

# Josine L Min

## List of Publications by Year in descending order

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Version: 2024-02-01

40  
papers

12,883  
citations

331670

21  
h-index

276875

41  
g-index

47  
all docs

47  
docs citations

47  
times ranked

24392  
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenetic Regulation of <i>F2RL3</i> Associates With Myocardial Infarction and Platelet Function. <i>Circulation Research</i> , 2022, 130, 384-400.	4.5	10
2	Genome-wide association meta-analysis identifies 29 new acne susceptibility loci. <i>Nature Communications</i> , 2022, 13, 702.	12.8	23
3	DNA methylome-wide association study of genetic risk for depression implicates antigen processing and immune responses. <i>Genome Medicine</i> , 2022, 14, 36.	8.2	16
4	Pulmonary Function and Blood DNA Methylation: A Multiancestry Epigenome-Wide Association Meta-analysis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2022, 206, 321-336.	5.6	15
5	Complex trait methylation scores in the prediction of major depressive disorder. <i>EBioMedicine</i> , 2022, 79, 104000.	6.1	4
6	Investigating DNA methylation as a potential mediator between pigmentation genes, pigimentary traits and skin cancer. <i>Pigment Cell and Melanoma Research</i> , 2021, 34, 892-904.	3.3	9
7	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021, 12, 24.	12.8	87
8	Comparison of DNA methylation clocks in Black South African men. <i>Epigenomics</i> , 2021, 13, 437-449.	2.1	4
9	Assessing the role of genome-wide DNA methylation between smoking and risk of lung cancer using repeated measurements: the HUNT study. <i>International Journal of Epidemiology</i> , 2021, 50, 1482-1497.	1.9	14
10	Triangulating Molecular Evidence to Prioritize Candidate Causal Genes at Established Atopic Dermatitis Loci. <i>Journal of Investigative Dermatology</i> , 2021, 141, 2620-2629.	0.7	12
11	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.	8.8	90
12	The BIOMarkers in Atopic Dermatitis and Psoriasis (BIOMAP) glossary: developing a lingua franca to facilitate data harmonization and cross-cohort analyses. <i>British Journal of Dermatology</i> , 2021, 185, 1066-1069.	1.5	10
13	Identical twins carry a persistent epigenetic signature of early genome programming. <i>Nature Communications</i> , 2021, 12, 5618.	12.8	26
14	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	21.4	218
15	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. <i>Nature Communications</i> , 2021, 12, 7173.	12.8	8
16	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021, 12, 7174.	12.8	30
17	Opportunities and Challenges in Functional Genomics Research in Osteoporosis: Report From a Workshop Held by the Causes Working Group of the Osteoporosis and Bone Research Academy of the Royal Osteoporosis Society on October 5th 2020. <i>Frontiers in Endocrinology</i> , 2020, 11, 630875.	3.5	5
18	Low-frequency variation in TP53 has large effects on head circumference and intracranial volume. <i>Nature Communications</i> , 2019, 10, 357.	12.8	30

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19	GARFIELD classifies disease-relevant genomic features through integration of functional annotations with association signals. <i>Nature Genetics</i> , 2019, 51, 343-353.	21.4	147
20	The Effect of Pre-Analytical Conditions on Blood Metabolomics in Epidemiological Studies. <i>Metabolites</i> , 2019, 9, 64.	2.9	18
21	Autosomal genetic variation is associated with DNA methylation in regions variably escaping X-chromosome inactivation. <i>Nature Communications</i> , 2018, 9, 3738.	12.8	24
22	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. <i>American Journal of Human Genetics</i> , 2017, 100, 865-884.	6.2	131
23	Systematic identification of genetic influences on methylation across the human life course. <i>Genome Biology</i> , 2016, 17, 61.	8.8	489
24	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. <i>Nature Genetics</i> , 2016, 48, 1303-1312.	21.4	66
25	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016, 48, 1279-1283.	21.4	2,421
26	Involvement of astrocyte and oligodendrocyte gene sets in migraine. <i>Cephalalgia</i> , 2016, 36, 640-647.	3.9	15
27	Whole-genome sequence-based analysis of thyroid function. <i>Nature Communications</i> , 2015, 6, 5681.	12.8	75
28	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	27.8	1,328
29	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	27.8	3,823
30	An interactive genome browser of association results from the UK10K cohorts project. <i>Bioinformatics</i> , 2015, 31, 4029-4031.	4.1	12
31	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. <i>Nature</i> , 2015, 526, 112-117.	27.8	483
32	The UK10K project identifies rare variants in health and disease. <i>Nature</i> , 2015, 526, 82-90.	27.8	1,014
33	Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. <i>Nature Communications</i> , 2015, 6, 8111.	12.8	300
34	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. <i>Nature Communications</i> , 2014, 5, 4871.	12.8	62
35	Distinct Developmental Profile of Lower-Body Adipose Tissue Defines Resistance Against Obesity-Associated Metabolic Complications. <i>Diabetes</i> , 2014, 63, 3785-3797.	0.6	148
36	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. <i>PLoS Genetics</i> , 2013, 9, e1003500.	3.5	371

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37	Coexpression Network Analysis in Abdominal and Gluteal Adipose Tissue Reveals Regulatory Genetic Loci for Metabolic Syndrome and Related Phenotypes. PLoS Genetics, 2012, 8, e1002505.	3.5	57
38	The Architecture of Gene Regulatory Variation across Multiple Human Tissues: The MuTHER Study. PLoS Genetics, 2011, 7, e1002003.	3.5	392
39	The Use of Genome-Wide eQTL Associations in Lymphoblastoid Cell Lines to Identify Novel Genetic Pathways Involved in Complex Traits. PLoS ONE, 2011, 6, e22070.	2.5	36
40	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	21.4	836