

Devin M Absher

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

17,740
citations

147801

31
h-index

223800

46
g-index

48
all docs

48
docs citations

48
times ranked

26335
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	27.8	3,823
2	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013, 45, 1274-1283.	21.4	2,641
3	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	21.4	2,634
4	Large-scale association analysis identifies new risk loci for coronary artery disease. <i>Nature Genetics</i> , 2013, 45, 25-33.	21.4	1,439
5	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010, 42, 949-960.	21.4	836
6	DNA methylation-based measures of biological age: meta-analysis predicting time to death. <i>Aging</i> , 2016, 8, 1844-1865.	3.1	786
7	Common variants associated with plasma triglycerides and risk for coronary artery disease. <i>Nature Genetics</i> , 2013, 45, 1345-1352.	21.4	754
8	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013, 45, 501-512.	21.4	578
9	An epigenetic clock analysis of race/ethnicity, sex, and coronary heart disease. <i>Genome Biology</i> , 2016, 17, 171.	8.8	535
10	Epigenetic clock analysis of diet, exercise, education, and lifestyle factors. <i>Aging</i> , 2017, 9, 419-446.	3.1	521
11	Menopause accelerates biological aging. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9327-9332.	7.1	363
12	Genome-Wide DNA Methylation Analysis of Systemic Lupus Erythematosus Reveals Persistent Hypomethylation of Interferon Genes and Compositional Changes to CD4+ T-cell Populations. <i>PLoS Genetics</i> , 2013, 9, e1003678.	3.5	312
13	Differential DNA methylation with age displays both common and dynamic features across human tissues that are influenced by CpG landscape. <i>Genome Biology</i> , 2013, 14, R102.	9.6	291
14	Epigenome-wide association study (EWAS) of BMI, BMI change and waist circumference in African American adults identifies multiple replicated loci. <i>Human Molecular Genetics</i> , 2015, 24, 4464-4479.	2.9	289
15	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
16	DNA methylation profiling reveals novel biomarkers and important roles for DNA methyltransferases in prostate cancer. <i>Genome Research</i> , 2011, 21, 1017-1027.	5.5	206
17	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
18	Epigenome-wide study identifies novel methylation loci associated with body mass index and waist circumference. <i>Obesity</i> , 2015, 23, 1493-1501.	3.0	152

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19	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. <i>Circulation</i> , 2019, 140, 645-657.	1.6	151
20	Epigenome-Wide Association Study of Fasting Measures of Glucose, Insulin, and HOMA-IR in the Genetics of Lipid Lowering Drugs and Diet Network Study. <i>Diabetes</i> , 2014, 63, 801-807.	0.6	149
21	Genome-wide association study meta-analysis identifies five new loci for systemic lupus erythematosus. <i>Arthritis Research and Therapy</i> , 2018, 20, 100.	3.5	102
22	Epigenome-wide association study of rheumatoid arthritis identifies differentially methylated loci in B cells. <i>Human Molecular Genetics</i> , 2017, 26, 2803-2811.	2.9	67
23	Methylation at CPT1A locus is associated with lipoprotein subfraction profiles. <i>Journal of Lipid Research</i> , 2014, 55, 1324-1330.	4.2	65
24	DNA Methylation Patterns Are Associated with ω -3 Fatty Acid Intake in Yup'ik People. <i>Journal of Nutrition</i> , 2014, 144, 425-430.	2.9	59
25	Epigenomics and metabolomics reveal the mechanism of the APOA2-saturated fat intake interaction affecting obesity. <i>American Journal of Clinical Nutrition</i> , 2018, 108, 188-200.	4.7	54
26	Association of DNA Methylation at CPT1A Locus with Metabolic Syndrome in the Genetics of Lipid Lowering Drugs and Diet Network (GOLDN) Study. <i>PLoS ONE</i> , 2016, 11, e0145789.	2.5	54
27	Carbohydrate and fat intake associated with risk of metabolic diseases through epigenetics of CPT1A. <i>American Journal of Clinical Nutrition</i> , 2020, 112, 1200-1211.	4.7	48
28	DNA methylation profiling reveals novel diagnostic biomarkers in renal cell carcinoma. <i>BMC Medicine</i> , 2014, 12, 235.	5.5	42
29	Leukocyte telomere length, T cell composition and DNA methylation age. <i>Aging</i> , 2017, 9, 1983-1995.	3.1	42
30	Epigenome-wide association study of triglyceride postprandial responses to a high-fat dietary challenge. <i>Journal of Lipid Research</i> , 2016, 57, 2200-2207.	4.2	40
31	Genetic variants modify the effect of age on APOE methylation in the genetics of lipid lowering drugs and diet network study. <i>Aging Cell</i> , 2015, 14, 49-59.	6.7	34
32	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor α . <i>JAMA Cardiology</i> , 2018, 3, 463.	6.1	33
33	Population-specific Patterns of Epigenetic Defects in the B Cell Lineage in Patients With Systemic Lupus Erythematosus. <i>Arthritis and Rheumatology</i> , 2020, 72, 282-291.	5.6	27
34	Genomics of Post-Prandial Lipidomic Phenotypes in the Genetics of Lipid Lowering Drugs and Diet Network (GOLDN) Study. <i>PLoS ONE</i> , 2014, 9, e99509.	2.5	21
35	Lipid changes due to fenofibrate treatment are not associated with changes in DNA methylation patterns in the GOLDN study. <i>Frontiers in Genetics</i> , 2015, 6, 304.	2.3	20
36	Skewed allelic expression on X chromosome associated with aberrant expression of XIST on systemic lupus erythematosus lymphocytes. <i>Human Molecular Genetics</i> , 2020, 29, 2523-2534.	2.9	19

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37	Heritable DNA Methylation in CD4+ Cells among Complex Families Displays Genetic and Non-Genetic Effects. PLoS ONE, 2016, 11, e0165488.	2.5	19
38	Estimation of Cell-Type Composition Including T and B Cell Subtypes for Whole Blood Methylation Microarray Data. Frontiers in Genetics, 2016, 7, 23.	2.3	18
39	An epigenome-wide association study of inflammatory response to fenofibrate in the Genetics of Lipid Lowering Drugs and Diet Network. Pharmacogenomics, 2017, 18, 1333-1341.	1.3	16
40	Targeted Sequencing of Large Genomic Regions with CATCH-Seq. PLoS ONE, 2014, 9, e111756.	2.5	16
41	<i>PRKCZ</i> methylation is associated with sunlight exposure in a North American but not a Mediterranean population. Chronobiology International, 2014, 31, 1034-1040.	2.0	12
42	Genome- and CD4 + T-cell methylome-wide association study of circulating trimethylamine-N-oxide in the Genetics of Lipid Lowering Drugs and Diet Network (GOLDN). Journal of Nutrition & Intermediary Metabolism, 2017, 8, 1-7.	1.7	11
43	Data for GAW20: genome-wide DNA sequence variation and epigenome-wide DNA methylation before and after fenofibrate treatment in a family study of metabolic phenotypes. BMC Proceedings, 2018, 12, 35.	1.6	11
44	STAT3-mediated allelic imbalance of novel genetic variant Rs1047643 and B-cell-specific super-enhancer in association with systemic lupus erythematosus. ELife, 2022, 11, .	6.0	5
45	dCATCH-Seq: improved sequencing of large continuous genomic targets with double-hybridization. BMC Genomics, 2017, 18, 811.	2.8	4
46	Evaluation of population-level pharmacogenetic actionability in Alabama. Clinical and Translational Science, 2021, 14, 2327-2338.	3.1	4