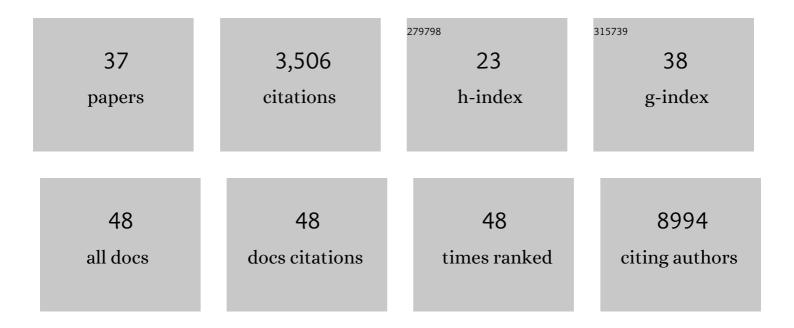
## Johanne Marie Justesen

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2626567/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
2	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
3	Identification of low-frequency and rare sequence variants associated with elevated or reduced risk of type 2 diabetes. Nature Genetics, 2014, 46, 294-298.	21.4	294
4	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.	21.4	294
5	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
6	Genome-wide physical activity interactions in adiposity ― A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
7	Exome sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. Diabetologia, 2013, 56, 298-310.	6.3	119
8	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.	3.5	95
9	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
10	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
11	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, 305-310.	0.8	68
12	Type 2 Diabetes Risk Alleles Near <i>BCAR1</i> and in <i>ANK1</i> Associate With Decreased Î <sup>2</sup> -Cell Function Whereas Risk Alleles Near <i>ANKRD55</i> and <i>GRB14</i> Associate With Decreased Insulin Sensitivity in the Danish Inter99 Cohort. Journal of Clinical Endocrinology and Metabolism, 2013, 98, E801-E806.	3.6	60
13	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.	2.5	49
14	Components of genetic associations across 2,138 phenotypes in the UK Biobank highlight adipocyte biology. Nature Communications, 2019, 10, 4064.	12.8	48
15	A Low-Frequency Inactivating <i>AKT2</i> Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.6	47
16	Genetic Risk Score of 46 Type 2 Diabetes Risk Variants Associates With Changes in Plasma Glucose and Estimates of Pancreatic β-Cell Function Over 5 Years of Follow-Up. Diabetes, 2013, 62, 3610-3617.	0.6	42
17	Implications of Central Obesity-Related Variants in LYPLAL1, NRXN3, MSRA, and TFAP2B on Quantitative Metabolic Traits in Adult Danes. PLoS ONE, 2011, 6, e20640.	2.5	42
18	Significant sparse polygenic risk scores across 813 traits in UK Biobank. PLoS Genetics, 2022, 18, e1010105.	3.5	40

#	Article	IF	CITATIONS
19	Cannabinoid receptor 1 antagonist genistein attenuates marijuana-induced vascular inflammation. Cell, 2022, 185, 1676-1693.e23.	28.9	40
20	The frequent UCP2 â^'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, 175-181.	3.4	36
21	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, 105-113.	6.3	32
22	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
23	The effect of GWAS identified BMI loci on changes in body weight among middleâ€aged danes during a fiveâ€year period. Obesity, 2014, 22, 901-908.	3.0	30
24	Interactions of Lipid Genetic Risk Scores With Estimates of Metabolic Health in a Danish Population. Circulation: Cardiovascular Genetics, 2015, 8, 465-472.	5.1	28
25	<i>Solute carrier family 2 member 1</i> is involved in the development of nonalcoholic fatty liver disease. Hepatology, 2013, 57, 505-514.	7.3	25
26	Combining Clinical and Polygenic Risk Improves Stroke Prediction Among Individuals With Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2021, 14, e003168.	3.6	24
27	Fast Lasso method for large-scale and ultrahigh-dimensional Cox model with applications to UK Biobank. Biostatistics, 2022, 23, 522-540.	1.5	22
28	Bioinformatics-Driven Identification and Examination of Candidate Genes for Non-Alcoholic Fatty Liver Disease. PLoS ONE, 2011, 6, e16542.	2.5	21
29	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 2018, 3, 4.	1.8	19
30	The minor C-allele of rs2014355 in ACADSis associated with reduced insulin release following an oral glucose load. BMC Medical Genetics, 2011, 12, 4.	2.1	11
31	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	1.8	11
32	Integration of rare expression outlier-associated variants improves polygenic risk prediction. American Journal of Human Genetics, 2022, 109, 1055-1064.	6.2	8
33	Interactions of physical activity, muscular fitness, adiposity, and genetic risk for NAFLD. Hepatology Communications, 2022, 6, 1516-1526.	4.3	7
34	Increasing insulin resistance accentuates the effect of triglyceride-associated loci on serum triglycerides during 5 years. Journal of Lipid Research, 2016, 57, 2193-2199.	4.2	5
35	PPARG 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.	2.3	3
36	Survival analysis on rare events using group-regularized multi-response Cox regression. Bioinformatics, 2021, 37, 4437-4443.	4.1	3

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