

# Johanne Marie Justesen

## List of Publications by Year in descending order

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Version: 2024-02-01

37  
papers

3,506  
citations

279798

23  
h-index

315739

38  
g-index

48  
all docs

48  
docs citations

48  
times ranked

8994  
citing authors

#	ARTICLE	IF	CITATIONS
1	Fast Lasso method for large-scale and ultrahigh-dimensional Cox model with applications to UK Biobank. <i>Biostatistics</i> , 2022, 23, 522-540.	1.5	22
2	Interactions of physical activity, muscular fitness, adiposity, and genetic risk for NAFLD. <i>Hepatology Communications</i> , 2022, 6, 1516-1526.	4.3	7
3	Significant sparse polygenic risk scores across 813 traits in UK Biobank. <i>PLoS Genetics</i> , 2022, 18, e1010105.	3.5	40
4	Cannabinoid receptor 1 antagonist genistein attenuates marijuana-induced vascular inflammation. <i>Cell</i> , 2022, 185, 1676-1693.e23.	28.9	40
5	Integration of rare expression outlier-associated variants improves polygenic risk prediction. <i>American Journal of Human Genetics</i> , 2022, 109, 1055-1064.	6.2	8
6	Survival analysis on rare events using group-regularized multi-response Cox regression. <i>Bioinformatics</i> , 2021, 37, 4437-4443.	4.1	3
7	Combining Clinical and Polygenic Risk Improves Stroke Prediction Among Individuals With Atrial Fibrillation. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003168.	3.6	24
8	Components of genetic associations across 2,138 phenotypes in the UK Biobank highlight adipocyte biology. <i>Nature Communications</i> , 2019, 10, 4064.	12.8	48
9	PPARG Pro12Ala Ala carriers exhibit greater improvements in peripheral insulin sensitivity in response to 12 weeks of aerobic exercise training. <i>Physiological Genomics</i> , 2019, 51, 254-260.	2.3	3
10	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.	21.4	89
11	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , 2018, 3, 4.	1.8	19
12	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, 14977.	12.8	169
13	A Low-Frequency Inactivating <i>AKT2</i> Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017, 66, 2019-2032.	0.6	47
14	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766.	21.4	470
15	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, 170179.	5.3	31
16	Genome-wide physical activity interactions in adiposity – A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	3.5	158
17	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	27.8	952
18	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, 13357.	12.8	74

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19	Increasing insulin resistance accentuates the effect of triglyceride-associated loci on serum triglycerides during 5 years. <i>Journal of Lipid Research</i> , 2016, 57, 2193-2199.	4.2	5
20	Interactions of Lipid Genetic Risk Scores With Estimates of Metabolic Health in a Danish Population. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 465-472.	5.1	28
21	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. <i>PLoS Genetics</i> , 2015, 11, e1004876.	3.5	95
22	A genetic risk score of 45 coronary artery disease risk variants associates with increased risk of myocardial infarction in 6041 Danish individuals. <i>Atherosclerosis</i> , 2015, 240, 305-310.	0.8	68
23	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. <i>Nature Genetics</i> , 2015, 47, 1282-1293.	21.4	294
24	Identification of low-frequency and rare sequence variants associated with elevated or reduced risk of type 2 diabetes. <i>Nature Genetics</i> , 2014, 46, 294-298.	21.4	294
25	The effect of GWAS identified BMI loci on changes in body weight among middle-aged danes during a five-year period. <i>Obesity</i> , 2014, 22, 901-908.	3.0	30
26	Exome sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. <i>Diabetologia</i> , 2013, 56, 298-310.	6.3	119
27	The frequent UCP2 $\sim$ 866G&gt;A polymorphism protects against insulin resistance and is associated with obesity: a study of obesity and related metabolic traits among 17%636 Danes. <i>International Journal of Obesity</i> , 2013, 37, 175-181.	3.4	36
28	Type 2 Diabetes Risk Alleles Near <i>BCAR1</i> and in <i>ANK1</i> Associate With Decreased $\beta$ -Cell Function Whereas Risk Alleles Near <i>ANKRD55</i> and <i>GRB14</i> Associate With Decreased Insulin Sensitivity in the Danish Inter99 Cohort. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2013, 98, E801-E806.	3.6	60
29	Genetic Risk Score of 46 Type 2 Diabetes Risk Variants Associates With Changes in Plasma Glucose and Estimates of Pancreatic $\beta$ -Cell Function Over 5 Years of Follow-Up. <i>Diabetes</i> , 2013, 62, 3610-3617.	0.6	42
30	<i>Solute carrier family 2 member 1</i> is involved in the development of nonalcoholic fatty liver disease. <i>Hepatology</i> , 2013, 57, 505-514.	7.3	25
31	Association studies of novel obesity-related gene variants with quantitative metabolic phenotypes in a population-based sample of 6,039 Danish individuals. <i>Diabetologia</i> , 2012, 55, 105-113.	6.3	32
32	Bioinformatics-Driven Identification and Examination of Candidate Genes for Non-Alcoholic Fatty Liver Disease. <i>PLoS ONE</i> , 2011, 6, e16542.	2.5	21
33	The minor C-allele of rs2014355 in <i>ACADS</i> is associated with reduced insulin release following an oral glucose load. <i>BMC Medical Genetics</i> , 2011, 12, 4.	2.1	11
34	Studies of the Association of Arg72Pro of Tumor Suppressor Protein p53 with Type 2 Diabetes in a Combined Analysis of 55,521 Europeans. <i>PLoS ONE</i> , 2011, 6, e15813.	2.5	49
35	Implications of Central Obesity-Related Variants in <i>LYPLAL1</i> , <i>NRXN3</i> , <i>MSRA</i> , and <i>TFAP2B</i> on Quantitative Metabolic Traits in Adult Danes. <i>PLoS ONE</i> , 2011, 6, e20640.	2.5	42
36	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , 0, 3, 4.	1.8	11

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37	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	1.8	1