

Jenny van Dongen

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

79
papers

3,586
citations

31
h-index

59
g-index

85
ext. papers

5,289
ext. citations

10.5
avg, IF

4.5
L-index

#	Paper	IF	Citations
79	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. <i>Nature Genetics</i> , 2017 , 49, 1752-1757	36.3	256
78	Disease variants alter transcription factor levels and methylation of their binding sites. <i>Nature Genetics</i> , 2017 , 49, 131-138	36.3	252
77	The continuing value of twin studies in the omics era. <i>Nature Reviews Genetics</i> , 2012 , 13, 640-53	30.1	250
76	Identification of context-dependent expression quantitative trait loci in whole blood. <i>Nature Genetics</i> , 2017 , 49, 139-145	36.3	240
75	Genetic and environmental influences interact with age and sex in shaping the human methylome. <i>Nature Communications</i> , 2016 , 7, 11115	17.4	200
74	Unraveling the polygenic architecture of complex traits using blood eQTL metaanalysis		175
73	The Adult Netherlands Twin Register: twenty-five years of survey and biological data collection. <i>Twin Research and Human Genetics</i> , 2013 , 16, 271-81	2.2	162
72	Prenatal famine and genetic variation are independently and additively associated with DNA methylation at regulatory loci within IGF2/H19. <i>PLoS ONE</i> , 2012 , 7, e37933	3.7	118
71	Blood lipids influence DNA methylation in circulating cells. <i>Genome Biology</i> , 2016 , 17, 138	18.3	118
70	Multiethnic meta-analysis of genome-wide association studies in >100 000 subjects identifies 23 fibrinogen-associated Loci but no strong evidence of a causal association between circulating fibrinogen and cardiovascular disease. <i>Circulation</i> , 2013 , 128, 1310-24	16.7	107
69	Multivariate genome-wide analyses of the well-being spectrum. <i>Nature Genetics</i> , 2019 , 51, 445-451	36.3	107
68	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. <i>American Journal of Human Genetics</i> , 2015 , 97, 75-85	11	85
67	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017 , 101, 888-902	11	83
66	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. <i>Genome Biology</i> , 2016 , 17, 191	18.3	80
65	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. <i>Nature Communications</i> , 2019 , 10, 1893	17.4	79
64	Circulating metabolites and general cognitive ability and dementia: Evidence from 11 cohort studies. <i>Alzheimers and Dementia</i> , 2018 , 14, 707-722	1.2	76
63	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. <i>Cell Reports</i> , 2016 , 17, 2137-2150	16.0	70

62	The evolutionary paradox and the missing heritability of schizophrenia. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2013 , 162B, 122-36	3.5	60
61	Heritability of metabolic syndrome traits in a large population-based sample. <i>Journal of Lipid Research</i> , 2013 , 54, 2914-23	6.3	60
60	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. <i>Nature Genetics</i> , 2021 , 53, 1300-1310	36.3	60
59	Sex differences in genetic architecture of complex phenotypes?. <i>PLoS ONE</i> , 2012 , 7, e47371	3.7	59
58	The Netherlands Twin Register: Longitudinal Research Based on Twin and Twin-Family Designs. <i>Twin Research and Human Genetics</i> , 2019 , 22, 623-636	2.2	53
57	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. <i>Nature Communications</i> , 2017 , 8, 15805	17.4	50
56	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016 , 7, 13357	17.4	46
55	Refined mapping of autoimmune disease associated genetic variants with gene expression suggests an important role for non-coding RNAs. <i>Journal of Autoimmunity</i> , 2016 , 68, 62-74	15.5	44
54	Epigenetic variation in monozygotic twins: a genome-wide analysis of DNA methylation in buccal cells. <i>Genes</i> , 2014 , 5, 347-65	4.2	43
53	Epigenome-wide association study of serum cotinine in current smokers reveals novel genetically driven loci. <i>Clinical Epigenetics</i> , 2019 , 11, 1	7.7	40
52	Childhood aggression and the co-occurrence of behavioural and emotional problems: results across ages 3-16 years from multiple raters in six cohorts in the EU-ACTION project. <i>European Child and Adolescent Psychiatry</i> , 2018 , 27, 1105-1121	5.5	40
51	The contribution of the functional IL6R polymorphism rs2228145, eQTLs and other genome-wide SNPs to the heritability of plasma sIL-6R levels. <i>Behavior Genetics</i> , 2014 , 44, 368-82	3.2	33
50	eFORGE v2.0: updated analysis of cell type-specific signal in epigenomic data. <i>Bioinformatics</i> , 2019 , 35, 4767-4769	7.2	32
49	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. <i>Nature Communications</i> , 2019 , 10, 2581	17.4	31
48	Epigenome-Wide Association Study of Aggressive Behavior. <i>Twin Research and Human Genetics</i> , 2015 , 18, 686-98	2.2	29
47	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021 , 53, 1311-1321	36.3	27
46	Epigenome-Wide Association Study of Tic Disorders. <i>Twin Research and Human Genetics</i> , 2015 , 18, 699-709	2.2	24
45	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. <i>Biological Psychiatry</i> , 2019 , 86, 599-607	7.9	24

44	Genome-wide analysis of DNA methylation in buccal cells: a study of monozygotic twins and mQTLs. <i>Epigenetics and Chromatin</i> , 2018 , 11, 54	5.8	23
43	Epigenome-wide meta-analysis of blood DNA methylation and its association with subcortical volumes: findings from the ENIGMA Epigenetics Working Group. <i>Molecular Psychiatry</i> , 2021 , 26, 3884-3895	15.1	22
42	Integrative DNA methylome analysis of pan-cancer biomarkers in cancer discordant monozygotic twin-pairs. <i>Clinical Epigenetics</i> , 2016 , 8, 7	7.7	21
41	Heritability estimates for 361 blood metabolites across 40 genome-wide association studies. <i>Nature Communications</i> , 2020 , 11, 39	17.4	21
40	DNA Methylation Changes in the IGF1R Gene in Birth Weight Discordant Adult Monozygotic Twins. <i>Twin Research and Human Genetics</i> , 2015 , 18, 635-46	2.2	20
39	DNA methylation and associated gene expression in blood prior to lung cancer diagnosis in the Norwegian Women and Cancer cohort. <i>Scientific Reports</i> , 2018 , 8, 16714	4.9	19
38	Low Birth Weight in MZ Twins Discordant for Birth Weight is Associated with Shorter Telomere Length and lower IQ, but not Anxiety/Depression in Later Life. <i>Twin Research and Human Genetics</i> , 2015 , 18, 198-209	2.2	17
37	Genetic architecture of the pro-inflammatory state in an extended twin-family design. <i>Twin Research and Human Genetics</i> , 2013 , 16, 931-40	2.2	16
36	DNA methylation signatures of educational attainment. <i>Npj Science of Learning</i> , 2018 , 3, 7	6	14
35	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021 , 22, 194	18.3	14
34	Identification, Heritability, and Relation With Gene Expression of Novel DNA Methylation Loci for Blood Pressure. <i>Hypertension</i> , 2020 , 76, 195-205	8.5	12
33	The relation between ADHD symptoms and fine motor control: a genetic study. <i>Child Neuropsychology</i> , 2011 , 17, 138-50	2.7	12
32	Evaluation of commonly used analysis strategies for epigenome- and transcriptome-wide association studies through replication of large-scale population studies. <i>Genome Biology</i> , 2019 , 20, 235	18.3	12
31	Longitudinal weight differences, gene expression and blood biomarkers in BMI-discordant identical twins. <i>International Journal of Obesity</i> , 2015 , 39, 899-909	5.5	11
30	Brain reward responses to food stimuli among female monozygotic twins discordant for BMI. <i>Brain Imaging and Behavior</i> , 2018 , 12, 718-727	4.1	11
29	DNA methylation age is associated with an altered hemostatic profile in a multiethnic meta-analysis. <i>Blood</i> , 2018 , 132, 1842-1850	2.2	11
28	Physical activity and dietary intake in BMI discordant identical twins. <i>Obesity</i> , 2016 , 24, 1349-55	8	11
27	Validated inference of smoking habits from blood with a finite DNA methylation marker set. <i>European Journal of Epidemiology</i> , 2019 , 34, 1055-1074	12.1	10

26	Epigenome-Wide Association Study of Wellbeing. <i>Twin Research and Human Genetics</i> , 2015 , 18, 710-9	2.2	10
25	DNA Methylation Signatures of Breastfeeding in Buccal Cells Collected in Mid-Childhood. <i>Nutrients</i> , 2019 , 11,	6.7	9
24	A characterization of cis- and trans-heritability of RNA-Seq-based gene expression. <i>European Journal of Human Genetics</i> , 2020 , 28, 253-263	5.3	8
23	Genomic and phenomic insights from an atlas of genetic effects on DNA methylation		7
22	DNA methylation signatures of aggression and closely related constructs: A meta-analysis of epigenome-wide studies across the lifespan. <i>Molecular Psychiatry</i> , 2021 , 26, 2148-2162	15.1	7
21	Refining Attention-Deficit/Hyperactivity Disorder and Autism Spectrum Disorder Genetic Loci by Integrating Summary Data From Genome-wide Association, Gene Expression, and DNA Methylation Studies. <i>Biological Psychiatry</i> , 2020 , 88, 470-479	7.9	6
20	Urinary Amine and Organic Acid Metabolites Evaluated as Markers for Childhood Aggression: The ACTION Biomarker Study. <i>Frontiers in Psychiatry</i> , 2020 , 11, 165	5	6
19	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. <i>Human Molecular Genetics</i> , 2021 , 30, 393-409	5.6	6
18	Identical twins carry a persistent epigenetic signature of early genome programming. <i>Nature Communications</i> , 2021 , 12, 5618	17.4	6
17	Pre- and Perinatal Characteristics Associated with Apgar Scores in a Review and in a New Study of Dutch Twins. <i>Twin Research and Human Genetics</i> , 2019 , 22, 164-176	2.2	5
16	No evidence for genome-wide interactions on plasma fibrinogen by smoking, alcohol consumption and body mass index: results from meta-analyses of 80,607 subjects. <i>PLoS ONE</i> , 2014 , 9, e1111156	3.7	5
15	Occupational exposure to gases/fumes and mineral dust affect DNA methylation levels of genes regulating expression. <i>Human Molecular Genetics</i> , 2019 , 28, 2477-2485	5.6	4
14	Predicting Complex Traits and Exposures From Polygenic Scores and Blood and Buccal DNA Methylation Profiles. <i>Frontiers in Psychiatry</i> , 2021 , 12, 688464	5	4
13	Genome-wide study of DNA methylation shows alterations in metabolic, inflammatory, and cholesterol pathways in ALS.. <i>Science Translational Medicine</i> , 2022 , 14, eabj0264	17.5	4
12	Genetics and Not Shared Environment Explains Familial Resemblance in Adult Metabolomics Data. <i>Twin Research and Human Genetics</i> , 2020 , 23, 145-155	2.2	3
11	Methylation as an epigenetic source of random genetic effects in the classical twin design. <i>Advances in Genomics and Genetics</i> , 2015 , 305		1
10	Integrative analysis of 3604 GWAS reveals multiple novel cell type-specific regulatory associations.. <i>Genome Biology</i> , 2022 , 23, 13	18.3	1
9	The genomic architecture of blood metabolites based on a decade of genome-wide analyses		1

8	Methylome-wide association study of antidepressant use in Generation Scotland and the Netherlands Twin Register implicates the innate immune system. <i>Molecular Psychiatry</i> , 2021 ,	15.1	1
7	Validating biomarkers and models for epigenetic inference of alcohol consumption from blood. <i>Clinical Epigenetics</i> , 2021 , 13, 198	7.7	0
6	DNA methylation in peripheral tissues and left-handedness.. <i>Scientific Reports</i> , 2022 , 12, 5606	4.9	0
5	Complex trait methylation scores in the prediction of major depressive disorder.. <i>EBioMedicine</i> , 2022 , 79, 104000	8.8	0
4	Heritability of Urinary Amines, Organic Acids, and Steroid Hormones in Children. <i>Metabolites</i> , 2022 , 12, 474	5.6	0
3	Examining the Vanishing Twin Hypothesis of Neural Tube Defects: Application of an Epigenetic Predictor for Monozygotic Twinning. <i>Twin Research and Human Genetics</i> , 2021 , 24, 155-159	2.2	
2	Discordant monozygotic twin studies of epigenetic mechanisms in mental health 2021 , 43-66		
1	Combining twin-family designs with measured genetic variants to study the causes of epigenetic variation 2021 , 239-259		