

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	Associations of carotid intima media thickness with gene expression in whole blood and genetically predicted gene expression across 48 tissues. <i>Human Molecular Genetics</i> , 2022, 31, 1171-1182.	1.4	4
2	Blood DNA methylation provides an accurate biomarker of <i>KMT2B</i>-related dystonia and predicts onset. <i>Brain</i> , 2022, 145, 644-654.	3.7	18
3	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function. <i>Nature Genetics</i> , 2022, 54, 18-29.	9.4	60
4	Epigenetic scores for the circulating proteome as tools for disease prediction. <i>ELife</i> , 2022, 11, .	2.8	37
5	Identification of Circulating lncRNAs Associated with Gallbladder Cancer Risk by Tissue-Based Preselection, Cis-eQTL Validation, and Analysis of Association with Genotype-Based Expression. <i>Cancers</i> , 2022, 14, 634.	1.7	3
6	The Role of Epigenetic Clocks in Explaining Educational Inequalities in Mortality: A Multicohort Study and Meta-analysis. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2022, 77, 1750-1759.	1.7	9
7	Genetic and clinical determinants of abdominal aortic diameter: genome-wide association studies, exome array data and Mendelian randomization study. <i>Human Molecular Genetics</i> , 2022, 31, 3566-3579.	1.4	5
8	Methylation risk scores for childhood aeroallergen sensitization: Results from the LISA birth cohort. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2022, 77, 2803-2817.	2.7	5
9	Integrative analysis of clinical and epigenetic biomarkers of mortality. <i>Aging Cell</i> , 2022, 21, e13608.	3.0	8
10	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
11	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> , 2022, 212, 113360.	3.7	7
12	Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. <i>Kidney International</i> , 2022, 102, 624-639.	2.6	18
13	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022, 5, .	2.0	17
14	Genetics and Epigenetics in Personalized Nutrition: Evidence, Expectations, and Experiences. <i>Molecular Nutrition and Food Research</i> , 2022, 66, .	1.5	8
15	Association between Usual Dietary Intake of Food Groups and DNA Methylation and Effect Modification by Metabotype in the KORA FF4 Cohort. <i>Life</i> , 2022, 12, 1064.	1.1	2
16	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
17	Robust Huber-LASSO for improved prediction of protein, metabolite and gene expression levels relying on individual genotype data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	10
18	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100013.	1.0	2

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19	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. <i>Kidney International</i> , 2021, 99, 926-939.	2.6	42
20	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
21	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
22	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. <i>Human Molecular Genetics</i> , 2021, 30, 393-409.	1.4	32
23	DNA methylation and lipid metabolism: an EWAS of 226 metabolic measures. <i>Clinical Epigenetics</i> , 2021, 13, 7.	1.8	36
24	Revealing the role of the human blood plasma proteome in obesity using genetic drivers. <i>Nature Communications</i> , 2021, 12, 1279.	5.8	50
25	Differences in Biomarkers of Inflammation Between Novel Subgroups of Recent-Onset Diabetes. <i>Diabetes</i> , 2021, 70, 1198-1208.	0.3	36
26	Epigenome-wide association study of whole blood gene expression in Framingham Heart Study participants provides molecular insight into the potential role of <i>CHRNA5</i> in cigarette smoking-related lung diseases. <i>Clinical Epigenetics</i> , 2021, 13, 60.	1.8	14
27	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
28	Multi-ancestry genome-wide gene-sleep interactions identify novel loci for blood pressure. <i>Molecular Psychiatry</i> , 2021, 26, 6293-6304.	4.1	13
29	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.	1.6	10
30	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. <i>Nature Communications</i> , 2021, 12, 2830.	5.8	35
31	Metabolic syndrome and the plasma proteome: from association to causation. <i>Cardiovascular Diabetology</i> , 2021, 20, 111.	2.7	19
32	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.	3.8	90
33	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. <i>Nature Communications</i> , 2021, 12, 3987.	5.8	18
34	DNAm-based signatures of accelerated aging and mortality in blood are associated with low renal function. <i>Clinical Epigenetics</i> , 2021, 13, 121.	1.8	13
35	Meta-analysis of epigenome-wide association studies of carotid intima-media thickness. <i>European Journal of Epidemiology</i> , 2021, 36, 1143-1155.	2.5	10
36	Plasma Proteomics of Renal Function: A Transethnic Meta-Analysis and Mendelian Randomization Study. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 1747-1763.	3.0	16

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37	Methylation status of nc886 epiallele reflects periconceptual conditions and is associated with glucose metabolism through nc886 RNAs. <i>Clinical Epigenetics</i> , 2021, 13, 143.	1.8	13
38	The blood metabolome of incident kidney cancer: A caseâ€“control study nested within the MetKid consortium. <i>PLoS Medicine</i> , 2021, 18, e1003786.	3.9	16
39	Validating biomarkers and models for epigenetic inference of alcohol consumption from blood. <i>Clinical Epigenetics</i> , 2021, 13, 198.	1.8	7
40	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. <i>Nature Communications</i> , 2021, 12, 7173.	5.8	8
41	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021, 12, 7174.	5.8	30
42	Abstract 14025: Atrial Fibrillation is Associated With Reduced Telomere Length. <i>Circulation</i> , 2021, 144, .	1.6	0
43	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
44	Arsenic and gallbladder cancer risk: Mendelian randomization analysis of European prospective data. <i>International Journal of Cancer</i> , 2020, 146, 2648-2650.	2.3	6
45	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
46	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
47	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.	2.4	5
48	Deciphering the Plasma Proteome of Type 2 Diabetes. <i>Diabetes</i> , 2020, 69, 2766-2778.	0.3	34
49	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, 387-395.	1.6	16
50	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. <i>Molecular Psychiatry</i> , 2020, 26, 2111-2125.	4.1	17
51	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020, 11, 2542.	5.8	59
52	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
53	DeepWAS: Multivariate genotype-phenotype associations by directly integrating regulatory information using deep learning. <i>PLoS Computational Biology</i> , 2020, 16, e1007616.	1.5	54
54	Epigenetic Link Between Statin Therapy and Type 2 Diabetes. <i>Diabetes Care</i> , 2020, 43, 875-884.	4.3	43

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55	ABCB1/4 gallbladder cancer risk variants identified in India also show strong effects in Chileans. <i>Cancer Epidemiology</i> , 2020, 65, 101643.	0.8	9
56	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
57	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.	1.1	8
58	Abstract 21: Deciphering the Plasma Proteome of Type 2 Diabetes. <i>Circulation</i> , 2020, 141, .	1.6	1
59	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. <i>Aging</i> , 2020, 12, 14092-14124.	1.4	15
60	Accelerated epigenetic aging as a risk factor for chronic obstructive pulmonary disease and decreased lung function in two prospective cohort studies. <i>Aging</i> , 2020, 12, 16539-16554.	1.4	13
61	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
62	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
63	Epigenome-wide association study of lung function level and its change. <i>European Respiratory Journal</i> , 2019, 54, 1900457.	3.1	49
64	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	5.8	84
65	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
66	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.	1.4	3
67	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
68	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019, 10, 4130.	5.8	133
69	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	9.4	251
70	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
71	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
72	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

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73	Methylation of the FKBP5 gene in association with FKBP5 genotypes, childhood maltreatment and depression. <i>Neuropsychopharmacology</i> , 2019, 44, 930-938.	2.8	52
74	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376.	5.8	64
75	Methylome-wide association study provides evidence of particulate matter air pollution-associated DNA methylation. <i>Environment International</i> , 2019, 132, 104723.	4.8	58
76	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
77	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
78	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.	3.3	193
79	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. <i>PLoS ONE</i> , 2019, 14, e0216222.	1.1	17
80	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.	1.4	14
81	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
82	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
83	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
84	Socioeconomic position, lifestyle habits and biomarkers of epigenetic aging: a multi-cohort analysis. <i>Aging</i> , 2019, 11, 2045-2070.	1.4	137
85	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor \pm . <i>JAMA Cardiology</i> , 2018, 3, 463.	3.0	33
86	DNA methylation in human lipid metabolism and related diseases. <i>Current Opinion in Lipidology</i> , 2018, 29, 116-124.	1.2	43
87	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
88	Deep molecular phenotypes link complex disorders and physiological insult to CpG methylation. <i>Human Molecular Genetics</i> , 2018, 27, 1106-1121.	1.4	30
89	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
90	Detecting heritable phenotypes without a model using fast permutation testing for heritability and set-tests. <i>Nature Communications</i> , 2018, 9, 4919.	5.8	6

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91	Association of maternal prenatal smoking GFI1-locus and cardio-metabolic phenotypes in 18,212 adults. EBioMedicine, 2018, 38, 206-216.	2.7	43
92	Analysis of repeated leukocyte DNA methylation assessments reveals persistent epigenetic alterations after an incident myocardial infarction. Clinical Epigenetics, 2018, 10, 161.	1.8	20
93	Long-term Air Pollution Exposure, Genome-wide DNA Methylation and Lung Function in the LifeLines Cohort Study. Environmental Health Perspectives, 2018, 126, 027004.	2.8	71
94	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.	1.6	27
95	Genetics of the thrombomodulin-endothelial cell protein C receptor system and the risk of early-onset ischemic stroke. PLoS ONE, 2018, 13, e0206554.	1.1	8
96	Circulating metabolic biomarkers of renal function in diabetic and non-diabetic populations. Scientific Reports, 2018, 8, 15249.	1.6	42
97	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.	2.6	326
98	Autosomal genetic variation is associated with DNA methylation in regions variably escaping X-chromosome inactivation. Nature Communications, 2018, 9, 3738.	5.8	24
99	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	1.6	19
100	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. Nature Communications, 2018, 9, 2904.	5.8	71
101	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.	0.4	13
102	DNA methylation age is associated with an altered hemostatic profile in a multiethnic meta-analysis. Blood, 2018, 132, 1842-1850.	0.6	16
103	Fatty liver is associated with blood pathways of inflammatory response, immune system activation and prothrombotic state in Young Finns Study. Scientific Reports, 2018, 8, 10358.	1.6	10
104	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. Genome Biology, 2018, 19, 87.	3.8	47
105	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. JAMA Psychiatry, 2018, 75, 949.	6.0	78
106	Novel DNA Methylation Sites Influence GPR15 Expression in Relation to Smoking. Biomolecules, 2018, 8, 74.	1.8	13
107	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	1.1	94
108	Improvement of myocardial infarction risk prediction via inflammation-associated metabolite biomarkers. Heart, 2017, 103, 1278-1285.	1.2	38

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109	Common coding variant in <i>SERPINA1</i> increases the risk for large artery stroke. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3613-3618.	3.3	46
110	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. Journal of the American College of Cardiology, 2017, 69, 823-836.	1.2	214
111	Discovery of novel heart rate-associated loci using the Exome Chip. Human Molecular Genetics, 2017, 26, 2346-2363.	1.4	29
112	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	9.4	279
113	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	5.8	169
114	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	1.6	98
115	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	5.8	95
116	Blood pathway analyses reveal differences between prediabetic subjects with or without dyslipidaemia. The Cardiovascular Risk in Young Finns Study. Diabetes/Metabolism Research and Reviews, 2017, 33, e2914.	1.7	3
117	DNA methylation signatures in peripheral blood strongly predict all-cause mortality. Nature Communications, 2017, 8, 14617.	5.8	221
118	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.	3.0	39
119	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. Nature, 2017, 541, 81-86.	13.7	743
120	Evidence for Stress-like Alterations in the HPA-Axis in Women Taking Oral Contraceptives. Scientific Reports, 2017, 7, 14111.	1.6	51
121	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
122	RL-SKAT: An Exact and Efficient Score Test for Heritability and Set Tests. Genetics, 2017, 207, 1275-1283.	1.2	19
123	Genetic Interactions with Age, Sex, Body Mass Index, and Hypertension in Relation to Atrial Fibrillation: The AFGen Consortium. Scientific Reports, 2017, 7, 11303.	1.6	15
124	Genetic variants including markers from the exome chip and metabolite traits of type 2 diabetes. Scientific Reports, 2017, 7, 6037.	1.6	12
125	Fifteen Genetic Loci Associated With the Electrocardiographic P Wave. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	38
126	Influence of Storage and Inter- and Intra-Assay Variability on the Measurement of Inflammatory Biomarkers in Population-Based Biobanking. Biopreservation and Biobanking, 2017, 15, 512-518.	0.5	3

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127	Genome-wide methylation data mirror ancestry information. <i>Epigenetics and Chromatin</i> , 2017, 10, 1.	1.8	120
128	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
129	pulver: an R package for parallel ultra-rapid p-value computation for linear regression interaction terms. <i>BMC Bioinformatics</i> , 2017, 18, 429.	1.2	1
130	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
131	Genetically defined elevated homocysteine levels do not result in widespread changes of DNA methylation in leukocytes. <i>PLoS ONE</i> , 2017, 12, e0182472.	1.1	10
132	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
133	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
134	Epigenetic Signatures at AQP3 and SOCS3 Engage in Low-Grade Inflammation across Different Tissues. <i>PLoS ONE</i> , 2016, 11, e0166015.	1.1	14
135	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
136	The Pharmacogenetic Footprint of ACE Inhibition: A Population-Based Metabolomics Study. <i>PLoS ONE</i> , 2016, 11, e0153163.	1.1	13
137	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016, 17, 255.	3.8	251
138	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
139	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
140	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
141	Cystatin C and Cardiovascular Disease. <i>Journal of the American College of Cardiology</i> , 2016, 68, 934-945.	1.2	109
142	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
143	A Whole-Blood Transcriptome Meta-Analysis Identifies Gene Expression Signatures of Cigarette Smoking. <i>Human Molecular Genetics</i> , 2016, 25, ddw288.	1.4	76
144	Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 436-447.	5.1	678

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145	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
146	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1435-1448.	1.2	113
147	Gene-gene Interaction Analyses for Atrial Fibrillation. <i>Scientific Reports</i> , 2016, 6, 35371.	1.6	15
148	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
149	Novel multiple sclerosis susceptibility loci implicated in epigenetic regulation. <i>Science Advances</i> , 2016, 2, e1501678.	4.7	133
150	Mendelian inheritance of trimodal CpG methylation sites suggests distal cis-acting genetic effects. <i>Clinical Epigenetics</i> , 2016, 8, 124.	1.8	16
151	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
152	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
153	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
154	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. <i>Diabetes</i> , 2016, 65, 803-817.	0.3	131
155	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
156	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
157	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
158	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
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