 2009, 19, 838-849.	2.4	139
102	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
103	A common Greenlandic Inuit BRCA1 RING domain founder mutation. <i>Breast Cancer Research and Treatment</i> , 2009, 115, 69-76.	1.1	19
104	Large BRCA1 and BRCA2 genomic rearrangements in Danish high risk breast-ovarian cancer families. <i>Breast Cancer Research and Treatment</i> , 2009, 115, 315-323.	1.1	61
105	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> , 2009, 52, 1308-1314.	2.9	53
106	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> , 2009, 52, 2122-2129.	2.9	29
107	Genetic variant near IRS1 is associated with type 2 diabetes, insulin resistance and hyperinsulinemia. <i>Nature Genetics</i> , 2009, 41, 1110-1115.	9.4	418
108	Functional <i>SOCS1</i> polymorphisms are associated with variation in obesity in whites. <i>Diabetes, Obesity and Metabolism</i> , 2009, 11, 196-203.	2.2	25

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109	The Validation and Assessment of Machine Learning: A Game of Prediction from High-Dimensional Data. PLoS ONE, 2009, 4, e6287.	1.1	22
110	Impact of polymorphisms in WFS1 on prediabetic phenotypes in a population-based sample of middle-aged people with normal and abnormal glucose regulation. Diabetologia, 2008, 51, 1646-1652.	2.9	44
111	Novel de novo BRCA2 mutation in a patient with a family history of breast cancer. BMC Medical Genetics, 2008, 9, 58.	2.1	33
112	Low Physical Activity Accentuates the Effect of the <i>FTO</i> rs9939609 Polymorphism on Body Fat Accumulation. Diabetes, 2008, 57, 95-101.	0.3	431
113	The $\sim 250$ g 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. Journal of Clinical Endocrinology and Metabolism, 2008, 93, 2294-2299.	1.8	33
114	Association Testing of Novel Type 2 Diabetes Risk Alleles in the <i>JAZF1</i> , <i>CDC123</i> , <i>CAMK1D</i> , <i>TSPAN8</i> , <i>THADA</i> , <i>ADAMTS9</i> , and <i>NOTCH2</i> Loci With Insulin Release, Insulin Sensitivity, and Obesity in a Population-Based Sample of 4,516 Glucose-Tolerant Middle-Aged Danes. Diabetes, 2008, 57, 2534-2540.	0.3	151
115	Studies of the Common <i>DIO2</i> Thr92Ala Polymorphism and Metabolic Phenotypes in 7342 Danish White Subjects. Journal of Clinical Endocrinology and Metabolism, 2007, 92, 363-366.	1.8	62
116	Studies of Association of Variants Near the <i>HHEX</i> , <i>CDKN2A/B</i> , and <i>IGF2BP2</i> Genes With Type 2 Diabetes and Impaired Insulin Release in 10,705 Danish Subjects. Diabetes, 2007, 56, 3105-3111.	0.3	230
117	A Bayesian Multilocus Association Method: Allowing for Higher-Order Interaction in Association Studies. Genetics, 2007, 176, 1197-1208.	1.2	12
118	Genetic analysis of the estrogen-related receptor $\beta$ and studies of association with obesity and type 2 diabetes. International Journal of Obesity, 2007, 31, 365-370.	1.6	21
119	Studies of associations between the Arg389Gly polymorphism of the $\beta$ 1-adrenergic receptor gene ( <i>ADRB1</i> ) and hypertension and obesity in 7677 Danish white subjects. Diabetic Medicine, 2007, 24, 392-397.	1.2	40
120	A T243A>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. Diabetic Medicine, 2007, 24, 702-706.	1.2	10
121	Variation in the peroxisome proliferator-activated receptor $\gamma$ gene in relation to common metabolic traits in 7,495 middle-aged white people. Diabetologia, 2007, 50, 1201-1208.	2.9	42
122	The GCKR rs780094 polymorphism is associated with elevated fasting serum triacylglycerol, reduced fasting and OGTT-related insulinaemia, and reduced risk of type 2 diabetes. Diabetologia, 2007, 51, 70-75.	2.9	153
123	Large-scale study of the T232C>T polymorphism of PCK1 in Type 2 diabetes. Diabetic Medicine, 2006, 23, 1140-1144.	1.2	9
124	Studies of the association of the GNB3 825C>T polymorphism with components of the metabolic syndrome in white Danes. Diabetologia, 2006, 49, 75-82.	2.9	43
125	Studies of the relationship between the ENPP1 K121Q polymorphism and type 2 diabetes, insulin resistance and obesity in 7,333 Danish white subjects. Diabetologia, 2006, 49, 2097-2104.	2.9	111
126	Variants in the 5' region of the neuropeptide Y receptor Y2 gene ( <i>NPY2R</i> ) are associated with obesity in 5,971 white subjects. Diabetologia, 2006, 49, 2653-2658.	2.9	35



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127	A Novel -192c/g Mutation in the Proximal P2 Promoter of the Hepatocyte Nuclear Factor-4 Gene (HNF4A) Associates With Late-Onset Diabetes. <i>Diabetes</i> , 2006, 55, 1869-1873.	0.3	12
128	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> , 0, , .	0.4	2
129	How robust are cross-population signatures of polygenic adaptation in humans?. , 0, 1, .		3