# Anders Albrechtsen

## List of Publications by Year
in descending order

| | | 26567 | 15218 |
|---|---|---|---|
| **129**<br>papers | **18,916**<br>citations | **56**<br>h-index | **126**<br>g-index |
| **149**<br>all docs | **149**<br>docs citations | **149**<br>times ranked | **23868**<br>citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | ANGSD: Analysis of Next Generation Sequencing Data. BMC Bioinformatics, 2014, 15, 356. | 1.2 | 1,935 |
| 2 | Genotype and SNP calling from next-generation sequencing data. Nature Reviews Genetics, 2011, 12, 443-451. | 7.7 | 1,238 |
| 3 | Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. Nature, 2014, 505, 87-91. | 13.7 | 821 |
| 4 | Ancient human genome sequence of an extinct Palaeo-Eskimo. Nature, 2010, 463, 757-762. | 13.7 | 750 |
| 5 | Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. Nature, 2013, 499, 74-78. | 13.7 | 717 |
| 6 | An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. Science, 2011, 334, 94-98. | 6.0 | 675 |
| 7 | Estimating Individual Admixture Proportions from Next Generation Sequencing Data. Genetics, 2013, 195, 693-702. | 1.2 | 515 |
| 8 | The genome of a Late Pleistocene human from a Clovis burial site in western Montana. Nature, 2014, 506, 225-229. | 13.7 | 500 |
| 9 | Genomic evidence for the Pleistocene and recent population history of Native Americans. Science, 2015, 349, aab3884. | 6.0 | 449 |
| 10 | A genomic history of Aboriginal Australia. Nature, 2016, 538, 207-214. | 13.7 | 439 |
| 11 | 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 |
| 12 | Inferring Population Structure and Admixture Proportions in Low-Depth NGS Data. Genetics, 2018, 210, 719-731. | 1.2 | 426 |
| 13 | Genetic variant near IRS1 is associated with type 2 diabetes, insulin resistance and hyperinsulinemia. Nature Genetics, 2009, 41, 1110-1115. | 9.4 | 418 |
| 14 | Greenlandic Inuit show genetic signatures of diet and climate adaptation. Science, 2015, 349, 1343-1347. | 6.0 | 397 |
| 15 | A common Greenlandic TBC1D4 variant confers muscle insulin resistance and type 2 diabetes. Nature, 2014, 512, 190-193. | 13.7 | 338 |
| 16 | SNP Calling, Genotype Calling, and Sample Allele Frequency Estimation from New-Generation Sequencing Data. PLoS ONE, 2012, 7, e37558. | 1.1 | 336 |
| 17 | Ascertainment Biases in SNP Chips Affect Measures of Population Divergence. Molecular Biology and Evolution, 2010, 27, 2534-2547. | 3.5 | 317 |
| 18 | Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. Nature, 2018, 553, 203-207. | 13.7 | 304 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 19 | Resequencing of 200 human exomes identifies an excess of low-frequency non-synonymous coding variants. Nature Genetics, 2010, 42, 969-972. | 9.4 | 297 |
| 20 | Genomic structure in Europeans dating back at least 36,200 years. Science, 2014, 346, 1113-1118. | 6.0 | 287 |
| 21 | The genetic prehistory of the New World Arctic. Science, 2014, 345, 1255832. | 6.0 | 264 |
| 22 | Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. Science, 2017, 358, 659-662. | 6.0 | 263 |
| 23 | Prehistoric genomes reveal the genetic foundation and cost of horse domestication. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5661-9. | 3.3 | 260 |
| 24 | The ancestry and affiliations of Kennewick Man. Nature, 2015, 523, 455-458. | 13.7 | 241 |
| 25 | Ancient genomes revisit the ancestry of domestic and Przewalski's horses. Science, 2018, 360, 111-114. | 6.0 | 241 |
| 26 | 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. Diabetes, 2007, 56, 3105-3111. | 0.3 | 230 |
| 27 | Genomic Analyses from Non-invasive Prenatal Testing Reveal Genetic Associations, Patterns of Viral Infections, and Chinese Population History. Cell, 2018, 175, 347-359.e14. | 13.5 | 213 |
| 28 | Calculation of Tajima's D and other neutrality test statistics from low depth next-generation sequencing data. BMC Bioinformatics, 2013, 14, 289. | 1.2 | 211 |
| 29 | Quantifying Population Genetic Differentiation from Next-Generation Sequencing Data. Genetics, 2013, 195, 979-992. | 1.2 | 187 |
| 30 | Ancient genomic changes associated with domestication of the horse. Science, 2017, 356, 442-445. | 6.0 | 185 |
| 31 | 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. | 3.3 | 183 |
| 32 | Weighting sequence variants based on their annotation increases power of whole-genome association studies. Nature Genetics, 2016, 48, 314-317. | 9.4 | 178 |
| 33 | Estimation of allele frequency and association mapping using next-generation sequencing data. BMC Bioinformatics, 2011, 12, 231. | 1.2 | 170 |
| 34 | Next-generation biology: Sequencing and data analysis approaches for non-model organisms. Marine Genomics, 2016, 30, 3-13. | 0.4 | 164 |
| 35 | Evolutionary Genomics and Conservation of the Endangered Przewalski's Horse. Current Biology, 2015, 25, 2577-2583. | 1.8 | 161 |
| 36 | Loss-of-function variants in ADCY3 increase risk of obesity and type 2 diabetes. Nature Genetics, 2018, 50, 172-174. | 9.4 | 156 |

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|---|---------|-----|-----------|
| 37 | 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 |
| 38 | 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. Diabetes, 2008, 57, 2534-2540. | 0.3 | 151 |
| 39 | Natural Selection Affects Multiple Aspects of Genetic Variation at Putatively Neutral Sites across the Human Genome. PLoS Genetics, 2011, 7, e1002326. | 1.5 | 146 |
| 40 | Population genomics of the Viking world. Nature, 2020, 585, 390-396. | 13.7 | 143 |
| 41 | Darwinian and demographic forces affecting human protein coding genes. Genome Research, 2009, 19, 838-849. | 2.4 | 139 |
| 42 | Tracking the origins of Yakutian horses and the genetic basis for their fast adaptation to subarctic environments. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6889-97. | 3.3 | 139 |
| 43 | The origin and evolution of maize in the Southwestern United States. Nature Plants, 2015, 1, 14003. | 4.7 | 138 |
| 44 | 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. | 2.6 | 124 |
| 45 | Detection of internal N7-methylguanosine (m7G) RNA modifications by mutational profiling sequencing. Nucleic Acids Research, 2019, 47, e126-e126. | 6.5 | 124 |
| 46 | Natural Selection and the Distribution of Identity-by-Descent in the Human Genome. Genetics, 2010, 186, 295-308. | 1.2 | 119 |
| 47 | Exome sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. Diabetologia, 2013, 56, 298-310. | 2.9 | 119 |
| 48 | Genetic Architecture of Vitamin B12 and Folate Levels Uncovered Applying Deeply Sequenced Large Datasets. PLoS Genetics, 2013, 9, e1003530. | 1.5 | 112 |
| 49 | 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 |
| 50 | Archaic adaptive introgression in *TBX15/WARS2*. Molecular Biology and Evolution, 2017, 34, msw283. | 3.5 | 101 |
| 51 | Relatedness mapping and tracts of relatedness for genome‐wide data in the presence of linkage disequilibrium. Genetic Epidemiology, 2009, 33, 266-274. | 0.6 | 99 |
| 52 | Estimating inbreeding coefficients from NGS data: Impact on genotype calling and allele frequency estimation. Genome Research, 2013, 23, 1852-1861. | 2.4 | 89 |
| 53 | Uncovering the Genetic History of the Present-Day Greenlandic Population. American Journal of Human Genetics, 2015, 96, 54-69. | 2.6 | 85 |
| 54 | Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. Current Biology, 2014, 24, R1035-R1037. | 1.8 | 73 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|----|-----------|
| 55 | Allele frequency–free inference of close familial relationships from genotypes or low–depth sequencing data. Molecular Ecology, 2019, 28, 35-48. | 2.0 | 73 |
| 56 | Powerful Inference with the D-Statistic on Low-Coverage Whole-Genome Data. G3: Genes, Genomes, Genetics, 2018, 8, 551-566. | 0.8 | 71 |
| 57 | Studies of the CommonDIO2Thr92Ala Polymorphism and Metabolic Phenotypes in 7342 Danish White Subjects. Journal of Clinical Endocrinology and Metabolism, 2007, 92, 363-366. | 1.8 | 62 |
| 58 | Large BRCA1 and BRCA2 genomic rearrangements in Danish high risk breast-ovarian cancer families. Breast Cancer Research and Treatment, 2009, 115, 315-323. | 1.1 | 61 |
| 59 | RelateAdmix: a software tool for estimating relatedness between admixed individuals. Bioinformatics, 2014, 30, 1027-1028. | 1.8 | 61 |
| 60 | Combined Analyses of 20 Common Obesity Susceptibility Variants. Diabetes, 2010, 59, 1667-1673. | 0.3 | 55 |
| 61 | The Effect of an Extreme and Prolonged Population Bottleneck on Patterns of Deleterious Variation: Insights from the Greenlandic Inuit. Genetics, 2017, 205, 787-801. | 1.2 | 54 |
| 62 | Combined analysis of 19 common validated type 2 diabetes susceptibility gene variants shows moderate discriminative value and no evidence of gene–gene interaction. Diabetologia, 2009, 52, 1308-1314. | 2.9 | 53 |
| 63 | Association Testing for Next–Generation Sequencing Data Using Score Statistics. Genetic Epidemiology, 2012, 36, 430-437. | 0.6 | 53 |
| 64 | Genomic diversity and novel genome-wide association with fruit morphology in Capsicum, from 746k polymorphic sites. Scientific Reports, 2019, 9, 10067. | 1.6 | 53 |
| 65 | 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 |
| 66 | 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 |
| 67 | Evaluation of model fit of inferred admixture proportions. Molecular Ecology Resources, 2020, 20, 936-949. | 2.2 | 43 |
| 68 | 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 |
| 69 | A method for detecting IBD regions simultaneously in multiple individuals—with applications to disease genetics. Genome Research, 2011, 21, 1168-1180. | 2.4 | 42 |
| 70 | High genetic diversity and low differentiation reflect the ecological versatility of the African leopard. Current Biology, 2021, 31, 1862-1871.e5. | 1.8 | 41 |
| 71 | Studies of associations between the Arg389Gly polymorphism of the $\beta$1-adrenergic receptor gene (ADRB1) and hypertension and obesity in 7677 Danish white subjects. Diabetic Medicine, 2007, 24, 392-397. | 1.2 | 40 |
| 72 | Estimating IBD tracts from low coverage NGS data. Bioinformatics, 2016, 32, 2096-2102. | 1.8 | 36 |

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|---|---------|----|-----------|
| 73 | Variants in the 5â€² region of the neuropeptide Y receptor Y2 gene (NPY2R) are associated with obesity in 5,971 white subjects. Diabetologia, 2006, 49, 2653-2658. | 2.9 | 35 |
| 74 | Novel de novo BRCA2mutation in a patient with a family history of breast cancer. BMC Medical Genetics, 2008, 9, 58. | 2.1 | 33 |
| 75 | The âˆ'250G&amp;gt;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 |
| 76 | Segregation distortion in chicken and the evolutionary consequences of female meiotic drive in birds. Heredity, 2010, 105, 290-298. | 1.2 | 33 |
| 77 | Life-threatening viral disease in a novel form of autosomal recessive <i>IFNAR2</i> deficiency in the Arctic. Journal of Experimental Medicine, 2022, 219, . | 4.2 | 33 |
| 78 | A southern African origin and cryptic structure in the highly mobile plains zebra. Nature Ecology and Evolution, 2018, 2, 491-498. | 3.4 | 32 |
| 79 | fastNGSadmix: admixture proportions and principal component analysis of a single NGS sample. Bioinformatics, 2017, 33, 3148-3150. | 1.8 | 31 |
| 80 | 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. Diabetologia, 2009, 52, 2122-2129. | 2.9 | 29 |
| 81 | 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. | 1.4 | 26 |
| 82 | Ancestryâ€specific association mapping in admixed populations. Genetic Epidemiology, 2019, 43, 506-521. | 0.6 | 26 |
| 83 | Testing for Hardyâ€"Weinberg equilibrium in structured populations using genotype or lowâ€depth next generation sequencing data. Molecular Ecology Resources, 2019, 19, 1144-1152. | 2.2 | 26 |
| 84 | Functional <i>SOCS1 </i>polymorphisms are associated with variation in obesity in whites. Diabetes, Obesity and Metabolism, 2009, 11, 196-203. | 2.2 | 25 |
| 85 | Interleukin-6 autoantibodies are involved in the pathogenesis of a subset of type 2 diabetes. Journal of Endocrinology, 2010, 204, 265-273. | 1.2 | 25 |
| 86 | Genetics of Type 2 Diabetes: the Power of Isolated Populations. Current Diabetes Reports, 2016, 16, 65. | 1.7 | 25 |
| 87 | The Validation and Assessment of Machine Learning: A Game of Prediction from High-Dimensional Data. PLoS ONE, 2009, 4, e6287. | 1.1 | 22 |
| 88 | Genetic analysis of the estrogen-related receptor Î± and studies of association with obesity and type 2 diabetes. International Journal of Obesity, 2007, 31, 365-370. | 1.6 | 21 |
| 89 | DamMet: ancient methylome mapping accounting for errors, true variants, and post-mortem DNA damage. GigaScience, 2019, 8, . | 3.3 | 20 |
| 90 | Identification of Novel Genetic Determinants of Erythrocyte Membrane Fatty Acid Composition among Greenlanders. PLoS Genetics, 2016, 12, e1006119. | 1.5 | 20 |

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|---|---------|-----|-----------|
| 91 | A common Greenlandic Inuit BRCA1 RING domain founder mutation. Breast Cancer Research and Treatment, 2009, 115, 69-76. | 1.1 | 19 |
| 92 | Genetic screening of the FLCN gene identify six novel variants and a Danish founder mutation. Journal of Human Genetics, 2017, 62, 151-157. | 1.1 | 19 |
| 93 | Joint identification of sex and sex-linked scaffolds in non-model organisms using low depth sequencing data. Molecular Ecology Resources, 2022, 22, 458-467. | 2.2 | 19 |
| 94 | Family and Population-Based Studies of Variation within the Ghrelin Receptor Locus in Relation to Measures of Obesity. PLoS ONE, 2010, 5, e10084. | 1.1 | 18 |
| 95 | Genetic and environmental determinants of 25-hydroxyvitamin D levels in multiple sclerosis. Multiple Sclerosis Journal, 2015, 21, 1414-1422. | 1.4 | 18 |
| 96 | Large-scale inference of population structure in presence of missingness using PCA. Bioinformatics, 2021, 37, 1868-1875. | 1.8 | 17 |
| 97 | Founder Effect of the $RET^{C611Y}$ Mutation in Multiple Endocrine Neoplasia 2A in Denmark: A Nationwide Study. Thyroid, 2017, 27, 1505-1510. | 2.4 | 16 |
| 98 | Identification of novel high-impact recessively inherited type 2 diabetes risk variants in the Greenlandic population. Diabetologia, 2018, 61, 2005-2015. | 2.9 | 14 |
| 99 | A likelihood method for estimating present-day human contamination in ancient male samples using low-depth X-chromosome data. Bioinformatics, 2020, 36, 828-841. | 1.8 | 14 |
| 100 | A Novel -192c/g Mutation in the Proximal P2 Promoter of the Hepatocyte Nuclear Factor-4Â Gene (HNF4A) Associates With Late-Onset Diabetes. Diabetes, 2006, 55, 1869-1873. | 0.3 | 12 |
| 101 | A Bayesian Multilocus Association Method: Allowing for Higher-Order Interaction in Association Studies. Genetics, 2007, 176, 1197-1208. | 1.2 | 12 |
| 102 | A reference-free approach to analyse RADseq data using standard next generation sequencing toolkits. Molecular Ecology Resources, 2021, 21, 1085-1097. | 2.2 | 12 |
| 103 | NGSremix: a software tool for estimating pairwise relatedness between admixed individuals from next-generation sequencing data. G3: Genes, Genomes, Genetics, 2021, 11, . | 0.8 | 12 |
| 104 | Vicariance followed by secondary gene flow in a young gazelle species complex. Molecular Ecology, 2021, 30, 528-544. | 2.0 | 11 |
| 105 | Diabetes in Population Isolates: Lessons from Greenland. Review of Diabetic Studies, 2015, 12, 320-329. | 0.5 | 11 |
| 106 | Warthog Genomes Resolve an Evolutionary Conundrum and Reveal Introgression of Disease Resistance Genes. Molecular Biology and Evolution, 2022, 39, . | 3.5 | 11 |
| 107 | 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. Diabetic Medicine, 2007, 24, 702-706. | 1.2 | 10 |
| 108 | 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. Breast Cancer Research and Treatment, 2010, 124, 259-264. | 1.1 | 10 |

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|---|---------|-----|-----------|
| 109 | Genetic study of the Arctic CPT1A variant suggests that its effect on fatty acid levels is modulated by traditional Inuit diet. European Journal of Human Genetics, 2020, 28, 1592-1601. | 1.4 | 10 |
| 110 | Predictors and trajectories of treatment response to SSRIs in patients suffering from PTSD. Psychiatry Research, 2021, 301, 113964. | 1.7 | 10 |
| 111 | Genome-Wide Association Study of Genetic Variants in LPS-Stimulated IL-6, IL-8, IL-10, IL-1ra and TNF-Î± Cytokine Response in a Danish Cohort. PLoS ONE, 2013, 8, e66262. | 1.1 | 10 |
| 112 | Large-scale study of the ?232Cï¿½>ï¿½G polymorphism of PCK1 in Typeï¿½2 diabetes. Diabetic Medicine, 2006, 23, 1140-1144. | 1.2 | 9 |
| 113 | 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. Neuropsychopharmacology, 2021, 46, 1324-1332. | 2.8 | 9 |
| 114 | The genetic history of Greenlandic-European contact. Current Biology, 2021, 31, 2214-2219.e4. | 1.8 | 9 |
| 115 | Loss of Sucrase-Isomaltase Function Increases Acetate Levels and Improves Metabolic Health in Greenlandic Cohorts. Gastroenterology, 2022, 162, 1171-1182.e3. | 0.6 | 9 |
| 116 | Partial USH2A deletions contribute to Usher syndrome in Denmark. European Journal of Human Genetics, 2015, 23, 1646-1651. | 1.4 | 8 |
| 117 | Identification of a novel locus for a USH3 like syndrome combined with congenital cataract. Clinical Genetics, 2010, 78, 388-397. | 1.0 | 6 |
| 118 | Genetic determinants of glycated hemoglobin levels in the Greenlandic Inuit population. European Journal of Human Genetics, 2018, 26, 868-875. | 1.4 | 6 |
| 119 | Omega-3 fatty acids and risk of cardiovascular disease in Inuit: First prospective cohort study. Atherosclerosis, 2020, 312, 28-34. | 0.4 | 6 |
| 120 | Estimating narrow-sense heritability using family data from admixed populations. Heredity, 2020, 124, 751-762. | 1.2 | 6 |
| 121 | Physical activity attenuates postprandial hyperglycaemia in homozygous TBC1D4 loss-of-function mutation carriers. Diabetologia, 2021, 64, 1795-1804. | 2.9 | 6 |
| 122 | Efficient approaches for large-scale GWAS with genotype uncertainty. G3: Genes, Genomes, Genetics, 2022, 12, . | 0.8 | 5 |
| 123 | The derived allele of a novel intergenic variant at chromosome 11 associates with lower body mass index and a favorable metabolic phenotype in Greenlanders. PLoS Genetics, 2020, 16, e1008544. | 1.5 | 4 |
| 124 | Detecting selection in low-coverage high-throughput sequencing data using principal component analysis. BMC Bioinformatics, 2021, 22, 470. | 1.2 | 4 |
| 125 | An LDLR missense variant poses high risk of familial hypercholesterolemia in 30% of Greenlanders and offers potential of early cardiovascular disease intervention. Human Genetics and Genomics Advances, 2022, 3, 100118. | 1.0 | 4 |
| 126 | Genetic architecture of obesity and related metabolic traits â€" recent insights from isolated populations. Current Opinion in Genetics and Development, 2018, 50, 74-78. | 1.5 | 3 |

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|---|---------|----|-----------| 
| 127 | How robust are cross-population signatures of polygenic adaptation in humans?. , 0, 1, . | | 3 |
| 128 | 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 |
| 129 | 246-OR: A Loss-of-Function Mutation in the Sucrase-Isomaltase Gene Is Linked to a Markedly Healthier Metabolic Profile in Greenlanders. Diabetes, 2020, 69, . | 0.3 | 0 |