Melanie Waldenberger

List of Publications by Year
in descending order

216 papers	23,659 citations	14655 66 h-index	10734 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. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
2	An atlas of genetic influences on human blood metabolites. Nature Genetics, 2014, 46, 543-550.	21.4	1,084
3	DNA methylation-based measures of biological age: meta-analysis predicting time to death. Aging, 2016, 8, 1844-1865.	3.1	786
4	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. Nature, 2017, 541, 81-86.	27.8	743
5	Tobacco Smoking Leads to Extensive Genome-Wide Changes in DNA Methylation. PLoS ONE, 2013, 8, e63812.	2.5	694
6	DNA methylation and body-mass index: a genome-wide analysis. Lancet, The, 2014, 383, 1990-1998.	13.7	686
7	Epigenetic Signatures of Cigarette Smoking. Circulation: Cardiovascular Genetics, 2016, 9, 436-447.	5.1	678
8	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
9	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. Nature Communications, 2016, 7, 11122.	12.8	576
10	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
11	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
12	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	12.8	533
13	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
14	The prevalence of metabolic syndrome and metabolically healthy obesity in Europe: a collaborative analysis of ten large cohort studies. BMC Endocrine Disorders, 2014, 14, 9.	2.2	440
15	Coding Variation in *ANGPTL4,* *LPL,* and *SVEP1* and the Risk of Coronary Disease. New England Journal of Medicine, 2016, 374, 1134-1144.	27.0	427
16	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
17	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	3.5	331
18	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	6.2	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. Nature Genetics, 2015, 47, 1282-1293.	21.4	294
20	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
21	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	21.4	279
22	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 126-135.	2.5	278
23	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. Genome Biology, 2016, 17, 255.	8.8	251
24	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
25	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	7.9	235
26	Meta-analysis of genome-wide association studies identifies ten loci influencing allergic sensitization. Nature Genetics, 2013, 45, 902-906.	21.4	221
27	DNA methylation signatures in peripheral blood strongly predict all-cause mortality. Nature Communications, 2017, 8, 14617.	12.8	221
28	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. Lancet Neurology, The, 2016, 15, 174-184.	10.2	217
29	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. Journal of the American College of Cardiology, 2017, 69, 823-836.	2.8	214
30	Prenatal and early life influences on epigenetic age in children: a study of mother–offspring pairs from two cohort studies. Human Molecular Genetics, 2016, 25, 191-201.	2.9	205
31	Epigenetic upregulation of FKBP5 by aging and stress contributes to NF-κB–driven inflammation and cardiovascular risk. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 11370-11379.	7.1	193
32	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	12.8	192
33	DataSHIELD: taking the analysis to the data, not the data to the analysis. International Journal of Epidemiology, 2014, 43, 1929-1944.	1.9	188
34	A metabolic profile of all-cause mortality risk identified in an observational study of 44,168 individuals. Nature Communications, 2019, 10, 3346.	12.8	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. Environmental Health Perspectives, 2015, 123, 193-199.	6.0	178
36	Characterization of whole-genome autosomal differences of DNA methylation between men and women. Epigenetics and Chromatin, 2015, 8, 43.	3.9	176

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37	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
38	Epigenetics meets metabolomics: an epigenome-wide association study with blood serum metabolic traits. Human Molecular Genetics, 2014, 23, 534-545.	2.9	169
39	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
40	DNA Methylation of Lipid-Related Genes Affects Blood Lipid Levels. Circulation: Cardiovascular Genetics, 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. Environmental Health Perspectives, 2016, 124, 983-990.	6.0	150
42	Socioeconomic position, lifestyle habits and biomarkers of epigenetic aging: a multi-cohort analysis. Aging, 2019, 11, 2045-2070.	3.1	137
43	Novel multiple sclerosis susceptibility loci implicated in epigenetic regulation. Science Advances, 2016, 2, e1501678.	10.3	133
44	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	12.8	133
45	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. Diabetes, 2016, 65, 803-817.	0.6	131
46	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
47	Genome-wide methylation data mirror ancestry information. Epigenetics and Chromatin, 2017, 10, 1.	3.9	120
48	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113
49	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
50	Cystatin C and Cardiovascular Disease. Journal of the American College of Cardiology, 2016, 68, 934-945.	2.8	109
51	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. PLoS Genetics, 2015, 11, e1005035.	3.5	107
52	Data harmonization and federated analysis of population-based studies: the BioSHaRE project. Emerging Themes in Epidemiology, 2013, 10, 12.	2.7	105
53	Telomere length in circulating leukocytes is associated with lung function and disease. European Respiratory Journal, 2014, 43, 983-992.	6.7	103
54	Restless Legs Syndrome-associated intronic common variant in <i>Meis1</i> alters enhancer function in the developing telencephalon. Genome Research, 2014, 24, 592-603.	5.5	102

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55	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	3.3	98
56	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	12.8	95
57	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
58	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	8.8	90
59	Pre-Analytical Sample Quality: Metabolite Ratios as an Intrinsic Marker for Prolonged Room Temperature Exposure of Serum Samples. PLoS ONE, 2015, 10, e0121495.	2.5	88
60	The dynamics of smoking-related disturbed methylation: a two time-point study of methylation change in smokers, non-smokers and former smokers. BMC Genomics, 2017, 18, 805.	2.8	85
61	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
62	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
63	Comprehensive catalog of European biobanks. Nature Biotechnology, 2011, 29, 795-797.	17.5	83
64	Genome-Wide Association Study with Targeted and Non-targeted NMR Metabolomics Identifies 15 Novel Loci of Urinary Human Metabolic Individuality. PLoS Genetics, 2015, 11, e1005487.	3.5	83
65	Association between DNA Methylation in Whole Blood and Measures of Glucose Metabolism: KORA F4 Study. PLoS ONE, 2016, 11, e0152314.	2.5	81
66	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. JAMA Psychiatry, 2018, 75, 949.	11.0	78
67	A Whole-Blood Transcriptome Meta-Analysis Identifies Gene Expression Signatures of Cigarette Smoking. Human Molecular Genetics, 2016, 25, ddw288.	2.9	76
68	Genetic Evidence for <i>PLASMINOGEN</i> as a Shared Genetic Risk Factor of Coronary Artery Disease and Periodontitis. Circulation: Cardiovascular Genetics, 2015, 8, 159-167.	5.1	74
69	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	2.9	73
70	Metabolomics approach reveals effects of antihypertensives and lipid-lowering drugs on the human metabolism. European Journal of Epidemiology, 2014, 29, 325-336.	5.7	72
71	Long-term Air Pollution Exposure, Genome-wide DNA Methylation and Lung Function in the LifeLines Cohort Study. Environmental Health Perspectives, 2018, 126, 027004.	6.0	71
72	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. Nature Communications, 2018, 9, 2904.	12.8	71

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73	Discovery and Fine Mapping of Serum Protein Loci through Transethnic Meta-analysis. American Journal of Human Genetics, 2012, 91, 744-753.	6.2	69
74	Multi-omic signature of body weight change: results from a population-based cohort study. BMC Medicine, 2015, 13, 48.	5.5	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. Molecular and Cellular Endocrinology, 2014, 391, 41-49.	3.2	65
76	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. Epigenomics, 2019, 11, 1487-1500.	2.1	64
77	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
78	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	2.5	64
79	Blood hsa-miR-122-5p and hsa-miR-885-5p levels associate with fatty liver and related lipoprotein metabolismâ€"The Young Finns Study. Scientific Reports, 2016, 6, 38262.	3.3	62
80	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
81	16p11.2 600 kb Duplications confer risk for typical and atypical Rolandic epilepsy. Human Molecular Genetics, 2014, 23, 6069-6080.	2.9	61
82	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function. Nature Genetics, 2022, 54, 18-29.	21.4	60
83	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
84	Methylome-wide association study provides evidence of particulate matter air pollution-associated DNA methylation. Environment International, 2019, 132, 104723.	10.0	58
85	Epigenetics meets proteomics in an epigenome-wide association study with circulating blood plasma protein traits. Nature Communications, 2020, 11, 15.	12.8	57
86	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. Human Molecular Genetics, 2014, 23, 2490-2497.	2.9	56
87	Compound Heterozygosity of Low-Frequency Promoter Deletions and Rare Loss-of-Function Mutations in TXNL4A Causes Burn-McKeown Syndrome. American Journal of Human Genetics, 2014, 95, 698-707.	6.2	55
88	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. Blood, 2015, 126, e19-e29.	1.4	55
89	Whole blood microRNA levels associate with glycemic status and correlate with target mRNAs in pathways important to type 2 diabetes. Scientific Reports, 2019, 9, 8887.	3.3	55
90	MASP1, THBS1, GPLD1 and ApoA-IV are novel biomarkers associated with prediabetes: the KORA F4 study. Diabetologia, 2016, 59, 1882-1892.	6.3	54

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91	Genome-Wide Association Analysis of Young-Onset Stroke Identifies a Locus on Chromosome 10q25 Near *HABP2*. Stroke, 2016, 47, 307-316.	2.0	54
92	DeepWAS: Multivariate genotype-phenotype associations by directly integrating regulatory information using deep learning. PLoS Computational Biology, 2020, 16, e1007616.	3.2	54
93	Methylation of the FKBP5 gene in association with FKBP5 genotypes, childhood maltreatment and depression. Neuropsychopharmacology, 2019, 44, 930-938.	5.4	52
94	Metabolite profiling reveals new insights into the regulation of serum urate in humans. Metabolomics, 2014, 10, 141-151.	3.0	51
95	A genome-wide association study reveals 2 new susceptibility loci for atopic dermatitis. Journal of Allergy and Clinical Immunology, 2015, 136, 802-806.	2.9	51
96	Evidence for Stress-like Alterations in the HPA-Axis in Women Taking Oral Contraceptives. Scientific Reports, 2017, 7, 14111.	3.3	51
97	Revealing the role of the human blood plasma proteome in obesity using genetic drivers. Nature Communications, 2021, 12, 1279.	12.8	50
98	Epigenome-wide association study of lung function level and its change. European Respiratory Journal, 2019, 54, 1900457.	6.7	49
99	Alcohol consumption is associated with widespread changes in blood DNA methylation: Analysis of cross€sectional and longitudinal data. Addiction Biology, 2021, 26, e12855.	2.6	49
100	Genome-wide association analysis in dilated cardiomyopathy reveals two new players in systolic heart failure on chromosomes 3p25.1 and 22q11.23. European Heart Journal, 2021, 42, 2000-2011.	2.2	49
101	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. Genome Biology, 2018, 19, 87.	8.8	47
102	FTO, obesity and the adolescent brain. Human Molecular Genetics, 2013, 22, 1050-1058.	2.9	46
103	Common coding variant in *SERPINA1* increases the risk for large artery stroke. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3613-3618.	7.1	46
104	DNA methylation in human lipid metabolism and related diseases. Current Opinion in Lipidology, 2018, 29, 116-124.	2.7	43
105	Anxiety Associated Increased CpG Methylation in the Promoter of Asb1: A Translational Approach Evidenced by Epidemiological and Clinical Studies and a Murine Model. Neuropsychopharmacology, 2018, 43, 342-353.	5.4	43
106	Association of maternal prenatal smoking GFI1-locus and cardio-metabolic phenotypes in 18,212 adults. EBioMedicine, 2018, 38, 206-216.	6.1	43
107	Epigenetic Link Between Statin Therapy and Type 2 Diabetes. Diabetes Care, 2020, 43, 875-884.	8.6	43
108	Circulating metabolic biomarkers of renal function in diabetic and non-diabetic populations. Scientific Reports, 2018, 8, 15249.	3.3	42

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109	Whole Blood DNA Methylation Signatures of Diet Are Associated With Cardiovascular Disease Risk Factors and All-Cause Mortality. Circulation Genomic and Precision Medicine, 2020, 13, e002766.	3.6	42
110	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	5.2	42
111	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. Journal of the American Society of Nephrology: JASN, 2017, 28, 981-994.	6.1	39
112	Improvement of myocardial infarction risk prediction via inflammation-associated metabolite biomarkers. Heart, 2017, 103, 1278-1285.	2.9	38
113	Fifteen Genetic Loci Associated With the Electrocardiographic P Wave. Circulation: Cardiovascular Genetics, 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. European Journal of Epidemiology, 2019, 34, 409-422.	5.7	37
115	Impact of long-term storage and freeze-thawing on eight circulating microRNAs in plasma samples. PLoS ONE, 2020, 15, e0227648.	2.5	37
116	Epigenetic scores for the circulating proteome as tools for disease prediction. ELife, 2022, 11, .	6.0	37
117	DNA methylation and lipid metabolism: an EWAS of 226 metabolic measures. Clinical Epigenetics, 2021, 13, 7.	4.1	36
118	Differences in Biomarkers of Inflammation Between Novel Subgroups of Recent-Onset Diabetes. Diabetes, 2021, 70, 1198-1208.	0.6	36
119	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. Nature Communications, 2021, 12, 2830.	12.8	35
120	Mitochondrial Genetic Variants Identified to Be Associated with BMI in Adults. PLoS ONE, 2014, 9, e105116.	2.5	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. Carcinogenesis, 2016, 37, 677-684.	2.8	34
122	Deciphering the Plasma Proteome of Type 2 Diabetes. Diabetes, 2020, 69, 2766-2778.	0.6	34
123	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor α. JAMA Cardiology, 2018, 3, 463.	6.1	33
124	Gallstones, Body Mass Index, C–Reactive Protein, and Gallbladder Cancer: Mendelian Randomization Analysis of Chilean and European Genotype Data. Hepatology, 2021, 73, 1783-1796.	7.3	32
125	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. Human Molecular Genetics, 2021, 30, 393-409.	2.9	32
126	Mapping the Genetic Architecture of Gene Regulation in Whole Blood. PLoS ONE, 2014, 9, e93844.	2.5	31

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127	Validated inference of smoking habits from blood with a finite DNA methylation marker set. European Journal of Epidemiology, 2019, 34, 1055-1074.	5.7	31
128	A multi-ancestry genome-wide study incorporating gene–smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
129	Smoking-related changes in DNA methylation and gene expression are associated with cardio-metabolic traits. Clinical Epigenetics, 2020, 12, 157.	4.1	31
130	Deep molecular phenotypes link complex disorders and physiological insult to CpG methylation. Human Molecular Genetics, 2018, 27, 1106-1121.	2.9	30
131	Meta-analyses identify DNA methylation associated with kidney function and damage. Nature Communications, 2021, 12, 7174.	12.8	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. Human Genetics, 2015, 134, 627-636.	3.8	29
133	Discovery of novel heart rate-associated loci using the Exome Chip. Human Molecular Genetics, 2017, 26, 2346-2363.	2.9	29
134	Genome-wide association meta-analysis of 30,000 samples identifies seven novel loci for quantitative ECG traits. European Journal of Human Genetics, 2019, 27, 952-962.	2.8	29
135	Protein-coding variants contribute to the risk of atopic dermatitis and skin-specific gene expression. Journal of Allergy and Clinical Immunology, 2020, 145, 1208-1218.	2.9	29
136	Harmonising and linking biomedical and clinical data across disparate data archives to enable integrative cross-biobank research. European Journal of Human Genetics, 2016, 24, 521-528.	2.8	27
137	ExomeChip-Wide Analysis of 95 626 Individuals Identifies 10 Novel Loci Associated With QT and JT Intervals. Circulation Genomic and Precision Medicine, 2018, 11, e001758.	3.6	27
138	Effects of Calcium, Magnesium, and Potassium Concentrations on Ventricular Repolarization in Unselected Individuals. Journal of the American College of Cardiology, 2019, 73, 3118-3131.	2.8	27
139	Layered genetic control of DNA methylation and gene expression: a locus of multiple sclerosis in healthy individuals. Human Molecular Genetics, 2015, 24, 5733-5745.	2.9	26
140	Predicting sudden cardiac death using common genetic risk variants for coronary artery disease. European Heart Journal, 2015, 36, 1669-1675.	2.2	26
141	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases. Nature Communications, 2022, 13, 2408.	12.8	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. PLoS Genetics, 2010, 6, e1001213.	3.5	24
143	Autosomal genetic variation is associated with DNA methylation in regions variably escaping X-chromosome inactivation. Nature Communications, 2018, 9, 3738.	12.8	24
144	Epigenome-Wide Analysis of Methylation Changes in the Sequence of Gallstone Disease, Dysplasia, and Gallbladder Cancer. Hepatology, 2021, 73, 2293-2310.	7.3	24

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145	Bayesian and frequentist analysis of an Austrian genome-wide association study of colorectal cancer and advanced adenomas. Oncotarget, 2017, 8, 98623-98634.	1.8	23
146	Molecular Characterization of the *NLRC4* Expression in Relation to Interleukin-18 Levels. Circulation: 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. Clinical Epigenetics, 2018, 10, 161.	4.1	20
148	Activated immune–inflammatory pathways are associated with long-standing depressive symptoms: Evidence from gene-set enrichment analyses in the Young Finns Study. Journal of Psychiatric Research, 2015, 71, 120-125.	3.1	19
149	Analysis with the exome array identifies multiple new independent variants in lipid loci. Human Molecular Genetics, 2016, 25, 4094-4106.	2.9	19
150	Characterization of the metabolic profile associated with serum 25-hydroxyvitamin D: a cross-sectional analysis in population-based data. International Journal of Epidemiology, 2016, 45, 1469-1481.	1.9	19
151	RL-SKAT: An Exact and Efficient Score Test for Heritability and Set Tests. Genetics, 2017, 207, 1275-1283.	2.9	19
152	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	3.6	19
153	Metabolic syndrome and the plasma proteome: from association to causation. Cardiovascular Diabetology, 2021, 20, 111.	6.8	19
154	Are Epigenetic Factors Implicated in Chronic Widespread Pain?. PLoS ONE, 2016, 11, e0165548.	2.5	19
155	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. Nature Communications, 2021, 12, 3987.	12.8	18
156	Blood DNA methylation provides an accurate biomarker of *KMT2B*-related dystonia and predicts onset. Brain, 2022, 145, 644-654.	7.6	18
157	Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. Kidney International, 2022, 102, 624-639.	5.2	18
158	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. PLoS ONE, 2019, 14, e0216222.	2.5	17
159	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
160	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	4.4	17
161	Mendelian inheritance of trimodal CpG methylation sites suggests distal cis-acting genetic effects. Clinical Epigenetics, 2016, 8, 124.	4.1	16
162	DNA methylation age is associated with an altered hemostatic profile in a multiethnic meta-analysis. Blood, 2018, 132, 1842-1850.	1.4	16

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163	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2020, 13, 387-395.	3.6	16
164	Plasma Proteomics of Renal Function: A Transethnic Meta-Analysis and Mendelian Randomization Study. Journal of the American Society of Nephrology: JASN, 2021, 32, 1747-1763.	6.1	16
165	The blood metabolome of incident kidney cancer: A case–control study nested within the MetKid consortium. PLoS Medicine, 2021, 18, e1003786.	8.4	16
166	Successful Replication of GWAS Hits for Multiple Sclerosis in 10,000 Germans Using the Exome Array. Genetic Epidemiology, 2015, 39, 601-608.	1.3	15
167	Associations between the 17q21 region and allergic rhinitis in 5 birth cohorts. Journal of Allergy and Clinical Immunology, 2015, 135, 573-576.e5.	2.9	15
168	Gene-gene Interaction Analyses for Atrial Fibrillation. Scientific Reports, 2016, 6, 35371.	3.3	15
169	Genetic Interactions with Age, Sex, Body Mass Index, and Hypertension in Relation to Atrial Fibrillation: The AFGen Consortium. Scientific Reports, 2017, 7, 11303.	3.3	15
170	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. Aging, 2020, 12, 14092-14124.	3.1	15
171	Mitochondrial GWA Analysis of Lipid Profile Identifies Genetic Variants to Be Associated with HDL Cholesterol and Triglyceride Levels. PLoS ONE, 2015, 10, e0126294.	2.5	14
172	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. British Journal of Nutrition, 2015, 113, 1782-1791.	2.3	14
173	Epigenetic Signatures at AQP3 and SOCS3 Engage in Low-Grade Inflammation across Different Tissues. PLoS ONE, 2016, 11, e0166015.	2.5	14
174	Exposure to disinfection byproducts and risk of type 2 diabetes: a nested case–control study in the HUNT and Lifelines cohorts. Metabolomics, 2019, 15, 60.	3.0	14
175	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. Clinical Epigenetics, 2021, 13, 60.	4.1	14
176	On the potential of models for location and scale for genome-wide DNA methylation data. BMC Bioinformatics, 2014, 15, 232.	2.6	13
177	The Pharmacogenetic Footprint of ACE Inhibition: A Population-Based Metabolomics Study. PLoS ONE, 2016, 11, e0153163.	2.5	13
178	Ldlr and ApoE mice better mimic the human metabolite signature of increased carotid intima media thickness compared to other animal models of cardiovascular disease. Atherosclerosis, 2018, 276, 140-147.	0.8	13
179	Novel DNA Methylation Sites Influence GPR15 Expression in Relation to Smoking. Biomolecules, 2018, 8, 74.	4.0	13
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