

# Melanie Waldenberger

## List of Publications by Year in Descending Order

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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	Epigenetic scores for the circulating proteome as tools for disease prediction.. <i>ELife</i> , <b>2022</b> , 11,	8.9	2
207	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function.. <i>Nature Genetics</i> , <b>2022</b> ,	36.3	6
206	Integrative analysis of clinical and epigenetic biomarkers of mortality.. <i>Aging Cell</i> , <b>2022</b> , e13608	9.9	1
205	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases.. <i>Nature Communications</i> , <b>2022</b> , 13, 2408	17.4	1
204	Gaseous air pollutants and DNA methylation in a methylome-wide association study of an ethnically and environmentally diverse population of U.S. adults.. <i>Environmental Research</i> , <b>2022</b> , 212, 113360	7.9	0
203	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , <b>2022</b> , 5,	6.7	1
202	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. <i>Molecular Psychiatry</i> , <b>2021</b> , 26, 2111-2125	15.1	3
201	Validating biomarkers and models for epigenetic inference of alcohol consumption from blood. <i>Clinical Epigenetics</i> , <b>2021</b> , 13, 198	7.7	0
200	Epigenome-Wide Analysis of Methylation Changes in the Sequence of Gallstone Disease, Dysplasia, and Gallbladder Cancer. <i>Hepatology</i> , <b>2021</b> , 73, 2293-2310	11.2	9
199	Robust Huber-LASSO for improved prediction of protein, metabolite and gene expression levels relying on individual genotype data. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	2
198	Epigenome-wide association study of whole blood gene expression in Framingham Heart Study participants provides molecular insight into the potential role of CHRNA5 in cigarette smoking-related lung diseases. <i>Clinical Epigenetics</i> , <b>2021</b> , 13, 60	7.7	3
197	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> , <b>2021</b> , 42, 2000-2011	9.5	14
196	Multi-ancestry genome-wide gene-sleep interactions identify novel loci for blood pressure. <i>Molecular Psychiatry</i> , <b>2021</b> ,	15.1	3
195	Adulthood blood levels of hsa-miR-29b-3p associate with preterm birth and adult metabolic and cognitive health. <i>Scientific Reports</i> , <b>2021</b> , 11, 9203	4.9	2
194	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. <i>Nature Communications</i> , <b>2021</b> , 12, 2830	17.4	9
193	Metabolic syndrome and the plasma proteome: from association to causation. <i>Cardiovascular Diabetology</i> , <b>2021</b> , 20, 111	8.7	4
192	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , <b>2021</b> , 22, 194	18.3	14

191	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. <i>Nature Communications</i> , <b>2021</b> , 12, 3987	17.4	3
190	DNA-based signatures of accelerated aging and mortality in blood are associated with low renal function. <i>Clinical Epigenetics</i> , <b>2021</b> , 13, 121	7.7	1
189	Meta-analysis of epigenome-wide association studies of carotid intima-media thickness. <i>European Journal of Epidemiology</i> , <b>2021</b> , 36, 1143-1155	12.1	4
188	Plasma Proteomics of Renal Function: A Trans-ethnic Meta-analysis and Mendelian Randomization Study. <i>Journal of the American Society of Nephrology: JASN</i> , <b>2021</b> ,	12.7	1
187	Methylation status of nc886 epiallele reflects periconceptional conditions and is associated with glucose metabolism through nc886 RNAs. <i>Clinical Epigenetics</i> , <b>2021</b> , 13, 143	7.7	1
186	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. <i>Kidney International</i> , <b>2021</b> , 99, 926-939	9.9	6
185	Gallstones, Body Mass Index, C-Reactive Protein, and Gallbladder Cancer: Mendelian Randomization Analysis of Chilean and European Genotype Data. <i>Hepatology</i> , <b>2021</b> , 73, 1783-1796	11.2	8
184	Alcohol consumption is associated with widespread changes in blood DNA methylation: Analysis of cross-sectional and longitudinal data. <i>Addiction Biology</i> , <b>2021</b> , 26, e12855	4.6	13
183	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. <i>Human Molecular Genetics</i> , <b>2021</b> , 30, 393-409	5.6	6
182	DNA methylation and lipid metabolism: an EWAS of 226 metabolic measures. <i>Clinical Epigenetics</i> , <b>2021</b> , 13, 7	7.7	11
181	Revealing the role of the human blood plasma proteome in obesity using genetic drivers. <i>Nature Communications</i> , <b>2021</b> , 12, 1279	17.4	14
180	Differences in Biomarkers of Inflammation Between Novel Subgroups of Recent-Onset Diabetes. <i>Diabetes</i> , <b>2021</b> , 70, 1198-1208	0.9	9
179	The blood metabolome of incident kidney cancer: A case-control study nested within the MetKid consortium. <i>PLoS Medicine</i> , <b>2021</b> , 18, e1003786	11.6	1
178	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. <i>Nature Communications</i> , <b>2021</b> , 12, 7173	17.4	1
177	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , <b>2021</b> , 12, 7174	17.4	0
176	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , <b>2020</b> , 11, 2542	17.4	16
175	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> , <b>2020</b> , 13, e002766	5.2	18
174	DeepWAS: Multivariate genotype-phenotype associations by directly integrating regulatory information using deep learning. <i>PLoS Computational Biology</i> , <b>2020</b> , 16, e1007616	5	14

173	Epigenetic Link Between Statin Therapy and Type 2 Diabetes. <i>Diabetes Care</i> , <b>2020</b> , 43, 875-884	14.6	16
172	ABCB1/4 gallbladder cancer risk variants identified in India also show strong effects in Chileans. <i>Cancer Epidemiology</i> , <b>2020</b> , 65, 101643	2.8	3
171	Impact of long-term storage and freeze-thawing on eight circulating microRNAs in plasma samples. <i>PLoS ONE</i> , <b>2020</b> , 15, e0227648	3.7	16
170	A genome-wide analysis of DNA methylation identifies a novel association signal for Lp(a) concentrations in the LPA promoter. <i>PLoS ONE</i> , <b>2020</b> , 15, e0232073	3.7	7
169	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. <i>Aging</i> , <b>2020</b> , 12, 14092-14124	5.6	6
168	Accelerated epigenetic aging as a risk factor for chronic obstructive pulmonary disease and decreased lung function in two prospective cohort studies. <i>Aging</i> , <b>2020</b> , 12, 16539-16554	5.6	3
167	Protein-coding variants contribute to the risk of atopic dermatitis and skin-specific gene expression. <i>Journal of Allergy and Clinical Immunology</i> , <b>2020</b> , 145, 1208-1218	11.5	19
166	Arsenic and gallbladder cancer risk: Mendelian randomization analysis of European prospective data. <i>International Journal of Cancer</i> , <b>2020</b> , 146, 2648-2650	7.5	1
165	Epigenetics meets proteomics in an epigenome-wide association study with circulating blood plasma protein traits. <i>Nature Communications</i> , <b>2020</b> , 11, 15	17.4	34
164	Smoking-related changes in DNA methylation and gene expression are associated with cardio-metabolic traits. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 157	7.7	5
163	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> , <b>2020</b> , 10, 323	8.6	1
162	Deciphering the Plasma Proteome of Type 2 Diabetes. <i>Diabetes</i> , <b>2020</b> , 69, 2766-2778	0.9	15
161	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. <i>Circulation Genomic and Precision Medicine</i> , <b>2020</b> , 13, 387-395	5.2	4
160	Discovery of mitochondrial DNA variants associated with genome-wide blood cell gene expression: a population-based mtDNA sequencing study. <i>Human Molecular Genetics</i> , <b>2019</b> , 28, 1381-1391	5.6	1
159	Validated inference of smoking habits from blood with a finite DNA methylation marker set. <i>European Journal of Epidemiology</i> , <b>2019</b> , 34, 1055-1074	12.1	10
158	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , <b>2019</b> , 10, 4130	17.4	43
157	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , <b>2019</b> , 51, 1459-1474	36.3	122
156	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. <i>Epigenomics</i> , <b>2019</b> , 11, 1487-1500	4.4	24

155	Genome-wide association meta-analysis of 30,000 samples identifies seven novel loci for quantitative ECG traits. <i>European Journal of Human Genetics</i> , <b>2019</b> , 27, 952-962	5.3	18
154	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , <b>2019</b> , 188, 1033-1054	3.8	39
153	Methylation of the FKBP5 gene in association with FKBP5 genotypes, childhood maltreatment and depression. <i>Neuropsychopharmacology</i> , <b>2019</b> , 44, 930-938	8.7	27
152	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , <b>2019</b> , 10, 376	17.4	41
151	Methylome-wide association study provides evidence of particulate matter air pollution-associated DNA methylation. <i>Environment International</i> , <b>2019</b> , 132, 104723	12.9	35
150	Whole blood microRNA levels associate with glycemic status and correlate with target mRNAs in pathways important to type 2 diabetes. <i>Scientific Reports</i> , <b>2019</b> , 9, 8887	4.9	28
149	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , <b>2019</b> , 51, 957-972	36.3	217
148	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> , <b>2019</b> , 116, 11370-11379	11.5	98
147	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. <i>PLoS ONE</i> , <b>2019</b> , 14, e0216222	3.7	11
146	Exposure to disinfection byproducts and risk of type 2 diabetes: a nested case-control study in the HUNT and Lifelines cohorts. <i>Metabolomics</i> , <b>2019</b> , 15, 60	4.7	12
145	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> , <b>2019</b> , 28, 2615-2633	5.6	14
144	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , <b>2019</b> , 51, 636-648	36.3	59
143	A metabolic profile of all-cause mortality risk identified in an observational study of 44,168 individuals. <i>Nature Communications</i> , <b>2019</b> , 10, 3346	17.4	89
142	Effects of Calcium, Magnesium, and Potassium Concentrations on Ventricular Repolarization in Unselected Individuals. <i>Journal of the American College of Cardiology</i> , <b>2019</b> , 73, 3118-3131	15.1	12
141	Epigenome-wide association study of lung function level and its change. <i>European Respiratory Journal</i> , <b>2019</b> , 54,	13.6	25
140	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , <b>2019</b> , 10, 4957	17.4	40
139	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. <i>Nature Communications</i> , <b>2019</b> , 10, 5121	17.4	31
138	Socioeconomic position, lifestyle habits and biomarkers of epigenetic aging: a multi-cohort analysis. <i>Aging</i> , <b>2019</b> , 11, 2045-2070	5.6	67

137	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> , <b>2019</b> , 34, 409-422	12.1	26
136	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor $\alpha$ <i>JAMA Cardiology</i> , <b>2018</b> , 3, 463-472	16.2	17
135	DNA methylation in human lipid metabolism and related diseases. <i>Current Opinion in Lipidology</i> , <b>2018</b> , 29, 116-124	4.4	28
134	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> , <b>2018</b> , 102, 375-400	11	59
133	Deep molecular phenotypes link complex disorders and physiological insult to CpG methylation. <i>Human Molecular Genetics</i> , <b>2018</b> , 27, 1106-1121	5.6	21
132	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> , <b>2018</b> , 43, 342-353	8.7	24
131	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. <i>Nature Communications</i> , <b>2018</b> , 9, 2904	17.4	39
130	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> , <b>2018</b> , 276, 140-147	3.1	7
129	DNA methylation age is associated with an altered hemostatic profile in a multiethnic meta-analysis. <i>Blood</i> , <b>2018</b> , 132, 1842-1850	2.2	11
128	Fatty liver is associated with blood pathways of inflammatory response, immune system activation and prothrombotic state in Young Finns Study. <i>Scientific Reports</i> , <b>2018</b> , 8, 10358	4.9	7
127	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. <i>Genome Biology</i> , <b>2018</b> , 19, 87	18.3	25
126	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons: Meta-analysis of Multiethnic Epigenome-wide Studies. <i>JAMA Psychiatry</i> , <b>2018</b> , 75, 949-959	14.5	51
125	Novel DNA Methylation Sites Influence Expression in Relation to Smoking. <i>Biomolecules</i> , <b>2018</b> , 8,	5.9	5
124	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , <b>2018</b> , 13, e0198166	3.7	31
123	Detecting heritable phenotypes without a model using fast permutation testing for heritability and set-tests. <i>Nature Communications</i> , <b>2018</b> , 9, 4919	17.4	4
122	Association of maternal prenatal smoking GFI1-locus and cardio-metabolic phenotypes in 18,212 adults. <i>EBioMedicine</i> , <b>2018</b> , 38, 206-216	8.8	19
121	Analysis of repeated leukocyte DNA methylation assessments reveals persistent epigenetic alterations after an incident myocardial infarction. <i>Clinical Epigenetics</i> , <b>2018</b> , 10, 161	7.7	14
120	Long-term Air Pollution Exposure, Genome-wide DNA Methylation and Lung Function in the LifeLines Cohort Study. <i>Environmental Health Perspectives</i> , <b>2018</b> , 126, 027004	8.4	50

119	ExomeChip-Wide Analysis of 95 626 Individuals Identifies 10 Novel Loci Associated With QT and JT Intervals. <i>Circulation Genomic and Precision Medicine</i> , <b>2018</b> , 11, e001758	5.2	14
118	Genetics of the thrombomodulin-endothelial cell protein C receptor system and the risk of early-onset ischemic stroke. <i>PLoS ONE</i> , <b>2018</b> , 13, e0206554	3.7	4
117	Circulating metabolic biomarkers of renal function in diabetic and non-diabetic populations. <i>Scientific Reports</i> , <b>2018</b> , 8, 15249	4.9	20
116	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> , <b>2018</b> , 103, 691-706	11	151
115	Autosomal genetic variation is associated with DNA methylation in regions variably escaping X-chromosome inactivation. <i>Nature Communications</i> , <b>2018</b> , 9, 3738	17.4	12
114	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. <i>Circulation Genomic and Precision Medicine</i> , <b>2018</b> , 11, e002037	5.2	11
113	Improvement of myocardial infarction risk prediction via inflammation-associated metabolite biomarkers. <i>Heart</i> , <b>2017</b> , 103, 1278-1285	5.1	27
112	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> , <b>2017</b> , 114, 3613-3618	11.5	28
111	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , <b>2017</b> , 69, 823-836	15.1	146
110	Discovery of novel heart rate-associated loci using the Exome Chip. <i>Human Molecular Genetics</i> , <b>2017</b> , 26, 2346-2363	5.6	17
109	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. <i>Nature Genetics</i> , <b>2017</b> , 49, 946-952	36.3	176
108	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , <b>2017</b> , 8, 14977	17.4	105
107	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. <i>Scientific Reports</i> , <b>2017</b> , 7, 45040	4.9	70
106	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. <i>Nature Communications</i> , <b>2017</b> , 8, 15805	17.4	50
105	Blood pathway analyses reveal differences between prediabetic subjects with or without dyslipidaemia. The Cardiovascular Risk in Young Finns Study. <i>Diabetes/Metabolism Research and Reviews</i> , <b>2017</b> , 33, e2914	7.5	2
104	DNA methylation signatures in peripheral blood strongly predict all-cause mortality. <i>Nature Communications</i> , <b>2017</b> , 8, 14617	17.4	148
103	and Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. <i>Journal of the American Society of Nephrology: JASN</i> , <b>2017</b> , 28, 981-994	12.7	30
102	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , <b>2017</b> , 541, 81-86	50.4	511



101	Evidence for Stress-like Alterations in the HPA-Axis in Women Taking Oral Contraceptives. <i>Scientific Reports</i> , <b>2017</b> , 7, 14111	4.9	24
100	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , <b>2017</b> , 49, 1758-1766	3.6	310
99	RL-SKAT: An Exact and Efficient Score Test for Heritability and Set Tests. <i>Genetics</i> , <b>2017</b> , 207, 1275-1283	4	12
98	Genetic Interactions with Age, Sex, Body Mass Index, and Hypertension in Relation to Atrial Fibrillation: The AFGen Consortium. <i>Scientific Reports</i> , <b>2017</b> , 7, 11303	4.9	14
97	Genetic variants including markers from the exome chip and metabolite traits of type 2 diabetes. <i>Scientific Reports</i> , <b>2017</b> , 7, 6037	4.9	10
96	Fifteen Genetic Loci Associated With the Electrocardiographic P Wave. <i>Circulation: Cardiovascular Genetics</i> , <b>2017</b> , 10,		24
95	Influence of Storage and Inter- and Intra-Assay Variability on the Measurement of Inflammatory Biomarkers in Population-Based Biobanking. <i>Biopreservation and Biobanking</i> , <b>2017</b> , 15, 512-518	2.1	3
94	Genome-wide methylation data mirror ancestry information. <i>Epigenetics and Chromatin</i> , <b>2017</b> , 10, 1	5.8	48
93	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2017</b> , 26, 126-135	4	183
92	pulver: an R package for parallel ultra-rapid p-value computation for linear regression interaction terms. <i>BMC Bioinformatics</i> , <b>2017</b> , 18, 429	3.6	0
91	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> , <b>2017</b> , 18, 805	4.5	50
90	Genetically defined elevated homocysteine levels do not result in widespread changes of DNA methylation in leukocytes. <i>PLoS ONE</i> , <b>2017</b> , 12, e0182472	3.7	8
89	Bayesian and frequentist analysis of an Austrian genome-wide association study of colorectal cancer and advanced adenomas. <i>Oncotarget</i> , <b>2017</b> , 8, 98623-98634	3.3	12
88	A whole-blood transcriptome meta-analysis identifies gene expression signatures of cigarette smoking. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 4611-4623	5.6	58
87	Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , <b>2016</b> , 9, 436-447		442
86	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> , <b>2016</b> , 45, 1469-1481	7.8	14
85	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , <b>2016</b> , 68, 1435-1448	15.1	76
84	Gene-gene Interaction Analyses for Atrial Fibrillation. <i>Scientific Reports</i> , <b>2016</b> , 6, 35371	4.9	11



83	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. <i>Nature Communications</i> , <b>2016</b> , 7, 11122	17.4	335
82	Novel multiple sclerosis susceptibility loci implicated in epigenetic regulation. <i>Science Advances</i> , <b>2016</b> , 2, e1501678	14.3	75
81	Mendelian inheritance of trimodal CpG methylation sites suggests distal cis-acting genetic effects. <i>Clinical Epigenetics</i> , <b>2016</b> , 8, 124	7.7	8
80	MASP1, THBS1, GPLD1 and ApoA-IV are novel biomarkers associated with prediabetes: the KORA F4 study. <i>Diabetologia</i> , <b>2016</b> , 59, 1882-92	10.3	40
79	Genome-Wide Association Analysis of Young-Onset Stroke Identifies a Locus on Chromosome 10q25 Near HABP2. <i>Stroke</i> , <b>2016</b> , 47, 307-16	6.7	39
78	Loci associated with ischaemic stroke and its subtypes (SIGN): a genome-wide association study. <i>Lancet Neurology</i> , <b>2016</b> , 15, 174-184	24.1	159
77	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. <i>Diabetes</i> , <b>2016</b> , 65, 803-17	0.9	96
76	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , <b>2016</b> , 7, 10023	17.4	295
75	Harmonising and linking biomedical and clinical data across disparate data archives to enable integrative cross-biobank research. <i>European Journal of Human Genetics</i> , <b>2016</b> , 24, 521-8	5.3	19
74	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 358-70	5.6	54
73	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> , <b>2016</b> , 25, 191-201	5.6	153
72	Are Epigenetic Factors Implicated in Chronic Widespread Pain?. <i>PLoS ONE</i> , <b>2016</b> , 11, e0165548	3.7	14
71	DNA methylation-based measures of biological age: meta-analysis predicting time to death. <i>Aging</i> , <b>2016</b> , 8, 1844-1865	5.6	531
70	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> , <b>2016</b> , 124, 983-90	8.4	113
69	Epigenetic Signatures at AQP3 and SOCS3 Engage in Low-Grade Inflammation across Different Tissues. <i>PLoS ONE</i> , <b>2016</b> , 11, e0166015	3.7	10
68	Association between DNA Methylation in Whole Blood and Measures of Glucose Metabolism: KORA F4 Study. <i>PLoS ONE</i> , <b>2016</b> , 11, e0152314	3.7	50
67	The Pharmacogenetic Footprint of ACE Inhibition: A Population-Based Metabolomics Study. <i>PLoS ONE</i> , <b>2016</b> , 11, e0153163	3.7	9
66	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , <b>2016</b> , 17, 255	18.3	171

65	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> , <b>2016</b> , 6, 38262	4.9	42
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5	Discovering patterns of pleiotropy in genome-wide association studies		1
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2	Epigenetic scores for the circulating proteome as tools for disease prediction		2
1	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