Josine L Min

List of Publications by Year
in descending order

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	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
2	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	21.4	2,421
3	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
4	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	27.8	1,014
5	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
6	Systematic identification of genetic influences on methylation across the human life course. Genome Biology, 2016, 17, 61.	8.8	489
7	Wholeâ€genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	27.8	483
8	The Architecture of Gene Regulatory Variation across Multiple Human Tissues: The MuTHER Study. PLoS Genetics, 2011, 7, e1002003.	3.5	392
9	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	3.5	371
10	Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. Nature Communications, 2015, 6, 8111.	12.8	300
11	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	21.4	218
12	Distinct Developmental Profile of Lower-Body Adipose Tissue Defines Resistance Against Obesity-Associated Metabolic Complications. Diabetes, 2014, 63, 3785-3797.	0.6	148
13	GARFIELD classifies disease-relevant genomic features through integration of functional annotations with association signals. Nature Genetics, 2019, 51, 343-353.	21.4	147
14	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	6.2	131
15	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	8.8	90
16	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
17	Whole-genome sequence-based analysis of thyroid function. Nature Communications, 2015, 6, 5681.	12.8	75
18	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	21.4	66

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19	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. Nature Communications, 2014, 5, 4871.	12.8	62
20	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
21	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
22	Low-frequency variation in TP53 has large effects on head circumference and intracranial volume. Nature Communications, 2019, 10, 357.	12.8	30
23	Meta-analyses identify DNA methylation associated with kidney function and damage. Nature Communications, 2021, 12, 7174.	12.8	30
24	Identical twins carry a persistent epigenetic signature of early genome programming. Nature Communications, 2021, 12, 5618.	12.8	26
25	Autosomal genetic variation is associated with DNA methylation in regions variably escaping X-chromosome inactivation. Nature Communications, 2018, 9, 3738.	12.8	24
26	Genome-wide association meta-analysis identifies 29 new acne susceptibility loci. Nature Communications, 2022, 13, 702.	12.8	23
27	The Effect of Pre-Analytical Conditions on Blood Metabolomics in Epidemiological Studies. Metabolites, 2019, 9, 64.	2.9	18
28	DNA methylome-wide association study of genetic risk for depression implicates antigen processing and immune responses. Genome Medicine, 2022, 14, 36.	8.2	16
29	Involvement of astrocyte and oligodendrocyte gene sets in migraine. Cephalalgia, 2016, 36, 640-647.	3.9	15
30	Pulmonary Function and Blood DNA Methylation: A Multiancestry Epigenome-Wide Association Meta-analysis. American Journal of Respiratory and Critical Care Medicine, 2022, 206, 321-336.	5.6	15
31	Assessing the role of genome-wide DNA methylation between smoking and risk of lung cancer using repeated measurements: the HUNT study. International Journal of Epidemiology, 2021, 50, 1482-1497.	1.9	14
32	An interactive genome browser of association results from the UK10K cohorts project. Bioinformatics, 2015, 31, 4029-4031.	4.1	12
33	Triangulating Molecular Evidence to Prioritize Candidate Causal Genes at Established Atopic Dermatitis Loci. Journal of Investigative Dermatology, 2021, 141, 2620-2629.	0.7	12
34	The BIOMarkers in Atopic Dermatitis and Psoriasis (BIOMAP) glossary: developing a lingua franca to facilitate data harmonization and crossâ€cohort analyses. British Journal of Dermatology, 2021, 185, 1066-1069.	1.5	10
35	Epigenetic Regulation of F2RL3 Associates With Myocardial Infarction and Platelet Function. Circulation Research, 2022, 130, 384-400.	4.5	10
36	Investigating DNA methylation as a potential mediator between pigmentation genes, pigmentary traits and skin cancer. Pigment Cell and Melanoma Research, 2021, 34, 892-904.	3.3	9

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37	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. Nature Communications, 2021, 12, 7173.	12.8	8
38	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. Frontiers in Endocrinology, 2020, 11, 630875.	3.5	5
39	Comparison of DNA methylation clocks in Black South African men. Epigenomics, 2021, 13, 437-449.	2.1	4
40	Complex trait methylation scores in the prediction of major depressive disorder. EBioMedicine, 2022, 79, 104000.	6.1	4