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List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

5,987
citations

186265
28
h-index

214800
47
g-index

53
all docs

53
docs citations

53
times ranked

11148
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA methylation age of blood predicts all-cause mortality in later life. <i>Genome Biology</i> , 2015, 16, 25.	8.8	928
2	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	21.4	924
3	Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 436-447.	5.1	678
4	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016, 48, 1171-1184.	21.4	362
5	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016, 17, 255.	8.8	251
6	Association of Body Mass Index with DNA Methylation and Gene Expression in Blood Cells and Relations to Cardiometabolic Disease: A Mendelian Randomization Approach. <i>PLoS Medicine</i> , 2017, 14, e1002215.	8.4	246
7	Epigenome-Wide Association Study of Fasting Blood Lipids in the Genetics of Lipid-Lowering Drugs and Diet Network Study. <i>Circulation</i> , 2014, 130, 565-572.	1.6	190
8	Integrated genome-wide analysis of expression quantitative trait loci aids interpretation of genomic association studies. <i>Genome Biology</i> , 2017, 18, 16.	8.8	151
9	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. <i>Nature Communications</i> , 2018, 9, 387.	12.8	151
10	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. <i>Circulation</i> , 2019, 140, 645-657.	1.6	151
11	Epigenome-wide association studies identify DNA methylation associated with kidney function. <i>Nature Communications</i> , 2017, 8, 1286.	12.8	145
12	Genome-wide identification of DNA methylation QTLs in whole blood highlights pathways for cardiovascular disease. <i>Nature Communications</i> , 2019, 10, 4267.	12.8	139
13	Genome-wide identification of microRNA expression quantitative trait loci. <i>Nature Communications</i> , 2015, 6, 6601.	12.8	134
14	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. <i>Hypertension</i> , 2017, 70, .	2.7	123
15	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018, 102, 375-400.	6.2	123
16	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. <i>American Journal of Human Genetics</i> , 2015, 97, 75-85.	6.2	116
17	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019, 51, 636-648.	21.4	112
18	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. <i>PLoS Genetics</i> , 2015, 11, e1005035.	3.5	107

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19	Gene Expression Signatures of Coronary Heart Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2013, 33, 1418-1426.	2.4	105
20	Epigenetic Patterns in Blood Associated With Lipid Traits Predict Incident Coronary Heart Disease Events and Are Enriched for Results From Genome-Wide Association Studies. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	104
21	Integrative network analysis reveals molecular mechanisms of blood pressure regulation. <i>Molecular Systems Biology</i> , 2015, 11, 799.	7.2	102
22	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. <i>Nature Communications</i> , 2018, 9, 2976.	12.8	85
23	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. <i>Epigenomics</i> , 2019, 11, 1487-1500.	2.1	64
24	Dissecting the Roles of MicroRNAs in Coronary Heart Disease via Integrative Genomic Analyses. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015, 35, 1011-1021.	2.4	53
25	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. <i>American Journal of Clinical Nutrition</i> , 2019, 110, 437-450.	4.7	46
26	Whole Blood DNA Methylation Signatures of Diet Are Associated With Cardiovascular Disease Risk Factors and All-Cause Mortality. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002766.	3.6	42
27	Higher diet quality relates to decelerated epigenetic aging. <i>American Journal of Clinical Nutrition</i> , 2022, 115, 163-170.	4.7	42
28	A Peripheral Blood DNA Methylation Signature of Hepatic Fat Reveals a Potential Causal Pathway for Nonalcoholic Fatty Liver Disease. <i>Diabetes</i> , 2019, 68, 1073-1083.	0.6	41
29	Messenger RNA and MicroRNA transcriptomic signatures of cardiometabolic risk factors. <i>BMC Genomics</i> , 2017, 18, 139.	2.8	33
30	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021, 12, 7174.	12.8	30
31	Common variants in signaling transcription-factor-binding sites drive phenotypic variability in red blood cell traits. <i>Nature Genetics</i> , 2020, 52, 1333-1345.	21.4	24
32	Arsenic Exposure, Blood DNA Methylation, and Cardiovascular Disease. <i>Circulation Research</i> , 2022, 131, .	4.5	20
33	Whole Blood Gene Expression Associated With Clinical Biological Age. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2019, 74, 81-88.	3.6	19
34	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. <i>Nature Communications</i> , 2021, 12, 3987.	12.8	18
35	Epigenome-wide association study of DNA methylation and microRNA expression highlights novel pathways for human complex traits. <i>Epigenetics</i> , 2020, 15, 183-198.	2.7	15
36	Transcriptome-wide association study of inflammatory biologic age. <i>Aging</i> , 2017, 9, 2288-2301.	3.1	12

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37	Meta-analysis of epigenome-wide association studies of carotid intima-media thickness. <i>European Journal of Epidemiology</i> , 2021, 36, 1143-1155.	5.7	10
38	Genetically defined elevated homocysteine levels do not result in widespread changes of DNA methylation in leukocytes. <i>PLoS ONE</i> , 2017, 12, e0182472.	2.5	10
39	Network Analysis of Gene Expression. <i>Methods in Molecular Biology</i> , 2018, 1783, 325-341.	0.9	9
40	Integrating genetic, transcriptional, and biological information provides insights into obesity. <i>International Journal of Obesity</i> , 2019, 43, 457-467.	3.4	8
41	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
42	Integrative analysis of clinical and epigenetic biomarkers of mortality. <i>Aging Cell</i> , 2022, 21, e13608.	6.7	8
43	Low oxygen saturation during sleep reduces CD1D and RAB20 expressions that are reversed by CPAP therapy. <i>EBioMedicine</i> , 2020, 56, 102803.	6.1	7
44	Homocysteine levels associate with subtle changes in leukocyte DNA methylation: an epigenome-wide analysis. <i>Epigenomics</i> , 2017, 9, 1403-1422.	2.1	6
45	Longitudinal change in blood DNA epigenetic signature after smoking cessation. <i>Epigenetics</i> , 2021, , 1-12.	2.7	5
46	Association of 71 cardiovascular disease-related plasma proteins with pulmonary function in the community. <i>PLoS ONE</i> , 2022, 17, e0266523.	2.5	0