

Roby Joehanes

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.

45
papers

3,661
citations

25
h-index

53
g-index

53
ext. papers

5,049
ext. citations

12.5
avg, IF

3.85
L-index

#	Paper	IF	Citations
45	DNA methylation age of blood predicts all-cause mortality in later life. <i>Genome Biology</i> , 2015 , 16, 25	18.3	670
44	Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , 2016 , 9, 436-447		442
43	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018 , 50, 1412-1425	36.3	386
42	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	36.3	251
41	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016 , 17, 255	18.3	171
40	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	11.6	162
39	Epigenome-wide association study of fasting blood lipids in the Genetics of Lipid-lowering Drugs and Diet Network study. <i>Circulation</i> , 2014 , 130, 565-72	16.7	161
38	Integrated genome-wide analysis of expression quantitative trait loci aids interpretation of genomic association studies. <i>Genome Biology</i> , 2017 , 18, 16	18.3	108
37	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. <i>Nature Communications</i> , 2018 , 9, 387	17.4	106
36	Genome-wide identification of microRNA expression quantitative trait loci. <i>Nature Communications</i> , 2015 , 6, 6601	17.4	104
35	Epigenome-wide association studies identify DNA methylation associated with kidney function. <i>Nature Communications</i> , 2017 , 8, 1286	17.4	92
34	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. <i>American Journal of Human Genetics</i> , 2015 , 97, 75-85	11	85
33	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 ,	8.5	85
32	A meta-analysis of gene expression signatures of blood pressure and hypertension. <i>PLoS Genetics</i> , 2015 , 11, e1005035	6	83
31	Gene expression signatures of coronary heart disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2013 , 33, 1418-26	9.4	80
30	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,		72
29	Integrative network analysis reveals molecular mechanisms of blood pressure regulation. <i>Molecular Systems Biology</i> , 2015 , 11, 799	12.2	72

28	Genome-wide identification of DNA methylation QTLs in whole blood highlights pathways for cardiovascular disease. <i>Nature Communications</i> , 2019 , 10, 4267	17.4	65
27	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. <i>Circulation</i> , 2019 , 140, 645-657	16.7	65
26	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	36.3	59
25	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	11	59
24	Dissecting the roles of microRNAs in coronary heart disease via integrative genomic analyses. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015 , 35, 1011-21	9.4	46
23	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. <i>Nature Communications</i> , 2018 , 9, 2976	17.4	45
22	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	0.9	25
21	Messenger RNA and MicroRNA transcriptomic signatures of cardiometabolic risk factors. <i>BMC Genomics</i> , 2017 , 18, 139	4.5	25
20	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. <i>Epigenomics</i> , 2019 , 11, 1487-1500	4.4	24
19	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	7	22
18	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	5.2	18
17	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	6.4	13
16	Genetically defined elevated homocysteine levels do not result in widespread changes of DNA methylation in leukocytes. <i>PLoS ONE</i> , 2017 , 12, e0182472	3.7	8
15	Common variants in signaling transcription-factor-binding sites drive phenotypic variability in red blood cell traits. <i>Nature Genetics</i> , 2020 , 52, 1333-1345	36.3	8
14	Transcriptome-wide association study of inflammatory biologic age. <i>Aging</i> , 2017 , 9, 2288-2301	5.6	5
13	Higher diet quality relates to decelerated epigenetic aging. <i>American Journal of Clinical Nutrition</i> , 2021 ,	7	5
12	Epigenome-wide association study of DNA methylation and microRNA expression highlights novel pathways for human complex traits. <i>Epigenetics</i> , 2020 , 15, 183-198	5.7	5
11	Homocysteine levels associate with subtle changes in leukocyte DNA methylation: an epigenome-wide analysis. <i>Epigenomics</i> , 2017 , 9, 1403-1422	4.4	4

10	Meta-analysis of epigenome-wide association studies of carotid intima-media thickness. <i>European Journal of Epidemiology</i> , 2021 , 36, 1143-1155	12.1	4
9	Integrating genetic, transcriptional, and biological information provides insights into obesity. <i>International Journal of Obesity</i> , 2019 , 43, 457-467	5.5	3
8	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. <i>Nature Communications</i> , 2021 , 12, 3987	17.4	3
7	Network Analysis of Gene Expression. <i>Methods in Molecular Biology</i> , 2018 , 1783, 325-341	1.4	3
6	Low oxygen saturation during sleep reduces CD1D and RAB20 expressions that are reversed by CPAP therapy. <i>EBioMedicine</i> , 2020 , 56, 102803	8.8	2
5	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. <i>Nature Communications</i> , 2021 , 12, 7173	17.4	1
4	Integrative analysis of clinical and epigenetic biomarkers of mortality.. <i>Aging Cell</i> , 2022 , e13608	9.9	1
3	Longitudinal change in blood DNA epigenetic signature after smoking cessation. <i>Epigenetics</i> , 2021 , 1-12	5.7	0
2	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021 , 12, 7174	17.4	0
1	Association of 71 cardiovascular disease-related plasma proteins with pulmonary function in the community.. <i>PLoS ONE</i> , 2022 , 17, e0266523	3.7	