

# Melanie Waldenberger

## List of Publications by Year in descending order

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Version: 2024-02-01

216  
papers

23,659  
citations

14614

66  
h-index

10708

138  
g-index

247  
all docs

247  
docs citations

247  
times ranked

36367  
citing authors

#	ARTICLE	IF	CITATIONS
1	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	9.4	1,818
2	An atlas of genetic influences on human blood metabolites. <i>Nature Genetics</i> , 2014, 46, 543-550.	9.4	1,084
3	DNA methylation-based measures of biological age: meta-analysis predicting time to death. <i>Aging</i> , 2016, 8, 1844-1865.	1.4	786
4	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , 2017, 541, 81-86.	13.7	743
5	Tobacco Smoking Leads to Extensive Genome-Wide Changes in DNA Methylation. <i>PLoS ONE</i> , 2013, 8, e63812.	1.1	694
6	DNA methylation and body-mass index: a genome-wide analysis. <i>Lancet</i> , The, 2014, 383, 1990-1998.	6.3	686
7	Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 436-447.	5.1	678
8	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2013, 45, 145-154.	9.4	675
9	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. <i>Nature Communications</i> , 2016, 7, 11122.	5.8	576
10	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	9.4	549
11	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	13.7	548
12	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015, 6, 8570.	5.8	533
13	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766.	9.4	470
14	The prevalence of metabolic syndrome and metabolically healthy obesity in Europe: a collaborative analysis of ten large cohort studies. <i>BMC Endocrine Disorders</i> , 2014, 14, 9.	0.9	440
15	Coding Variation in <i>ANGPTL4</i> , <i>LPL</i> , and <i>SVEP1</i> and the Risk of Coronary Disease. <i>New England Journal of Medicine</i> , 2016, 374, 1134-1144.	13.9	427
16	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016, 7, 10023.	5.8	412
17	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	1.5	331
18	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , 2018, 103, 691-706.	2.6	326

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19	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. <i>Nature Genetics</i> , 2015, 47, 1282-1293.	9.4	294
20	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. <i>Nature Genetics</i> , 2014, 46, 826-836.	9.4	281
21	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. <i>Nature Genetics</i> , 2017, 49, 946-952.	9.4	279
22	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 126-135.	1.1	278
23	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016, 17, 255.	3.8	251
24	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	9.4	251
25	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015, 20, 647-656.	4.1	235
26	Meta-analysis of genome-wide association studies identifies ten loci influencing allergic sensitization. <i>Nature Genetics</i> , 2013, 45, 902-906.	9.4	221
27	DNA methylation signatures in peripheral blood strongly predict all-cause mortality. <i>Nature Communications</i> , 2017, 8, 14617.	5.8	221
28	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. <i>Lancet Neurology</i> , The, 2016, 15, 174-184.	4.9	217
29	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2017, 69, 823-836.	1.2	214
30	Prenatal and early life influences on epigenetic age in children: a study of mother-offspring pairs from two cohort studies. <i>Human Molecular Genetics</i> , 2016, 25, 191-201.	1.4	205
31	Epigenetic upregulation of FKBP5 by aging and stress contributes to NF- $\kappa$ B-driven inflammation and cardiovascular risk. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11370-11379.	3.3	193
32	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. <i>Nature Communications</i> , 2014, 5, 4926.	5.8	192
33	DataSHIELD: taking the analysis to the data, not the data to the analysis. <i>International Journal of Epidemiology</i> , 2014, 43, 1929-1944.	0.9	188
34	A metabolic profile of all-cause mortality risk identified in an observational study of 44,168 individuals. <i>Nature Communications</i> , 2019, 10, 3346.	5.8	188
35	Prenatal Exposure to Maternal Cigarette Smoking and DNA Methylation: Epigenome-Wide Association in a Discovery Sample of Adolescents and Replication in an Independent Cohort at Birth through 17 Years of Age. <i>Environmental Health Perspectives</i> , 2015, 123, 193-199.	2.8	178
36	Characterization of whole-genome autosomal differences of DNA methylation between men and women. <i>Epigenetics and Chromatin</i> , 2015, 8, 43.	1.8	176

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37	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	13.7	173
38	Epigenetics meets metabolomics: an epigenome-wide association study with blood serum metabolic traits. <i>Human Molecular Genetics</i> , 2014, 23, 534-545.	1.4	169
39	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, 14977.	5.8	169
40	DNA Methylation of Lipid-Related Genes Affects Blood Lipid Levels. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 334-342.	5.1	151
41	Genome-Wide Analysis of DNA Methylation and Fine Particulate Matter Air Pollution in Three Study Populations: KORA F3, KORA F4, and the Normative Aging Study. <i>Environmental Health Perspectives</i> , 2016, 124, 983-990.	2.8	150
42	Socioeconomic position, lifestyle habits and biomarkers of epigenetic aging: a multi-cohort analysis. <i>Aging</i> , 2019, 11, 2045-2070.	1.4	137
43	Novel multiple sclerosis susceptibility loci implicated in epigenetic regulation. <i>Science Advances</i> , 2016, 2, e1501678.	4.7	133
44	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019, 10, 4130.	5.8	133
45	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. <i>Diabetes</i> , 2016, 65, 803-817.	0.3	131
46	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
47	Genome-wide methylation data mirror ancestry information. <i>Epigenetics and Chromatin</i> , 2017, 10, 1.	1.8	120
48	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1435-1448.	1.2	113
49	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
50	Cystatin C and Cardiovascular Disease. <i>Journal of the American College of Cardiology</i> , 2016, 68, 934-945.	1.2	109
51	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. <i>PLoS Genetics</i> , 2015, 11, e1005035.	1.5	107
52	Data harmonization and federated analysis of population-based studies: the BioSHaRE project. <i>Emerging Themes in Epidemiology</i> , 2013, 10, 12.	1.2	105
53	Telomere length in circulating leukocytes is associated with lung function and disease. <i>European Respiratory Journal</i> , 2014, 43, 983-992.	3.1	103
54	Restless Legs Syndrome-associated intronic common variant in <i>Meis1</i> alters enhancer function in the developing telencephalon. <i>Genome Research</i> , 2014, 24, 592-603.	2.4	102

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55	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. <i>Scientific Reports</i> , 2017, 7, 45040.	1.6	98
56	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. <i>Nature Communications</i> , 2017, 8, 15805.	5.8	95
57	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018, 13, e0198166.	1.1	94
58	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.	3.8	90
59	Pre-Analytical Sample Quality: Metabolite Ratios as an Intrinsic Marker for Prolonged Room Temperature Exposure of Serum Samples. <i>PLoS ONE</i> , 2015, 10, e0121495.	1.1	88
60	The dynamics of smoking-related disturbed methylation: a two time-point study of methylation change in smokers, non-smokers and former smokers. <i>BMC Genomics</i> , 2017, 18, 805.	1.2	85
61	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019, 188, 1033-1054.	1.6	85
62	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	5.8	84
63	Comprehensive catalog of European biobanks. <i>Nature Biotechnology</i> , 2011, 29, 795-797.	9.4	83
64	Genome-Wide Association Study with Targeted and Non-targeted NMR Metabolomics Identifies 15 Novel Loci of Urinary Human Metabolic Individuality. <i>PLoS Genetics</i> , 2015, 11, e1005487.	1.5	83
65	Association between DNA Methylation in Whole Blood and Measures of Glucose Metabolism: KORA F4 Study. <i>PLoS ONE</i> , 2016, 11, e0152314.	1.1	81
66	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. <i>JAMA Psychiatry</i> , 2018, 75, 949.	6.0	78
67	A Whole-Blood Transcriptome Meta-Analysis Identifies Gene Expression Signatures of Cigarette Smoking. <i>Human Molecular Genetics</i> , 2016, 25, ddw288.	1.4	76
68	Genetic Evidence for <i>PLASMINOGEN</i> as a Shared Genetic Risk Factor of Coronary Artery Disease and Periodontitis. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 159-167.	5.1	74
69	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. <i>Human Molecular Genetics</i> , 2016, 25, 358-370.	1.4	73
70	Metabolomics approach reveals effects of antihypertensives and lipid-lowering drugs on the human metabolism. <i>European Journal of Epidemiology</i> , 2014, 29, 325-336.	2.5	72
71	Long-term Air Pollution Exposure, Genome-wide DNA Methylation and Lung Function in the LifeLines Cohort Study. <i>Environmental Health Perspectives</i> , 2018, 126, 027004.	2.8	71
72	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. <i>Nature Communications</i> , 2018, 9, 2904.	5.8	71

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73	Discovery and Fine Mapping of Serum Protein Loci through Transethnic Meta-analysis. <i>American Journal of Human Genetics</i> , 2012, 91, 744-753.	2.6	69
74	Multi-omic signature of body weight change: results from a population-based cohort study. <i>BMC Medicine</i> , 2015, 13, 48.	2.3	69
75	Blood microRNA profile associates with the levels of serum lipids and metabolites associated with glucose metabolism and insulin resistance and pinpoints pathways underlying metabolic syndrome. <i>Molecular and Cellular Endocrinology</i> , 2014, 391, 41-49.	1.6	65
76	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
77	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376.	5.8	64
78	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. <i>PLoS ONE</i> , 2015, 10, e0119752.	1.1	64
79	Blood hsa-miR-122-5p and hsa-miR-885-5p levels associate with fatty liver and related lipoprotein metabolism in the Young Finns Study. <i>Scientific Reports</i> , 2016, 6, 38262.	1.6	62
80	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. <i>Nature Communications</i> , 2019, 10, 5121.	5.8	62
81	16p11.2 600 kb Duplications confer risk for typical and atypical Rolandic epilepsy. <i>Human Molecular Genetics</i> , 2014, 23, 6069-6080.	1.4	61
82	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function. <i>Nature Genetics</i> , 2022, 54, 18-29.	9.4	60
83	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020, 11, 2542.	5.8	59
84	Methylome-wide association study provides evidence of particulate matter air pollution-associated DNA methylation. <i>Environment International</i> , 2019, 132, 104723.	4.8	58
85	Epigenetics meets proteomics in an epigenome-wide association study with circulating blood plasma protein traits. <i>Nature Communications</i> , 2020, 11, 15.	5.8	57
86	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. <i>Human Molecular Genetics</i> , 2014, 23, 2490-2497.	1.4	56
87	Compound Heterozygosity of Low-Frequency Promoter Deletions and Rare Loss-of-Function Mutations in TXNL4A Causes Burn-McKeown Syndrome. <i>American Journal of Human Genetics</i> , 2014, 95, 698-707.	2.6	55
88	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. <i>Blood</i> , 2015, 126, e19-e29.	0.6	55
89	Whole blood microRNA levels associate with glycemic status and correlate with target mRNAs in pathways important to type 2 diabetes. <i>Scientific Reports</i> , 2019, 9, 8887.	1.6	55
90	MASP1, THBS1, GPLD1 and ApoA-IV are novel biomarkers associated with prediabetes: the KORA F4 study. <i>Diabetologia</i> , 2016, 59, 1882-1892.	2.9	54

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91	Genome-Wide Association Analysis of Young-Onset Stroke Identifies a Locus on Chromosome 10q25 Near <i>HABP2</i> . <i>Stroke</i> , 2016, 47, 307-316.	1.0	54
92	DeepWAS: Multivariate genotype-phenotype associations by directly integrating regulatory information using deep learning. <i>PLoS Computational Biology</i> , 2020, 16, e1007616.	1.5	54
93	Methylation of the FKBP5 gene in association with FKBP5 genotypes, childhood maltreatment and depression. <i>Neuropsychopharmacology</i> , 2019, 44, 930-938.	2.8	52
94	Metabolite profiling reveals new insights into the regulation of serum urate in humans. <i>Metabolomics</i> , 2014, 10, 141-151.	1.4	51
95	A genome-wide association study reveals 2 new susceptibility loci for atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 136, 802-806.	1.5	51
96	Evidence for Stress-like Alterations in the HPA-Axis in Women Taking Oral Contraceptives. <i>Scientific Reports</i> , 2017, 7, 14111.	1.6	51
97	Revealing the role of the human blood plasma proteome in obesity using genetic drivers. <i>Nature Communications</i> , 2021, 12, 1279.	5.8	50
98	Epigenome-wide association study of lung function level and its change. <i>European Respiratory Journal</i> , 2019, 54, 1900457.	3.1	49
99	Alcohol consumption is associated with widespread changes in blood DNA methylation: Analysis of cross-sectional and longitudinal data. <i>Addiction Biology</i> , 2021, 26, e12855.	1.4	49
100	Genome-wide association analysis in dilated cardiomyopathy reveals two new players in systolic heart failure on chromosomes 3p25.1 and 22q11.23. <i>European Heart Journal</i> , 2021, 42, 2000-2011.	1.0	49
101	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including <i>ADAMTS6</i> . <i>Genome Biology</i> , 2018, 19, 87.	3.8	47
102	FTO, obesity and the adolescent brain. <i>Human Molecular Genetics</i> , 2013, 22, 1050-1058.	1.4	46
103	Common coding variant in <i>SERPINA1</i> increases the risk for large artery stroke. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 3613-3618.	3.3	46
104	DNA methylation in human lipid metabolism and related diseases. <i>Current Opinion in Lipidology</i> , 2018, 29, 116-124.	1.2	43
105	Anxiety Associated Increased CpG Methylation in the Promoter of <i>Asb1</i> : A Translational Approach Evidenced by Epidemiological and Clinical Studies and a Murine Model. <i>Neuropsychopharmacology</i> , 2018, 43, 342-353.	2.8	43
106	Association of maternal prenatal smoking <i>GFI1</i> -locus and cardio-metabolic phenotypes in 18,212 adults. <i>EBioMedicine</i> , 2018, 38, 206-216.	2.7	43
107	Epigenetic Link Between Statin Therapy and Type 2 Diabetes. <i>Diabetes Care</i> , 2020, 43, 875-884.	4.3	43
108	Circulating metabolic biomarkers of renal function in diabetic and non-diabetic populations. <i>Scientific Reports</i> , 2018, 8, 15249.	1.6	42

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109	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
110	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. <i>Kidney International</i> , 2021, 99, 926-939.	2.6	42
111	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 981-994.	3.0	39
112	Improvement of myocardial infarction risk prediction via inflammation-associated metabolite biomarkers. <i>Heart</i> , 2017, 103, 1278-1285.	1.2	38
113	Fifteen Genetic Loci Associated With the Electrocardiographic P Wave. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	38
114	Protein markers and risk of type 2 diabetes and prediabetes: a targeted proteomics approach in the KORA F4/FF4 study. <i>European Journal of Epidemiology</i> , 2019, 34, 409-422.	2.5	37
115	Impact of long-term storage and freeze-thawing on eight circulating microRNAs in plasma samples. <i>PLoS ONE</i> , 2020, 15, e0227648.	1.1	37
116	Epigenetic scores for the circulating proteome as tools for disease prediction. <i>ELife</i> , 2022, 11, .	2.8	37
117	DNA methylation and lipid metabolism: an EWAS of 226 metabolic measures. <i>Clinical Epigenetics</i> , 2021, 13, 7.	1.8	36
118	Differences in Biomarkers of Inflammation Between Novel Subgroups of Recent-Onset Diabetes. <i>Diabetes</i> , 2021, 70, 1198-1208.	0.3	36
119	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. <i>Nature Communications</i> , 2021, 12, 2830.	5.8	35
120	Mitochondrial Genetic Variants Identified to Be Associated with BMI in Adults. <i>PLoS ONE</i> , 2014, 9, e105116.	1.1	34
121	Selected single-nucleotide polymorphisms in <i>FOXE1</i> , <i>SERPINA5</i> , <i>FTO</i> , <i>EVPL</i> , <i>TICAM1</i> and <i>SCARB1</i> are associated with papillary and follicular thyroid cancer risk: replication study in a German population. <i>Carcinogenesis</i> , 2016, 37, 677-684.	1.3	34
122	Deciphering the Plasma Proteome of Type 2 Diabetes. <i>Diabetes</i> , 2020, 69, 2766-2778.	0.3	34
123	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor $\uparrow$ . <i>JAMA Cardiology</i> , 2018, 3, 463.	3.0	33
124	Gallstones, Body Mass Index, C-reactive Protein, and Gallbladder Cancer: Mendelian Randomization Analysis of Chilean and European Genotype Data. <i>Hepatology</i> , 2021, 73, 1783-1796.	3.6	32
125	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. <i>Human Molecular Genetics</i> , 2021, 30, 393-409.	1.4	32
126	Mapping the Genetic Architecture of Gene Regulation in Whole Blood. <i>PLoS ONE</i> , 2014, 9, e93844.	1.1	31



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127	Validated inference of smoking habits from blood with a finite DNA methylation marker set. <i>European Journal of Epidemiology</i> , 2019, 34, 1055-1074.	2.5	31
128	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. <i>Human Molecular Genetics</i> , 2019, 28, 2615-2633.	1.4	31
129	Smoking-related changes in DNA methylation and gene expression are associated with cardio-metabolic traits. <i>Clinical Epigenetics</i> , 2020, 12, 157.	1.8	31
130	Deep molecular phenotypes link complex disorders and physiological insult to CpG methylation. <i>Human Molecular Genetics</i> , 2018, 27, 1106-1121.	1.4	30
131	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021, 12, 7174.	5.8	30
132	A genome-wide expression quantitative trait loci analysis of proprotein convertase subtilisin/kexin enzymes identifies a novel regulatory gene variant for FURIN expression and blood pressure. <i>Human Genetics</i> , 2015, 134, 627-636.	1.8	29
133	Discovery of novel heart rate-associated loci using the Exome Chip. <i>Human Molecular Genetics</i> , 2017, 26, 2346-2363.	1.4	29
134	Genome-wide association meta-analysis of 30,000 samples identifies seven novel loci for quantitative ECG traits. <i>European Journal of Human Genetics</i> , 2019, 27, 952-962.	1.4	29
135	Protein-coding variants contribute to the risk of atopic dermatitis and skin-specific gene expression. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 1208-1218.	1.5	29
136	Harmonising and linking biomedical and clinical data across disparate data archives to enable integrative cross-biobank research. <i>European Journal of Human Genetics</i> , 2016, 24, 521-528.	1.4	27
137	ExomeChip-Wide Analysis of 95 626 Individuals Identifies 10 Novel Loci Associated With QT and JT Intervals. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e001758.	1.6	27
138	Effects of Calcium, Magnesium, and Potassium Concentrations on Ventricular Repolarization in Unselected Individuals. <i>Journal of the American College of Cardiology</i> , 2019, 73, 3118-3131.	1.2	27
139	Layered genetic control of DNA methylation and gene expression: a locus of multiple sclerosis in healthy individuals. <i>Human Molecular Genetics</i> , 2015, 24, 5733-5745.	1.4	26
140	Predicting sudden cardiac death using common genetic risk variants for coronary artery disease. <i>European Heart Journal</i> , 2015, 36, 1669-1675.	1.0	26
141	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases. <i>Nature Communications</i> , 2022, 13, 2408.	5.8	26
142	Genome-Wide Association Study Identifies Two Novel Regions at 11p15.5-p13 and 1p31 with Major Impact on Acute-Phase Serum Amyloid A. <i>PLoS Genetics</i> , 2010, 6, e1001213.	1.5	24
143	Autosomal genetic variation is associated with DNA methylation in regions variably escaping X-chromosome inactivation. <i>Nature Communications</i> , 2018, 9, 3738.	5.8	24
144	Epigenome-Wide Analysis of Methylation Changes in the Sequence of Gallstone Disease, Dysplasia, and Gallbladder Cancer. <i>Hepatology</i> , 2021, 73, 2293-2310.	3.6	24

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145	Bayesian and frequentist analysis of an Austrian genome-wide association study of colorectal cancer and advanced adenomas. <i>Oncotarget</i> , 2017, 8, 98623-98634.	0.8	23
146	Molecular Characterization of the <i>NLR4</i> Expression in Relation to Interleukin-18 Levels. <i>Circulation</i> : Cardiovascular Genetics, 2015, 8, 717-726.	5.1	22
147	Analysis of repeated leukocyte DNA methylation assessments reveals persistent epigenetic alterations after an incident myocardial infarction. <i>Clinical Epigenetics</i> , 2018, 10, 161.	1.8	20
148	Activated immune-inflammatory pathways are associated with long-standing depressive symptoms: Evidence from gene-set enrichment analyses in the Young Finns Study. <i>Journal of Psychiatric Research</i> , 2015, 71, 120-125.	1.5	19
149	Analysis with the exome array identifies multiple new independent variants in lipid loci. <i>Human Molecular Genetics</i> , 2016, 25, 4094-4106.	1.4	19
150	Characterization of the metabolic profile associated with serum 25-hydroxyvitamin D: a cross-sectional analysis in population-based data. <i>International Journal of Epidemiology</i> , 2016, 45, 1469-1481.	0.9	19
151	RL-SKAT: An Exact and Efficient Score Test for Heritability and Set Tests. <i>Genetics</i> , 2017, 207, 1275-1283.	1.2	19
152	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002037.	1.6	19
153	Metabolic syndrome and the plasma proteome: from association to causation. <i>Cardiovascular Diabetology</i> , 2021, 20, 111.	2.7	19
154	Are Epigenetic Factors Implicated in Chronic Widespread Pain?. <i>PLoS ONE</i> , 2016, 11, e0165548.	1.1	19
155	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. <i>Nature Communications</i> , 2021, 12, 3987.	5.8	18
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