

Roby Joehanes

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/262903/publications.pdf>

Version: 2024-02-01

46
papers

5,987
citations

185998

28
h-index

214527

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. | 3.8 | 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. | 9.4 | 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. | 9.4 | 362 |
| 5 | DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016, 17, 255. | 3.8 | 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. | 3.9 | 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. | 3.8 | 151 |
| 9 | GWAS of epigenetic aging rates in blood reveals a critical role for TERT. <i>Nature Communications</i> , 2018, 9, 387. | 5.8 | 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. | 5.8 | 145 |
| 12 | Genome-wide identification of DNA methylation QTLs in whole blood highlights pathways for cardiovascular disease. <i>Nature Communications</i> , 2019, 10, 4267. | 5.8 | 139 |
| 13 | Genome-wide identification of microRNA expression quantitative trait loci. <i>Nature Communications</i> , 2015, 6, 6601. | 5.8 | 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, . | 1.3 | 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. | 2.6 | 123 |
| 16 | Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. <i>American Journal of Human Genetics</i> , 2015, 97, 75-85. | 2.6 | 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. | 9.4 | 112 |
| 18 | A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. <i>PLoS Genetics</i> , 2015, 11, e1005035. | 1.5 | 107 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | Gene Expression Signatures of Coronary Heart Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2013, 33, 1418-1426. | 1.1 | 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. | 3.2 | 102 |
| 22 | Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. <i>Nature Communications</i> , 2018, 9, 2976. | 5.8 | 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. | 1.0 | 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. | 1.1 | 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. | 2.2 | 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. | 1.6 | 42 |
| 27 | Higher diet quality relates to decelerated epigenetic aging. <i>American Journal of Clinical Nutrition</i> , 2022, 115, 163-170. | 2.2 | 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. | 0.3 | 41 |
| 29 | Messenger RNA and MicroRNA transcriptomic signatures of cardiometabolic risk factors. <i>BMC Genomics</i> , 2017, 18, 139. | 1.2 | 33 |
| 30 | Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021, 12, 7174. | 5.8 | 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. | 9.4 | 24 |
| 32 | Arsenic Exposure, Blood DNA Methylation, and Cardiovascular Disease. <i>Circulation Research</i> , 2022, 131, . | 2.0 | 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. | 1.7 | 19 |
| 34 | A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. <i>Nature Communications</i> , 2021, 12, 3987. | 5.8 | 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. | 1.3 | 15 |
| 36 | Transcriptome-wide association study of inflammatory biologic age. <i>Aging</i> , 2017, 9, 2288-2301. | 1.4 | 12 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 37 | Meta-analysis of epigenome-wide association studies of carotid intima-media thickness. <i>European Journal of Epidemiology</i> , 2021, 36, 1143-1155. | 2.5 | 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. | 1.1 | 10 |
| 39 | Network Analysis of Gene Expression. <i>Methods in Molecular Biology</i> , 2018, 1783, 325-341. | 0.4 | 9 |
| 40 | Integrating genetic, transcriptional, and biological information provides insights into obesity. <i>International Journal of Obesity</i> , 2019, 43, 457-467. | 1.6 | 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. | 5.8 | 8 |
| 42 | Integrative analysis of clinical and epigenetic biomarkers of mortality. <i>Aging Cell</i> , 2022, 21, e13608. | 3.0 | 8 |
| 43 | Low oxygen saturation during sleep reduces CD1D and RAB20 expressions that are reversed by CPAP therapy. <i>EBioMedicine</i> , 2020, 56, 102803. | 2.7 | 7 |
| 44 | Homocysteine levels associate with subtle changes in leukocyte DNA methylation: an epigenome-wide analysis. <i>Epigenomics</i> , 2017, 9, 1403-1422. | 1.0 | 6 |
| 45 | Longitudinal change in blood DNA epigenetic signature after smoking cessation. <i>Epigenetics</i> , 2021, , 1-12. | 1.3 | 5 |
| 46 | Association of 71 cardiovascular disease-related plasma proteins with pulmonary function in the community. <i>PLoS ONE</i> , 2022, 17, e0266523. | 1.1 | 0 |