

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	STAT3-mediated allelic imbalance of novel genetic variant Rs1047643 and B-cell-specific super-enhancer in association with systemic lupus erythematosus. <i>ELife</i> , 2022, 11, .	6.0	5
2	Evaluation of population-level pharmacogenetic actionability in Alabama. <i>Clinical and Translational Science</i> , 2021, 14, 2327-2338.	3.1	4
3	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
4	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
5	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
6	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. <i>Circulation</i> , 2019, 140, 645-657.	1.6	151
7	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor β . <i>JAMA Cardiology</i> , 2018, 3, 463.	6.1	33
8	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. <i>BMC Proceedings</i> , 2018, 12, 35.	1.6	11
9	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
10	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
11	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). <i>Journal of Nutrition & Intermediary Metabolism</i> , 2017, 8, 1-7.	1.7	11
12	An epigenome-wide association study of inflammatory response to fenofibrate in the Genetics of Lipid Lowering Drugs and Diet Network. <i>Pharmacogenomics</i> , 2017, 18, 1333-1341.	1.3	16
13	dCATCH-Seq: improved sequencing of large continuous genomic targets with double-hybridization. <i>BMC Genomics</i> , 2017, 18, 811.	2.8	4
14	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
15	Epigenetic clock analysis of diet, exercise, education, and lifestyle factors. <i>Aging</i> , 2017, 9, 419-446.	3.1	521
16	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
17	Leukocyte telomere length, T cell composition and DNA methylation age. <i>Aging</i> , 2017, 9, 1983-1995.	3.1	42
18	Estimation of Cell-Type Composition Including T and B Cell Subtypes for Whole Blood Methylation Microarray Data. <i>Frontiers in Genetics</i> , 2016, 7, 23.	2.3	18

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19	An epigenetic clock analysis of race/ethnicity, sex, and coronary heart disease. <i>Genome Biology</i> , 2016, 17, 171.	8.8	535
20	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
21	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
22	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
23	Heritable DNA Methylation in CD4+ Cells among Complex Families Displays Genetic and Non-Genetic Effects. <i>PLoS ONE</i> , 2016, 11, e0165488.	2.5	19
24	DNA methylation-based measures of biological age: meta-analysis predicting time to death. <i>Aging</i> , 2016, 8, 1844-1865.	3.1	786
25	Genetic variants modify the effect of age on <i>APOE</i> methylation in the <i>Genetics of Lipid Lowering Drugs and Diet Network</i> study. <i>Aging Cell</i> , 2015, 14, 49-59.	6.7	34
26	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
27	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
28	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	27.8	3,823
29	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
30	DNA methylation profiling reveals novel diagnostic biomarkers in renal cell carcinoma. <i>BMC Medicine</i> , 2014, 12, 235.	5.5	42
31	Methylation at CPT1A locus is associated with lipoprotein subfraction profiles. <i>Journal of Lipid Research</i> , 2014, 55, 1324-1330.	4.2	65
32	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
33	<i>PRKCZ</i> methylation is associated with sunlight exposure in a North American but not a Mediterranean population. <i>Chronobiology International</i> , 2014, 31, 1034-1040.	2.0	12
34	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
35	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
36	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

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37	Targeted Sequencing of Large Genomic Regions with CATCH-Seq. PLoS ONE, 2014, 9, e111756.	2.5	16
38	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
39	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	21.4	754
40	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	21.4	1,439
41	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	21.4	578
42	Genome-Wide DNA Methylation Analysis of Systemic Lupus Erythematosus Reveals Persistent Hypomethylation of Interferon Genes and Compositional Changes to CD4+ T-cell Populations. PLoS Genetics, 2013, 9, e1003678.	3.5	312
43	Differential DNA methylation with age displays both common and dynamic features across human tissues that are influenced by CpG landscape. Genome Biology, 2013, 14, R102.	9.6	291
44	DNA methylation profiling reveals novel biomarkers and important roles for DNA methyltransferases in prostate cancer. Genome Research, 2011, 21, 1017-1027.	5.5	206
45	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	21.4	836
46	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	21.4	2,634