Johanne Marie Justesen

List of Publications by Citations

39 papers	2,459 citations	22 h-index	48 g-index
48 ext. papers	3,119 ext. citations	12.2 avg, IF	2.95 L-index

#	Paper	IF	Citations
39	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
38	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
37	Identification of low-frequency and rare sequence variants associated with elevated or reduced risk of type 2 diabetes. *Nature Genetics*, **2014**, 46, 294-8	36.3	241
36	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. *Nature Genetics*, **2015**, 47, 1282-1293	36.3	223
35	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. *Nature Communications*, **2017**, 8, 14977	17.4	105
34	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. *PLoS Genetics*, **2017**, 13, e1006528	6	103
33	Exome sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. *Diabetologia*, **2013**, 56, 298-310	10.3	102
32	Identification and functional characterization of G6PC2 coding variants influencing glycemic traits define an effector transcript at the G6PC2-ABCB11 locus. *PLoS Genetics*, **2015**, 11, e1004876	6	76
31	A genetic risk score of 45 coronary artery disease risk variants associates with increased risk of myocardial infarction in 6041 Danish individuals. *Atherosclerosis*, **2015**, 240, 305-10	3.1	50
30	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. *Nature Communications*, **2016**, 7, 13357	17.4	46
29	Type 2 diabetes risk alleles near BCAR1 and in ANK1 associate with decreased ß-cell function whereas risk alleles near ANKRD55 and GRB14 associate with decreased insulin sensitivity in the Danish Inter99 cohort. *Journal of Clinical Endocrinology and Metabolism*, **2013**, 98, E801-6	5.6	46
28	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
27	Studies of the association of Arg72Pro of tumor suppressor protein p53 with type 2 diabetes in a combined analysis of 55,521 Europeans. *PLoS ONE*, **2011**, 6, e15813	3.7	41
26	Genetic risk score of 46 type 2 diabetes risk variants associates with changes in plasma glucose and estimates of pancreatic ß-cell function over 5 years of follow-up. *Diabetes*, **2013**, 62, 3610-7	0.9	36
25	Implications of central obesity-related variants in LYPLAL1, NRXN3, MSRA, and TFAP2B on quantitative metabolic traits in adult Danes. *PLoS ONE*, **2011**, 6, e20640	3.7	36
24	Association studies of novel obesity-related gene variants with quantitative metabolic phenotypes in a population-based sample of 6,039 Danish individuals. *Diabetologia*, **2012**, 55, 105-13	10.3	31
23	The frequent UCP2 -866G>A polymorphism protects against insulin resistance and is associated with obesity: a study of obesity and related metabolic traits among 17 636 Danes. *International Journal of Obesity*, **2013**, 37, 175-81	5.5	31

22	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. *Diabetes*, **2017**, 66, 2019-2032	0.9	29
21	Components of genetic associations across 2,138 phenotypes in the UK Biobank highlight adipocyte biology. *Nature Communications*, **2019**, 10, 4064	17.4	26
20	Interactions of Lipid Genetic Risk Scores With Estimates of Metabolic Health in a Danish Population. *Circulation: Cardiovascular Genetics*, **2015**, 8, 465-72		25
19	The effect of GWAS identified BMI loci on changes in body weight among middle-aged Danes during a five-year period. *Obesity*, **2014**, 22, 901-8	8	24
18	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
17	Bioinformatics-driven identification and examination of candidate genes for non-alcoholic fatty liver disease. *PLoS ONE*, **2011**, 6, e16542	3.7	19
16	Solute carrier family 2 member 1 is involved in the development of nonalcoholic fatty liver disease. *Hepatology*, **2013**, 57, 505-14	11.2	18
15	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*, **2018**, 3, 4	4.8	16
14	The minor C-allele of rs2014355 in ACADS is associated with reduced insulin release following an oral glucose load. *BMC Medical Genetics*, **2011**, 12, 4	2.1	10
13	Fast Lasso method for large-scale and ultrahigh-dimensional Cox model with applications to UK Biobank. *Biostatistics*, **2020**,	3.7	7
12	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*,3, 4	4.8	6
11	Cannabinoid receptor 1 antagonist genistein attenuates marijuana-induced vascular inflammation.. *Cell*, **2022**,	56.2	5
10	Combining Clinical and Polygenic Risk Improves Stroke Prediction Among Individuals With Atrial Fibrillation. *Circulation Genomic and Precision Medicine*, **2021**, 14, e003168	5.2	3
9	Pro12Ala Ala carriers exhibit greater improvements in peripheral insulin sensitivity in response to 12 weeks of aerobic exercise training. *Physiological Genomics*, **2019**, 51, 254-260	3.6	2
8	Increasing insulin resistance accentuates the effect of triglyceride-associated loci on serum triglycerides during 5 years. *Journal of Lipid Research*, **2016**, 57, 2193-2199	6.3	2
7	Components of genetic associations across 2,138 phenotypes in the UK Biobank highlight novel adipocyte biology		2
6	Fast Lasso method for Large-scale and Ultrahigh-dimensional Cox Model with applications to UK Biobank		2
5	Pervasive additive and non-additive effects within the HLA region contribute to disease risk in the UK Biobank		2

4 Combining clinical and polygenic risk improves stroke prediction among individuals with atrial fibrillation 2

3 Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*, 3, 4 4.8 1

2 Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution 1

1 Significant sparse polygenic risk scores across 813 traits in UK Biobank.. *PLoS Genetics*, **2022**, 18, e1010105 0