Melissa A Richard

List of Publications by Year
in descending order

36 papers	1,363 citations	516710 16 h-index	454955 30 g-index
40 all docs	40 docs citations	40 times ranked	3906 citing authors

#	Article	IF	Citations
1	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	6.2	154
2	Genome-wide identification of DNA methylation QTLs in whole blood highlights pathways for cardiovascular disease. Nature Communications, 2019, 10, 4267.	12.8	139
3	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	6.2	123
4	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
5	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
6	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	21.4	91
7	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
8	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	6.2	82
9	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
10	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	12.8	62
11	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	6.2	60
12	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. American Journal of Human Genetics, 2016, 99, 22-39.	6.2	50
13	Exosome miR-371b-5p promotes proliferation of lung alveolar progenitor type II cells by using PTEN to orchestrate the PI3K/Akt signaling. Stem Cell Research and Therapy, 2017, 8, 138.	5.5	43
14	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
15	Fine mapping of QT interval regions in global populations refines previously identified QT interval loci and identifies signals unique to African and Hispanic descent populations. Heart Rhythm, 2017, 14, 572-580.	0.7	19
16	An Empirical Comparison of Joint and Stratified Frameworks for Studying G Ã— E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Geneâ€Lifestyle Interactions Working Group. Genetic Epidemiology, 2016, 40, 404-415.	1.3	18
17	Discovery and fine-mapping of loci associated with MUFAs through trans-ethnic meta-analysis in Chinese and European populations. Journal of Lipid Research, 2017, 58, 974-981.	4.2	18
18	Genetic variation in POT1 and risk of thyroid subsequent malignant neoplasm: A report from the Childhood Cancer Survivor Study. PLoS ONE, 2020, 15, e0228887.	2.5	18

#	Article	IF	Citations
19	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	7.9	17
20	Associations of plasma clusterin and Alzheimerâ€™s disease-related MRI markers in adults at mid-life: The CARDIA Brain MRI sub-study. PLoS ONE, 2018, 13, e0190478.	2.5	15
21	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
22	Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. Circulation Genomic and Precision Medicine, 2020, 13, e002772.	3.6	11
23	Altered mechanisms of genital development identified through integration of DNA methylation and genomic measures in hypospadias. Scientific Reports, 2020, 10, 12715.	3.3	10
24	Epilepsy Risk Prediction Model for Patients With Tuberous Sclerosis Complex. Pediatric Neurology, 2020, 113, 46-50.	2.1	9
25	Utilization of archived neonatal dried blood spots for genome-wide genotyping. PLoS ONE, 2020, 15, e0229352.	2.5	7
26	Genetic variation in the body mass index of adult survivors of childhood acute lymphoblastic leukemia: A report from the Childhood Cancer Survivor Study and the St. Jude Lifetime Cohort. Cancer, 2021, 127, 310-318.	4.1	6
27	The role of genetic variation in DGKK on moderate and severe hypospadias. Birth Defects Research, 2019, 111, 932-937.	1.5	5
28	Short NK- and NaÃ¯ve T-Cell Telomere Length Is Associated with Thyroid Cancer in Childhood Cancer Survivors: A Report from the Childhood Cancer Survivor Study. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 453-460.	2.5	3
29	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. Human Genetics and Genomics Advances, 2021, 2, 100013.	1.7	2
30	A Role for Genetics in Racial Disparities of Therapy-Related Cardiomyopathy. Cancer Research, 2021, 81, 2272-2274.	0.9	1
31	Genetic and treatment risks for diabetes mellitus (DM) in survivors of childhood cancer: A report from the Childhood Cancer Survivor Study (CCSS) and St. Jude Lifetime (SJLIFE) cohorts.. Journal of Clinical Oncology, 2021, 39, 10014-10014.	1.6	0
32	Utilization of archived neonatal dried blood spots for genome-wide genotyping. , 2020, 15, e0229352.		0
33	Utilization of archived neonatal dried blood spots for genome-wide genotyping. , 2020, 15, e0229352.		0
34	Utilization of archived neonatal dried blood spots for genome-wide genotyping. , 2020, 15, e0229352.		0
35	Utilization of archived neonatal dried blood spots for genome-wide genotyping. , 2020, 15, e0229352.		0
36	Associations between DNA methylation age and chronic health conditions in survivors of childhood leukemia and CNS tumor.. Journal of Clinical Oncology, 2022, 40, 12088-12088.	1.6	0