

# Jette Bork-Jensen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/12155389/publications.pdf>

Version: 2024-02-01

38  
papers

7,286  
citations

201674

27  
h-index

276875

41  
g-index

51  
all docs

51  
docs citations

51  
times ranked

14037  
citing authors

#	ARTICLE	IF	CITATIONS
1	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. <i>Nature Genetics</i> , 2018, 50, 1505-1513.	21.4	1,331
2	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	27.8	952
3	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	27.8	544
4	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766.	21.4	470
5	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11.	28.9	388
6	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018, 50, 559-571.	21.4	356
7	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. <i>Cell</i> , 2020, 182, 1198-1213.e14.	28.9	353
8	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	27.8	353
9	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018, 50, 26-41.	21.4	286
10	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016, 48, 1151-1161.	21.4	261
11	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. <i>Nature Genetics</i> , 2022, 54, 560-572.	21.4	250
12	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. <i>Nature Communications</i> , 2015, 6, 5897.	12.8	173
13	Genome-Wide Analysis of DNA Methylation Differences in Muscle and Fat from Monozygotic Twins Discordant for Type 2 Diabetes. <i>PLoS ONE</i> , 2012, 7, e51302.	2.5	171
14	Novel variation and de novo mutation rates in population-wide de novo assembled Danish trios. <i>Nature Communications</i> , 2015, 6, 5969.	12.8	164
15	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. <i>Nature</i> , 2017, 548, 87-91.	27.8	130
16	A genomic approach to therapeutic target validation identifies a glucose-lowering <i>GLP1R</i> variant protective for coronary heart disease. <i>Science Translational Medicine</i> , 2016, 8, 341ra76.	12.4	100
17	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
18	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. <i>Nature Genetics</i> , 2020, 52, 1314-1332.	21.4	91

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19	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
20	Young men with low birthweight exhibit decreased plasticity of genome-wide muscle DNA methylation by high-fat overfeeding. <i>Diabetologia</i> , 2014, 57, 1154-1158.	6.3	67
21	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. <i>American Journal of Human Genetics</i> , 2016, 99, 8-21.	6.2	60
22	Human biallelic MFN2 mutations induce mitochondrial dysfunction, upper body adipose hyperplasia, and suppression of leptin expression. <i>ELife</i> , 2017, 6, .	6.0	60
23	Glucose tolerance is associated with differential expression of microRNAs in skeletal muscle: results from studies of twins with and without type 2 diabetes. <i>Diabetologia</i> , 2015, 58, 363-373.	6.3	53
24	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475,000 Individuals. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	48
25	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
26	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. <i>Genome Biology</i> , 2018, 19, 87.	8.8	47
27	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 981-994.	6.1	39
28	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, 170179.	5.3	31
29	A novel rare CUBN variant and three additional genes identified in Europeans with and without diabetes: results from an exome-wide association study of albuminuria. <i>Diabetologia</i> , 2019, 62, 292-305.	6.3	29
30	Skeletal muscle enhancer interactions identify genes controlling whole-body metabolism. <i>Nature Communications</i> , 2020, 11, 2695.	12.8	29
31	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. <i>Diabetes</i> , 2020, 69, 2806-2818.	0.6	26
32	Genetic versus Non-Genetic Regulation of miR-103, miR-143 and miR-483-3p Expression in Adipose Tissue and Their Metabolic Implications—A Twin Study. <i>Genes</i> , 2014, 5, 508-517.	2.4	21
33	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. <i>American Journal of Human Genetics</i> , 2019, 105, 15-28.	6.2	21
34	FUT2-ABO epistasis increases the risk of early childhood asthma and <i>Streptococcus pneumoniae</i> respiratory illnesses. <i>Nature Communications</i> , 2020, 11, 6398.	12.8	21
35	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002037.	3.6	19
36	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

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37	Carriers of a <i>VEGFA</i> enhancer polymorphism selectively binding CHOP/DDIT3 are predisposed to increased circulating levels of thyroid-stimulating hormone. <i>Journal of Medical Genetics</i> , 2017, 54, 166-175.	3.2	12
38	Genome-wide study of early and severe childhood asthma identifies interaction between CDHR3 and GSDMB. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 150, 622-630.	2.9	8