

Melanie Waldenberger

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

208 papers	15,200 citations	58 h-index	120 g-index
247 ext. papers	20,304 ext. citations	10.7 avg, IF	5.12 L-index

#	Paper	IF	Citations
208	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014 , 46, 1173-86	36.3	1339
207	An atlas of genetic influences on human blood metabolites. <i>Nature Genetics</i> , 2014 , 46, 543-550	36.3	695
206	DNA methylation and body-mass index: a genome-wide analysis. <i>Lancet, The</i> , 2014 , 383, 1990-8	40	569
205	DNA methylation-based measures of biological age: meta-analysis predicting time to death. <i>Aging</i> , 2016 , 8, 1844-1865	5.6	531
204	Tobacco smoking leads to extensive genome-wide changes in DNA methylation. <i>PLoS ONE</i> , 2013 , 8, e63812	3.7	523
203	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , 2017 , 541, 81-86	50.4	511
202	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2013 , 45, 145-54	36.3	505
201	Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , 2016 , 9, 436-447		442
200	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014 , 514, 92-97	50.4	401
199	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015 , 6, 8570	17.4	335
198	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. <i>Nature Communications</i> , 2016 , 7, 11122	17.4	335
197	Coding Variation in ANGPTL4, LPL, and SVEP1 and the Risk of Coronary Disease. <i>New England Journal of Medicine</i> , 2016 , 374, 1134-44	59.2	325
196	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	3.3	311
195	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017 , 49, 1758-1766	36.3	310
194	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016 , 7, 10023	17.4	295
193	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	36.3	223
192	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	6	220

191	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019 , 51, 957-972	36.3	217
190	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. <i>Nature Genetics</i> , 2014 , 46, 826-36	36.3	199
189	Meta-analysis of genome-wide association studies identifies ten loci influencing allergic sensitization. <i>Nature Genetics</i> , 2013 , 45, 902-906	36.3	191
188	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017 , 26, 126-135	4	183
187	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. <i>Nature Genetics</i> , 2017 , 49, 946-952	36.3	176
186	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016 , 17, 255	18.3	171
185	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015 , 20, 647-656	15.1	167
184	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. <i>Lancet Neurology</i> , 2016 , 15, 174-184	24.1	159
183	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	5.6	153
182	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	11	151
181	DNA methylation signatures in peripheral blood strongly predict all-cause mortality. <i>Nature Communications</i> , 2017 , 8, 14617	17.4	148
180	Epigenetics meets metabolomics: an epigenome-wide association study with blood serum metabolic traits. <i>Human Molecular Genetics</i> , 2014 , 23, 534-45	5.6	147
179	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	15.1	146
178	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, 193-9	8.4	127
177	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019 , 51, 1459-1474	36.3	122
176	DNA methylation of lipid-related genes affects blood lipid levels. <i>Circulation: Cardiovascular Genetics</i> , 2015 , 8, 334-42		122
175	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. <i>Nature Communications</i> , 2014 , 5, 4926	17.4	121
174	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015 , 523, 459-463	30.4	119

173	DataSHIELD: taking the analysis to the data, not the data to the analysis. <i>International Journal of Epidemiology</i> , 2014 , 43, 1929-44	7.8	116
172	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, 983-90	8.4	113
171	Characterization of whole-genome autosomal differences of DNA methylation between men and women. <i>Epigenetics and Chromatin</i> , 2015 , 8, 43	5.8	111
170	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	17.4	105
169	Epigenetic upregulation of FKBP5 by aging and stress contributes to NF- κ 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	11.5	98
168	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. <i>Diabetes</i> , 2016 , 65, 803-17	0.9	96
167	A metabolic profile of all-cause mortality risk identified in an observational study of 44,168 individuals. <i>Nature Communications</i> , 2019 , 10, 3346	17.4	89
166	A meta-analysis of gene expression signatures of blood pressure and hypertension. <i>PLoS Genetics</i> , 2015 , 11, e1005035	6	83
165	Telomere length in circulating leukocytes is associated with lung function and disease. <i>European Respiratory Journal</i> , 2014 , 43, 983-92	13.6	83
164	Data harmonization and federated analysis of population-based studies: the BioSHaRE project. <i>Emerging Themes in Epidemiology</i> , 2013 , 10, 12	3.9	80
163	Restless legs syndrome-associated intronic common variant in Meis1 alters enhancer function in the developing telencephalon. <i>Genome Research</i> , 2014 , 24, 592-603	9.7	79
162	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016 , 68, 1435-1448	15.1	76
161	Novel multiple sclerosis susceptibility loci implicated in epigenetic regulation. <i>Science Advances</i> , 2016 , 2, e1501678	14.3	75
160	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. <i>Scientific Reports</i> , 2017 , 7, 45040	4.9	70
159	Socioeconomic position, lifestyle habits and biomarkers of epigenetic aging: a multi-cohort analysis. <i>Aging</i> , 2019 , 11, 2045-2070	5.6	67
158	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	6	66
157	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	3.7	65
156	Comprehensive catalog of European biobanks. <i>Nature Biotechnology</i> , 2011 , 29, 795-7	44.5	65

155	Cystatin C and Cardiovascular Disease: A Mendelian Randomization Study. <i>Journal of the American College of Cardiology</i> , 2016 , 68, 934-45	15.1	65
154	Genetic evidence for PLASMINOGEN as a shared genetic risk factor of coronary artery disease and periodontitis. <i>Circulation: Cardiovascular Genetics</i> , 2015 , 8, 159-67		61
153	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	36.3	59
152	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	11	59
151	A whole-blood transcriptome meta-analysis identifies gene expression signatures of cigarette smoking. <i>Human Molecular Genetics</i> , 2016 , 25, 4611-4623	5.6	58
150	Discovery and fine mapping of serum protein loci through transethnic meta-analysis. <i>American Journal of Human Genetics</i> , 2012 , 91, 744-53	11	58
149	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. <i>Human Molecular Genetics</i> , 2016 , 25, 358-70	5.6	54
148	Multi-omic signature of body weight change: results from a population-based cohort study. <i>BMC Medicine</i> , 2015 , 13, 48	11.4	51
147	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons: Meta-analysis of Multiethnic Epigenome-wide Studies. <i>JAMA Psychiatry</i> , 2018 , 75, 949-959	14.5	51
146	Metabolomics approach reveals effects of antihypertensives and lipid-lowering drugs on the human metabolism. <i>European Journal of Epidemiology</i> , 2014 , 29, 325-36	12.1	51
145	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. <i>Nature Communications</i> , 2017 , 8, 15805	17.4	50
144	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: the cardiovascular risk in Young Finns Study. <i>Molecular and Cellular Endocrinology</i> , 2014 , 391, 41-9	4.4	50
143	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	4.5	50
142	Association between DNA Methylation in Whole Blood and Measures of Glucose Metabolism: KORA F4 Study. <i>PLoS ONE</i> , 2016 , 11, e0152314	3.7	50
141	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	8.4	50
140	Genome-wide methylation data mirror ancestry information. <i>Epigenetics and Chromatin</i> , 2017 , 10, 1	5.8	48
139	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. <i>Blood</i> , 2015 , 126, e19-29	2.2	45
138	16p11.2 600 kb Duplications confer risk for typical and atypical Rolandic epilepsy. <i>Human Molecular Genetics</i> , 2014 , 23, 6069-80	5.6	45

137	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	11	45
136	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019 , 10, 4130	17.4	43
135	Blood hsa-miR-122-5p and hsa-miR-885-5p levels associate with fatty liver and related lipoprotein metabolism-The Young Finns Study. <i>Scientific Reports</i> , 2016 , 6, 38262	4.9	42
134	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019 , 10, 376	17.4	41
133	MASP1, THBS1, GPLD1 and ApoA-IV are novel biomarkers associated with prediabetes: the KORA F4 study. <i>Diabetologia</i> , 2016 , 59, 1882-92	10.3	40
132	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019 , 10, 4957	17.4	40
131	FTO, obesity and the adolescent brain. <i>Human Molecular Genetics</i> , 2013 , 22, 1050-8	5.6	40
130	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019 , 188, 1033-1054	3.8	39
129	Genome-Wide Association Analysis of Young-Onset Stroke Identifies a Locus on Chromosome 10q25 Near HABP2. <i>Stroke</i> , 2016 , 47, 307-16	6.7	39
128	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. <i>Nature Communications</i> , 2018 , 9, 2904	17.4	39
127	Metabolite profiling reveals new insights into the regulation of serum urate in humans. <i>Metabolomics</i> , 2014 , 10, 141-151	4.7	36
126	Methylome-wide association study provides evidence of particulate matter air pollution-associated DNA methylation. <i>Environment International</i> , 2019 , 132, 104723	12.9	35
125	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. <i>Human Molecular Genetics</i> , 2014 , 23, 2490-7	5.6	35
124	Epigenetics meets proteomics in an epigenome-wide association study with circulating blood plasma protein traits. <i>Nature Communications</i> , 2020 , 11, 15	17.4	34
123	A genome-wide association study reveals 2 new susceptibility loci for atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2015 , 136, 802-6	11.5	32
122	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	3.7	31
121	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	17.4	31
120	Modulation of genetic associations with serum urate levels by body-mass-index in humans. <i>PLoS ONE</i> , 2015 , 10, e0119752	3.7	31

119	and 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	12.7	30
118	Common coding variant in 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	11.5	28
117	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	4.9	28
116	DNA methylation in human lipid metabolism and related diseases. <i>Current Opinion in Lipidology</i> , 2018 , 29, 116-124	4.4	28
115	Improvement of myocardial infarction risk prediction via inflammation-associated metabolite biomarkers. <i>Heart</i> , 2017 , 103, 1278-1285	5.1	27
114	Methylation of the FKBP5 gene in association with FKBP5 genotypes, childhood maltreatment and depression. <i>Neuropsychopharmacology</i> , 2019 , 44, 930-938	8.7	27
113	Mapping the genetic architecture of gene regulation in whole blood. <i>PLoS ONE</i> , 2014 , 9, e93844	3.7	27
112	Selected single-nucleotide polymorphisms in FOXE1, SERPINA5, FTO, EVPL, TICAM1 and SCARB1 are associated with papillary and follicular thyroid cancer risk: replication study in a German population. <i>Carcinogenesis</i> , 2016 , 37, 677-684	4.6	26
111	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	12.1	26
110	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. <i>Genome Biology</i> , 2018 , 19, 87	18.3	25
109	Epigenome-wide association study of lung function level and its change. <i>European Respiratory Journal</i> , 2019 , 54,	13.6	25
108	Evidence for Stress-like Alterations in the HPA-Axis in Women Taking Oral Contraceptives. <i>Scientific Reports</i> , 2017 , 7, 14111	4.9	24
107	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. <i>Epigenomics</i> , 2019 , 11, 1487-1500	4.4	24
106	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, 627-36	6.3	24
105	Anxiety Associated Increased CpG Methylation in the Promoter of Asb1: A Translational Approach Evidenced by Epidemiological and Clinical Studies and a Murine Model. <i>Neuropsychopharmacology</i> , 2018 , 43, 342-353	8.7	24
104	Fifteen Genetic Loci Associated With the Electrocardiographic P Wave. <i>Circulation: Cardiovascular Genetics</i> , 2017 , 10,		24
103	Deep molecular phenotypes link complex disorders and physiological insult to CpG methylation. <i>Human Molecular Genetics</i> , 2018 , 27, 1106-1121	5.6	21
102	Mitochondrial genetic variants identified to be associated with BMI in adults. <i>PLoS ONE</i> , 2014 , 9, e105116	5.7	21

101	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	6	20
100	Circulating metabolic biomarkers of renal function in diabetic and non-diabetic populations. <i>Scientific Reports</i> , 2018 , 8, 15249	4.9	20
99	Predicting sudden cardiac death using common genetic risk variants for coronary artery disease. <i>European Heart Journal</i> , 2015 , 36, 1669-75	9.5	19
98	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, 521-8	5.3	19
97	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	11.5	19
96	Association of maternal prenatal smoking GFI1-locus and cardio-metabolic phenotypes in 18,212 adults. <i>EBioMedicine</i> , 2018 , 38, 206-216	8.8	19
95	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	5.3	18
94	Molecular Characterization of the NLRC4 Expression in Relation to Interleukin-18 Levels. <i>Circulation: Cardiovascular Genetics</i> , 2015 , 8, 717-26		18
93	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	5.2	18
92	Discovery of novel heart rate-associated loci using the Exome Chip. <i>Human Molecular Genetics</i> , 2017 , 26, 2346-2363	5.6	17
91	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, 120-5	5.2	17
90	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, 463-472	16.2	17
89	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020 , 11, 2542	17.4	16
88	Epigenetic Link Between Statin Therapy and Type 2 Diabetes. <i>Diabetes Care</i> , 2020 , 43, 875-884	14.6	16
87	Impact of long-term storage and freeze-thawing on eight circulating microRNAs in plasma samples. <i>PLoS ONE</i> , 2020 , 15, e0227648	3.7	16
86	Deciphering the Plasma Proteome of Type 2 Diabetes. <i>Diabetes</i> , 2020 , 69, 2766-2778	0.9	15
85	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	5.6	14
84	DeepWAS: Multivariate genotype-phenotype associations by directly integrating regulatory information using deep learning. <i>PLoS Computational Biology</i> , 2020 , 16, e1007616	5	14

83	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	7.8	14
82	Genetic Interactions with Age, Sex, Body Mass Index, and Hypertension in Relation to Atrial Fibrillation: The AFGen Consortium. <i>Scientific Reports</i> , 2017 , 7, 11303	4.9	14
81	Are Epigenetic Factors Implicated in Chronic Widespread Pain?. <i>PLoS ONE</i> , 2016 , 11, e0165548	3.7	14
80	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	9.5	14
79	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021 , 22, 194	18.3	14
78	Analysis with the exome array identifies multiple new independent variants in lipid loci. <i>Human Molecular Genetics</i> , 2016 , 25, 4094-4106	5.6	14
77	Revealing the role of the human blood plasma proteome in obesity using genetic drivers. <i>Nature Communications</i> , 2021 , 12, 1279	17.4	14
76	Analysis of repeated leukocyte DNA methylation assessments reveals persistent epigenetic alterations after an incident myocardial infarction. <i>Clinical Epigenetics</i> , 2018 , 10, 161	7.7	14
75	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	5.2	14
74	Vitamin E supplementation is associated with lower levels of C-reactive protein only in higher dosages and combined with other antioxidants: The Cooperative Health Research in the Region of Augsburg (KORA) F4 study. <i>British Journal of Nutrition</i> , 2015 , 113, 1782-91	3.6	13
73	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	4.6	13
72	RL-SKAT: An Exact and Efficient Score Test for Heritability and Set Tests. <i>Genetics</i> , 2017 , 207, 1275-1283	4	12
71	Exposure to disinfection byproducts and risk of type 2 diabetes: a nested case-control study in the HUNT and Lifelines cohorts. <i>Metabolomics</i> , 2019 , 15, 60	4.7	12
70	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	15.1	12
69	Associations between the 17q21 region and allergic rhinitis in 5 birth cohorts. <i>Journal of Allergy and Clinical Immunology</i> , 2015 , 135, 573-6	11.5	12
68	Bayesian and frequentist analysis of an Austrian genome-wide association study of colorectal cancer and advanced adenomas. <i>Oncotarget</i> , 2017 , 8, 98623-98634	3.3	12
67	Autosomal genetic variation is associated with DNA methylation in regions variably escaping X-chromosome inactivation. <i>Nature Communications</i> , 2018 , 9, 3738	17.4	12
66	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. <i>PLoS ONE</i> , 2019 , 14, e0216222	3.7	11

65	Layered genetic control of DNA methylation and gene expression: a locus of multiple sclerosis in healthy individuals. <i>Human Molecular Genetics</i> , 2015 , 24, 5733-45	5.6	11
64	Gene-gene Interaction Analyses for Atrial Fibrillation. <i>Scientific Reports</i> , 2016 , 6, 35371	4.9	11
63	DNA methylation age is associated with an altered hemostatic profile in a multiethnic meta-analysis. <i>Blood</i> , 2018 , 132, 1842-1850	2.2	11
62	On the potential of models for location and scale for genome-wide DNA methylation data. <i>BMC Bioinformatics</i> , 2014 , 15, 232	3.6	11
61	DNA methylation and lipid metabolism: an EWAS of 226 metabolic measures. <i>Clinical Epigenetics</i> , 2021 , 13, 7	7.7	11
60	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. <i>Circulation Genomic and Precision Medicine</i> , 2018 , 11, e002037	5.2	11
59	Validated inference of smoking habits from blood with a finite DNA methylation marker set. <i>European Journal of Epidemiology</i> , 2019 , 34, 1055-1074	12.1	10
58	Genetic variants including markers from the exome chip and metabolite traits of type 2 diabetes. <i>Scientific Reports</i> , 2017 , 7, 6037	4.9	10
57	Epigenetic Signatures at AQP3 and SOCS3 Engage in Low-Grade Inflammation across Different Tissues. <i>PLoS ONE</i> , 2016 , 11, e0166015	3.7	10
56	Successful Replication of GWAS Hits for Multiple Sclerosis in 10,000 Germans Using the Exome Array. <i>Genetic Epidemiology</i> , 2015 , 39, 601-8	2.6	9
55	Epigenome-Wide Analysis of Methylation Changes in the Sequence of Gallstone Disease, Dysplasia, and Gallbladder Cancer. <i>Hepatology</i> , 2021 , 73, 2293-2310	11.2	9
54	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. <i>Nature Communications</i> , 2021 , 12, 2830	17.4	9
53	The Pharmacogenetic Footprint of ACE Inhibition: A Population-Based Metabolomics Study. <i>PLoS ONE</i> , 2016 , 11, e0153163	3.7	9
52	Differences in Biomarkers of Inflammation Between Novel Subgroups of Recent-Onset Diabetes. <i>Diabetes</i> , 2021 , 70, 1198-1208	0.9	9
51	Mendelian inheritance of trimodal CpG methylation sites suggests distal cis-acting genetic effects. <i>Clinical Epigenetics</i> , 2016 , 8, 124	7.7	8
50	Genetically defined elevated homocysteine levels do not result in widespread changes of DNA methylation in leukocytes. <i>PLoS ONE</i> , 2017 , 12, e0182472	3.7	8
49	Genome-wide association studies identify 137 loci for DNA methylation biomarkers of ageing		8
48	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	11.2	8

47	A genome-wide analysis of DNA methylation identifies a novel association signal for Lp(a) concentrations in the LPA promoter. <i>PLoS ONE</i> , 2020 , 15, e0232073	3.7	7
46	Ldlr and ApoE mice better mimic the human metabolite signature of increased carotid intima media thickness compared to other animal models of cardiovascular disease. <i>Atherosclerosis</i> , 2018 , 276, 140-147	3.1	7
45	Fatty liver is associated with blood pathways of inflammatory response, immune system activation and prothrombotic state in Young Finns Study. <i>Scientific Reports</i> , 2018 , 8, 10358	4.9	7
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39	Novel DNA Methylation Sites Influence Expression in Relation to Smoking. <i>Biomolecules</i> , 2018 , 8,	5.9	5
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21	Epigenetic scores for the circulating proteome as tools for disease prediction.. <i>ELife</i> , 2022 , 11,	8.9	2
20	Epigenetic scores for the circulating proteome as tools for disease prediction		2
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18	Adulthood blood levels of hsa-miR-29b-3p associate with preterm birth and adult metabolic and cognitive health. <i>Scientific Reports</i> , 2021 , 11, 9203	4.9	2
17	Discovery of mitochondrial DNA variants associated with genome-wide blood cell gene expression: a population-based mtDNA sequencing study. <i>Human Molecular Genetics</i> , 2019 , 28, 1381-1391	5.6	1
16	Discovering patterns of pleiotropy in genome-wide association studies		1
15	Multi-ancestry analysis of gene-sleep interactions in 126,926 individuals identifies multiple novel blood lipid loci that contribute to our understanding of sleep-associated adverse blood lipid profile		1
14	Arsenic and gallbladder cancer risk: Mendelian randomization analysis of European prospective data. <i>International Journal of Cancer</i> , 2020 , 146, 2648-2650	7.5	1
13	Subjective mental health, incidence of depressive symptoms in later life, and the role of epigenetics: results from two longitudinal cohort studies. <i>Translational Psychiatry</i> , 2020 , 10, 323	8.6	1
12	DNAm-based signatures of accelerated aging and mortality in blood are associated with low renal function. <i>Clinical Epigenetics</i> , 2021 , 13, 121	7.7	1

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