Bastiaan T Heijmans

List of Publications by Year
in descending order

131 papers	16,668 citations	28190 55 h-index	17055 122 g-index
142 all docs	142 docs citations	142 times ranked	20693 citing authors

#	Article	IF	Citations
1	Persistent epigenetic differences associated with prenatal exposure to famine in humans. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17046-17049.	3.3	2,683
2	DNA methylation differences after exposure to prenatal famine are common and timing- and sex-specific. Human Molecular Genetics, 2009, 18, 4046-4053.	1.4	1,042
3	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. Nature, 2017, 541, 81-86.	13.7	743
4	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature Genetics, 2021, 53, 1300-1310.	9.4	590
5	DNA methylation aging clocks: challenges and recommendations. Genome Biology, 2019, 20, 249.	3.8	552
6	DNA methylation signatures link prenatal famine exposure to growth and metabolism. Nature Communications, 2014, 5, 5592.	5.8	494
7	Periconceptional Maternal Folic Acid Use of 400 Âµg per Day Is Related to Increased Methylation of the IGF2 Gene in the Very Young Child. PLoS ONE, 2009, 4, e7845.	1.1	410
8	Disease variants alter transcription factor levels and methylation of their binding sites. Nature Genetics, 2017, 49, 131-138.	9.4	390
9	Identification of context-dependent expression quantitative trait loci in whole blood. Nature Genetics, 2017, 49, 139-145.	9.4	363
10	From promises to practical strategies in epigenetic epidemiology. Nature Reviews Genetics, 2013, 14, 585-594.	7.7	314
11	Genetic and environmental influences interact with age and sex in shaping the human methylome. Nature Communications, 2016, 7, 11115.	5.8	299
12	Reduced insulin/IGF-1 signalling and human longevity. Aging Cell, 2005, 4, 79-85.	3.0	288
13	Variation, patterns, and temporal stability of DNA methylation: considerations for epigenetic epidemiology. FASEB Journal, 2010, 24, 3135-3144.	0.2	287
14	Nonagenarian Siblings and Their Offspring Display Lower Risk of Mortality and Morbidity than Sporadic Nonagenarians: The Leiden Longevity Study. Journal of the American Geriatrics Society, 2009, 57, 1634-1637.	1.3	258
15	Epigenetic variation during the adult lifespan: crossâ€sectional and longitudinal data on monozygotic twin pairs. Aging Cell, 2012, 11, 694-703.	3.0	257
16	Controlling bias and inflation in epigenome- and transcriptome-wide association studies using the empirical null distribution. Genome Biology, 2017, 18, 19.	3.8	256
17	Transcription of the IL10 gene reveals allele-specific regulation at the mRNA level. Human Molecular Genetics, 2004, 13, 1755-1762.	1.4	249
18	Genomeâ€wide association study identifies a single major locus contributing to survival into old age; the APOE locus revisited. Aging Cell, 2011, 10, 686-698.	3.0	249

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19	Data Resource Profile: Accessible Resource for Integrated Epigenomic Studies (ARIES). International Journal of Epidemiology, 2015, 44, 1181-1190.	0.9	238
20	Inflammation underlying cardiovascular mortality is a late consequence of evolutionary programming. FASEB Journal, 2004, 18, 1022-1024.	0.2	231
21	Genome-wide association meta-analysis of human longevity identifies a novel locus conferring survival beyond 90 years of age. Human Molecular Genetics, 2014, 23, 4420-4432.	1.4	227
22	DNA methylation as a mediator of the association between prenatal adversity and risk factors for metabolic disease in adulthood. Science Advances, 2018, 4, eaao4364.	4.7	219
23	Heritable rather than age-related environmental and stochastic factors dominate variation in DNA methylation of the human IGF2/H19 locus. Human Molecular Genetics, 2007, 16, 547-554.	1.4	218
24	The epigenome: Archive of the prenatal environment. Epigenetics, 2009, 4, 526-531.	1.3	218
25	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	9.4	218
26	Identification and systematic annotation of tissue-specific differentially methylated regions using the Illumina 450k array. Epigenetics and Chromatin, 2013, 6, 26.	1.8	192
27	Commentary: The seven plagues of epigenetic epidemiology. International Journal of Epidemiology, 2012, 41, 74-78.	0.9	182
28	Epigenetic histone acetylation modifiers in vascular remodelling: new targets for therapy in cardiovascular disease. European Heart Journal, 2008, 30, 266-277.	1.0	154
29	MethylAid: visual and interactive quality control of large Illumina 450k datasets. Bioinformatics, 2014, 30, 3435-3437.	1.8	154
30	Blood lipids influence DNA methylation in circulating cells. Genome Biology, 2016, 17, 138.	3.8	154
31	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	2.6	154
32	Apolipoprotein E genotype, cardiovascular biomarkers and risk of stroke: Systematic review and meta-analysis of 14 015 stroke cases and pooled analysis of primary biomarker data from up to 60 883 individuals. International Journal of Epidemiology, 2013, 42, 475-492.	0.9	145
33	Early gestation as the critical time-window for changes in the prenatal environment to affect the adult human blood methylome. International Journal of Epidemiology, 2015, 44, 1211-1223.	0.9	139
34	Genome-wide association study (GWAS)-identified disease risk alleles do not compromise human longevity. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 18046-18049.	3.3	138
35	Prenatal Famine and Genetic Variation Are Independently and Additively Associated with DNA Methylation at Regulatory Loci within IGF2/H19. PLoS ONE, 2012, 7, e37933.	1.1	132
36	Age-related DNA methylation changes are tissue-specific with ELOVL2 promoter methylation as exception. Epigenetics and Chromatin, 2018, 11, 25.	1.8	130

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37	DNA methylation ofIGF2,GNASAS,INSIGFandLEPand being born small for gestational age. Epigenetics, 2011, 6, 171-176.	1.3	126
38	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. Genome Biology, 2016, 17, 191.	3.8	120
39	Skewed X-inactivation is common in the general female population. European Journal of Human Genetics, 2019, 27, 455-465.	1.4	119
40	Alternative Routes to Induce NaÃ¯ve Pluripotency in Human Embryonic Stem Cells. Stem Cells, 2015, 33, 2686-2698.	1.4	118
41	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. American Journal of Human Genetics, 2015, 97, 75-85.	2.6	116
42	A common variant of the methylenetetrahydrofolate reductase gene (1p36) is associated with an increased risk of cancer. Cancer Research, 2003, 63, 1249-53.	0.4	106
43	Impaired innate immunity predicts frailty in old age. The Leiden 85-plus study. Experimental Gerontology, 2004, 39, 1407-1414.	1.2	105
44	Duration of breastfeeding and gender are associated with methylation of the LEPTIN gene in very young children. Pediatric Research, 2013, 74, 344-349.	1.1	96
45	DNA methylation profiles at birth and child ADHD symptoms. Journal of Psychiatric Research, 2014, 49, 51-59.	1.5	93
46	Epigenetic drift in the aging genome: a ten-year follow-up in an elderly twin cohort. International Journal of Epidemiology, 2016, 45, dyw132.	0.9	82
47	Favorable Glucose Tolerance and Lower Prevalence of Metabolic Syndrome in Offspring without Diabetes Mellitus of Nonagenarian Siblings: The Leiden Longevity Study. Journal of the American Geriatrics Society, 2010, 58, 564-569.	1.3	75
48	Lipid metabolism in long-lived families: the Leiden Longevity Study. Age, 2011, 33, 219-227.	3.0	75
49	Underlying molecular mechanisms ofDIO2susceptibility in symptomatic osteoarthritis. Annals of the Rheumatic Diseases, 2015, 74, 1571-1579.	0.5	75
50	A metabolomic profile is associated with the risk of incident coronary heart disease. American Heart Journal, 2014, 168, 45-52.e7.	1.2	74
51	DNA Methylation Landscapes of Human Fetal Development. PLoS Genetics, 2015, 11, e1005583.	1.5	73
52	Heritabilities of Apolipoprotein and Lipid Levels in Three Countries. Twin Research and Human Genetics, 2002, 5, 87-97.	1.5	72
53	Common paraoxonase gene variants, mortality risk and fatal cardiovascular events in elderly subjects. Atherosclerosis, 2000, 149, 91-97.	0.4	66
54	Design, measurement and processing of region-specific DNA methylation assays: the mass spectrometry-based method EpiTYPER. Frontiers in Genetics, 2015, 6, 287.	1.1	66

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55	Epigenome-wide change and variation in DNA methylation in childhood: trajectories from birth to late adolescence. Human Molecular Genetics, 2021, 30, 119-134.	1.4	65
56	Association of the tumour necrosis factor Î± â^'308G/A polymorphism with the risk of diabetes in an elderly population-based cohort. Genes and Immunity, 2002, 3, 225-228.	2.2	57
57	Literature-Based Genetic Risk Scores for Coronary Heart Disease. Circulation: Cardiovascular Genetics, 2012, 5, 202-209.	5.1	53
58	Epigenome-Wide Association Study of Aggressive Behavior. Twin Research and Human Genetics, 2015, 18, 686-698.	0.3	53
59	DNA methylation and transcriptional trajectories during human development and reprogramming of isogenic pluripotent stem cells. Nature Communications, 2017, 8, 908.	5.8	53
60	Lipoprotein Particle Profiles Mark Familial and Sporadic Human Longevity. PLoS Medicine, 2006, 3, e495.	3.9	51
61	Prenatal parental tobacco smoking, gene specific DNA methylation, and newborns size: the Generation R study. Clinical Epigenetics, 2015, 7, 83.	1.8	51
62	DNA Methylation of IGF2DMR and H19 Is Associated with Fetal and Infant Growth: The Generation R Study. PLoS ONE, 2013, 8, e81731.	1.1	49
63	Epigenetic Variation in Monozygotic Twins: A Genome-Wide Analysis of DNA Methylation in Buccal Cells. Genes, 2014, 5, 347-365.	1.0	49
64	Mortality risk in men is associated with a common mutation in the methylenetetrahydrofolate reductase gene (MTHFR). European Journal of Human Genetics, 1999, 7, 197-204.	1.4	48
65	Association ofAPOE ?2/?3/?4 and promoter gene variants with dementia but not cardiovascular mortality in old age. American Journal of Medical Genetics Part A, 2002, 107, 201-208.	2.4	47
66	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. Biological Psychiatry, 2019, 86, 599-607.	0.7	47
67	Meta-analysis of four new genome scans for lipid parameters and analysis of positional candidates in positive linkage regions. European Journal of Human Genetics, 2005, 13, 1143-1153.	1.4	46
68	Association of dietary folate and vitamin B-12 intake with genome-wide DNA methylation in blood: a large-scale epigenome-wide association analysis in 5841 individuals. American Journal of Clinical Nutrition, 2019, 110, 437-450.	2.2	46
69	Markers of Endogenous Desaturase Activity and Risk of Coronary Heart Disease in the CAREMA Cohort Study. PLoS ONE, 2012, 7, e41681.	1.1	45
70	Selective Survival of Embryos Can Explain DNA Methylation Signatures of Adverse Prenatal Environments. Cell Reports, 2018, 25, 2660-2667.e4.	2.9	44
71	Association of maternal prenatal smoking GFI1-locus and cardio-metabolic phenotypes in 18,212 adults. EBioMedicine, 2018, 38, 206-216.	2.7	43
72	LDL cholesterol still a problem in old age? A Mendelian randomization study. International Journal of Epidemiology, 2015, 44, 604-612.	0.9	42

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73	DNA methylation signatures of educational attainment. Npj Science of Learning, 2018, 3, 7.	1.5	42
74	Genome-wide analysis of DNA methylation in buccal cells: a study of monozygotic twins and mQTLs. Epigenetics and Chromatin, 2018, 11, 54.	1.8	39
75	Sex-Limited Genome-Wide Linkage Scan for Body Mass Index in an Unselected Sample of 933 Australian Twin Families. Twin Research and Human Genetics, 2005, 8, 616-632.	0.3	38
76	Prolonged high-fat diet induces gradual and fat depot-specific DNA methylation changes in adult mice. Scientific Reports, 2017, 7, 43261.	1.6	38
77	Genome-wide study of DNA methylation shows alterations in metabolic, inflammatory, and cholesterol pathways in ALS. Science Translational Medicine, 2022, 14, eabj0264.	5.8	38
78	Human monocyte-to-macrophage differentiation involves highly localized gain and loss of DNA methylation at transcription factor binding sites. Epigenetics and Chromatin, 2019, 12, 34.	1.8	37
79	The effect of the Chinese Famine on type 2 diabetes mellitus epidemics. Nature Reviews Endocrinology, 2019, 15, 313-314.	4.3	35
80	IgG glycosylation and DNA methylation are interconnected with smoking. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 637-648.	1.1	33
81	Angiotensin Iâ€“converting enzyme and plasminogen activator inhibitor-1 gene variants: risk of mortality and fatal cardiovascular disease in an elderly population-based cohort. Journal of the American College of Cardiology, 1999, 34, 1176-1183.	1.2	32
82	Genetics of Human Aging: The Search for Genes Contributing to Human Longevity and Diseases of the Old. Annals of the New York Academy of Sciences, 2000, 908, 50-63.	1.8	32
83	Functional genomics analysis identifies T and NK cell activation as a driver of epigenetic clock progression. Genome Biology, 2022, 23, 24.	3.8	30
84	Evidence for a QTL on chromosome 19 influencing LDL cholesterol levels in the general population. European Journal of Human Genetics, 2003, 11, 845-850.	1.4	29
85	A characterization of cis- and trans-heritability of RNA-Seq-based gene expression. European Journal of Human Genetics, 2020, 28, 253-263.	1.4	29
86	omicsPrint: detection of data linkage errors in multiple omics studies. Bioinformatics, 2018, 34, 2142-2143.	1.8	28
87	Value of platelet pharmacogenetics in common clinical practice of patients with ST-segment elevation myocardial infarction. International Journal of Cardiology, 2013, 167, 2882-2888.	0.8	27
88	Genome-wide identification of genes regulating DNA methylation using genetic anchors for causal inference. Genome Biology, 2020, 21, 220.	3.8	27
89	Evaluation of commonly used analysis strategies for epigenome- and transcriptome-wide association studies through replication of large-scale population studies. Genome Biology, 2019, 20, 235.	3.8	26
90	Identical twins carry a persistent epigenetic signature of early genome programming. Nature Communications, 2021, 12, 5618.	5.8	26

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91	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases. Nature Communications, 2022, 13, 2408.	5.8	26
92	Chromatin remodeling of human subtelomeres and TERRA promoters upon cellular senescence. Epigenetics, 2013, 8, 512-521.	1.3	25
93	Tea and coffee consumption in relation to DNA methylation in four European cohorts. Human Molecular Genetics, 2017, 26, 3221-3231.	1.4	25
94	Effects of fatty acids on T cell function: role in atherosclerosis. Nature Reviews Cardiology, 2021, 18, 824-837.	6.1	25
95	Relationship between genome and epigenome - challenges and requirements for future research. BMC Genomics, 2014, 15, 487.	1.2	24
96	Autosomal genetic variation is associated with DNA methylation in regions variably escaping X-chromosome inactivation. Nature Communications, 2018, 9, 3738.	5.8	24
97	RNA-Seq in 296 phased trios provides a high-resolution map of genomic imprinting. BMC Biology, 2019, 17, 50.	1.7	23
98	DNA methylation signatures of aggression and closely related constructs: A meta-analysis of epigenome-wide studies across the lifespan. Molecular Psychiatry, 2021, 26, 2148-2162.	4.1	21
99	Respiratory distress syndrome and bronchopulmonary dysplasia after fetal growth restriction: Lessons from a natural experiment in identical twins. EClinicalMedicine, 2021, 32, 100725.	3.2	20
100	Integrating protein-protein interaction networks with gene-gene co-expression networks improves gene signatures for classifying breast cancer metastasis. Journal of Integrative Bioinformatics, 2011, 8, 188.	1.0	20
101	Genome-wide identification of directed gene networks using large-scale population genomics data. Nature Communications, 2018, 9, 3097.	5.8	18
102	Further Evidence for a QTL Influencing Body Mass Index on Chromosome 7p from a Genome-wide Scan in Dutch Families. Twin Research and Human Genetics, 2004, 7, 192-196.	1.5	17
103	Non-Homologous End-Joining Pathway Associated with Occurrence of Myocardial Infarction: Gene Set Analysis of Genome-Wide Association Study Data. PLoS ONE, 2013, 8, e56262.	1.1	17
104	Visit-to-visit lipid variability: Clinical significance, effects of lipid-lowering treatment, and (pharmaco) genetics. Journal of Clinical Lipidology, 2018, 12, 266-276.e3.	0.6	17
105	An alternative approach to multiple testing for methylation QTL mapping reduces the proportion of falsely identified CpGs. Bioinformatics, 2015, 31, 340-345.	1.8	15
106	Differential methylation within the major histocompatibility complex region in rheumatoid arthritis: a replication study. Rheumatology, 2014, 53, 2317-2318.	0.9	14
107	Investigating the relationships between unfavourable habitual sleep and metabolomic traits: evidence from multi-cohort multivariable regression and Mendelian randomization analyses. BMC Medicine, 2021, 19, 69.	2.3	14
108	A genome-wide association study identifies a region at chromosome 12 as a potential susceptibility locus for restenosis after percutaneous coronary intervention. Human Molecular Genetics, 2011, 20, 4748-4757.	1.4	13

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109	The tissue-specific aspect of genome-wide DNA methylation in newborn and placental tissues: implications for epigenetic epidemiologic studies. Journal of Developmental Origins of Health and Disease, 2021, 12, 113-123.	0.7	13
110	Sex-Limited Genome-Wide Linkage Scan for Body Mass Index in an Unselected Sample of 933 Australian Twin Families. , 0, .		13
111	Combined association and linkage analysis applied to theAPOE locus. Genetic Epidemiology, 2004, 26, 328-337.	0.6	12
112	Pathway Analysis Using Genome-Wide Association Study Data for Coronary Restenosis â€“ A Potential Role for the PARVB Gene. PLoS ONE, 2013, 8, e70676.	1.1	12
113	DNA methylation in peripheral tissues and left-handedness. Scientific Reports, 2022, 12, 5606.	1.6	12
114	Omixer: multivariate and reproducible sample randomization to proactively counter batch effects in omics studies. Bioinformatics, 2021, 37, 3051-3052.	1.8	11
115	Environmentally induced DNA methylation is inherited across generations in an aquatic keystone species. IScience, 2022, 25, 104303.	1.9	11
116	The multifaceted interplay between lipids and epigenetics. Current Opinion in Lipidology, 2016, 27, 288-294.	1.2	10
117	Genetically defined elevated homocysteine levels do not result in widespread changes of DNA methylation in leukocytes. PLoS ONE, 2017, 12, e0182472.	1.1	10
118	Two-locus Linkage Analysis Applied to Putative Quantitative Trait Loci for Lipoprotein(a) Levels. Twin Research and Human Genetics, 2003, 6, 322-324.	1.5	10
119	Integrating Protein-Protein Interaction Networks with Gene- Gene Co-Expression Networks improves Gene Signatures for Classifying Breast Cancer Metastasis. Journal of Integrative Bioinformatics, 2011, 8, 222-238.	1.0	9
120	TwinLIFE: The Twin Longitudinal Investigation of FEtal Discordance. Twin Research and Human Genetics, 2019, 22, 617-622.	0.3	7
121	Homocysteine levels associate with subtle changes in leukocyte DNA methylation: an epigenome-wide analysis. Epigenomics, 2017, 9, 1403-1422.	1.0	6
122	Handling blood cell composition in epigenetic studies on ageing. International Journal of Epidemiology, 2017, 46, 1717-1718.	0.9	6
123	DNA methylation differences at birth after conception through ART. Human Reproduction, 2020, 36, 248-259.	0.4	6
124	Reply to â€˜Early-life exposure to the Chinese Famine and subsequent T2DMâ€™. Nature Reviews Endocrinology, 2020, 16, 125-126.	4.3	5
125	Reply to â€˜Chinese famine and the diabetes mellitus epidemicâ€™. Nature Reviews Endocrinology, 2020, 16, 123-124.	4.3	4
126	Genome-wide analysis of constitutional DNA methylation in familial melanoma. Clinical Epigenetics, 2020, 12, 43.	1.8	4

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127	Repeat UVA exposure of human skin fibroblasts induces both a transitionary and recovery DNA methylation response. Epigenomics, 2020, 12, 563-573.	1.0	2
128	Molecular epidemiology, candidate genes versus genome-wide scans. Genes and Nutrition, 2007, 2, 27-29.	1.2	1
129	Two-locus Linkage Analysis Applied to Putative Quantitative Trait Loci for Lipoprotein(a) Levels. , 0, .		1
130	Further Evidence for a QTL Influencing Body Mass Index on Chromosome 7p from a Genome-wide Scan in Dutch Families. , 0, .		1
131	Environmental Studies as a Tool for Detecting Epigenetic Mechanisms in Schizophrenia. , 2011, , 97-118.		0