

# AndrÃ© G Uitterlinden

## List of Publications by Year in descending order

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Version: 2024-02-01

606  
papers

110,994  
citations

219

146  
h-index

259

300  
g-index

635  
all docs

635  
docs citations

635  
times ranked

88481  
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	Serum Phosphate, BMI, and Body Composition of Middle-Aged and Older Adults: A Cross-Sectional Association Analysis and Bidirectional Mendelian Randomization Study. <i>Journal of Nutrition</i> , 2022, 152, 276-285.	1.3	6
3	Skin Autofluorescence, a Noninvasive Biomarker for Advanced Glycation End-products, Is Associated With Sarcopenia. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2022, 107, e793-e803.	1.8	13
4	Impact of SNP microarray analysis of compromised DNA on kinship classification success in the context of investigative genetic genealogy. <i>Forensic Science International: Genetics</i> , 2022, 56, 102625.	1.6	32
5	Obesity Partially Mediates the Diabetogenic Effect of Lowering LDL Cholesterol. <i>Diabetes Care</i> , 2022, 45, 232-240.	4.3	10
6	Genome-wide analysis of mitochondrial DNA copy number reveals loci implicated in nucleotide metabolism, platelet activation, and megakaryocyte proliferation. <i>Human Genetics</i> , 2022, 141, 127-146.	1.8	30
7	Skin Autofluorescence, a Noninvasive Biomarker of Advanced Glycation End-products, Is Associated With Frailty: The Rotterdam Study. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2022, 77, 2032-2039.	1.7	5
8	Elucidating the relationship between migraine risk and brain structure using genetic data. <i>Brain</i> , 2022, 145, 3214-3224.	3.7	7
9	Genome-wide study of DNA methylation shows alterations in metabolic, inflammatory, and cholesterol pathways in ALS. <i>Science Translational Medicine</i> , 2022, 14, eabj0264.	5.8	38
10	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
11	Diversity in human genetics studies accelerates discovery and improves health care. <i>Nature Reviews Cardiology</i> , 2022, 19, 289-290.	6.1	4
12	Development of the AD <i>&gt;</i> F <i>&lt;</i> /i>ICE_IT Models for Predicting Falls and Recurrent Falls in Community-Dwelling Older Adults: Pooled Analyses of European Cohorts With Special Attention to Medication. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2022, 77, 1446-1454.	1.7	8
13	DNA methylation in peripheral tissues and left-handedness. <i>Scientific Reports</i> , 2022, 12, 5606.	1.6	12
14	New insights into the genetic etiology of Alzheimer's disease and related dementias. <i>Nature Genetics</i> , 2022, 54, 412-436.	9.4	700
15	Role of the Microbiome in Regulating Bone Metabolism and Susceptibility to Osteoporosis. <i>Calcified Tissue International</i> , 2022, 110, 273-284.	1.5	22
16	OUP accepted manuscript. <i>Human Reproduction</i> , 2022, , .	0.4	2
17	Candidate genetic variants and antidepressant-related fall risk in middle-aged and older adults. <i>PLoS ONE</i> , 2022, 17, e0266590.	1.1	1
18	Whole-exome sequencing of 14%389 individuals from the ESP and CHARGE consortia identifies novel rare variation associated with hemostatic factors. <i>Human Molecular Genetics</i> , 2022, 31, 3120-3132.	1.4	3

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19	Genomic analysis of diet composition finds novel loci and associations with health and lifestyle. <i>Molecular Psychiatry</i> , 2021, 26, 2056-2069.	4.1	79
20	Microbiomics, Metabolomics, Predicted Metagenomics, and Hepatic Steatosis in a Population-Based Study of 1,355 Adults. <i>Hepatology</i> , 2021, 73, 968-982.	3.6	43
21	Genome-wide association study identifies 48 common genetic variants associated with handedness. <i>Nature Human Behaviour</i> , 2021, 5, 59-70.	6.2	79
22	Genome-wide association of phenotypes based on clustering patterns of hand osteoarthritis identify <i>WNT9A</i> as novel osteoarthritis gene. <i>Annals of the Rheumatic Diseases</i> , 2021, 80, 367-375.	0.5	26
23	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
24	Long-term effects of folic acid and vitamin-B12 supplementation on fracture risk and cardiovascular disease: Extended follow-up of the B-PROOF trial. <i>Clinical Nutrition</i> , 2021, 40, 1199-1206.	2.3	9
25	Assessment of Advanced Glycation End Products and Receptors and the Risk of Dementia. <i>JAMA Network Open</i> , 2021, 4, e2033012.	2.8	29
26	Genetics of osteoporosis. , 2021, , 405-451.		5
27	Genome-wide meta-analysis of muscle weakness identifies 15 susceptibility loci in older men and women. <i>Nature Communications</i> , 2021, 12, 654.	5.8	75
28	DNA methylation signatures of aggression and closely related constructs: A meta-analysis of epigenome-wide studies across the lifespan. <i>Molecular Psychiatry</i> , 2021, 26, 2148-2162.	4.1	21
29	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	9.4	676
30	Age-dependent sex differences in calcium and phosphate homeostasis. <i>Endocrine Connections</i> , 2021, 10, 273-282.	0.8	19
31	Multi-ancestry genome-wide gene-sleep interactions identify novel loci for blood pressure. <i>Molecular Psychiatry</i> , 2021, 26, 6293-6304.	4.1	13
32	Vitamin K antagonist anticoagulant usage is associated with increased incidence and progression of osteoarthritis. <i>Annals of the Rheumatic Diseases</i> , 2021, 80, 598-604.	0.5	21
33	Plasma amyloid $\beta$ levels are driven by genetic variants near <i>APOE</i> , <i>BACE1</i> , <i>APP</i> , <i>PSEN2</i> : A genome-wide association study in over 12,000 non-demented participants. <i>Alzheimer's and Dementia</i> , 2021, 17, 1663-1674.	0.4	20
34	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. <i>Nature Communications</i> , 2021, 12, 2830.	5.8	35
35	Genetic analysis in European ancestry individuals identifies 517 loci associated with liver enzymes. <i>Nature Communications</i> , 2021, 12, 2579.	5.8	51
36	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	9.4	341

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37	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.	3.8	90
38	A comparison of genotyping arrays. <i>European Journal of Human Genetics</i> , 2021, 29, 1611-1624.	1.4	43
39	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. <i>Nature Communications</i> , 2021, 12, 3987.	5.8	18
40	Genetic association study of childhood aggression across raters, instruments, and age. <i>Translational Psychiatry</i> , 2021, 11, 413.	2.4	31
41	TCERG1L allelic variation is associated with cisplatin-induced hearing loss in childhood cancer, a PanCareLIFE study. <i>Npj Precision Oncology</i> , 2021, 5, 64.	2.3	8
42	Association of Insulin Resistance and Type 2 Diabetes With Gut Microbial Diversity. <i>JAMA Network Open</i> , 2021, 4, e2118811.	2.8	119
43	Multiethnic Genome-Wide Association Study of Subclinical Atherosclerosis in Individuals With Type 2 Diabetes. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003258.	1.6	4
44	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	13.7	183
45	Continuity of Genetic Risk for Aggressive Behavior Across the Life-Course. <i>Behavior Genetics</i> , 2021, 51, 592-606.	1.4	13
46	The genomics of heart failure: design and rationale of the HERMES consortium. <i>ESC Heart Failure</i> , 2021, 8, 5531-5541.	1.4	11
47	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	9.4	218
48	Prevalence of and risk factors for extended-spectrum beta-lactamase genes carriership in a population-based cohort of middle-aged and elderly. <i>International Journal of Antimicrobial Agents</i> , 2021, 58, 106388.	1.1	4
49	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. <i>Cell</i> , 2021, 184, 4784-4818.e17.	13.5	188
50	Genome-wide association study of frontotemporal dementia identifies a C9ORF72 haplotype with a median of 12-G4C2 repeats that predisposes to pathological repeat expansions. <i>Translational Psychiatry</i> , 2021, 11, 451.	2.4	6
51	Validating biomarkers and models for epigenetic inference of alcohol consumption from blood. <i>Clinical Epigenetics</i> , 2021, 13, 198.	1.8	7
52	CYP11B1 variants influence skeletal maturation via alternative splicing. <i>Communications Biology</i> , 2021, 4, 1274.	2.0	3
53	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. <i>Nature Genetics</i> , 2021, 53, 1636-1648.	9.4	223
54	B-vitamins and body composition: integrating observational and experimental evidence from the B-PROOF study. <i>European Journal of Nutrition</i> , 2020, 59, 1253-1262.	1.8	8

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55	Do Vitamin D Level and Dietary Calcium Intake Modify the Association Between Loop Diuretics and Bone Health?. <i>Calcified Tissue International</i> , 2020, 106, 104-114.	1.5	4
56	Maternal environmental risk factors and the development of internalizing and externalizing problems in childhood: The complex role of genetic factors. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2020, 183, 17-25.	1.1	18
57	Vertebral Fractures in Individuals With Type 2 Diabetes: More Than Skeletal Complications Alone. <i>Diabetes Care</i> , 2020, 43, 137-144.	4.3	82
58	Genetic variation of cisplatin-induced ototoxicity in non-cranial-irradiated pediatric patients using a candidate gene approach: The International PanCareLIFE Study. <i>Pharmacogenomics Journal</i> , 2020, 20, 294-305.	0.9	28
59	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. <i>Nature Communications</i> , 2020, 11, 163.	5.8	466
60	Genome-wide meta-analysis of variant-by-diuretic interactions as modulators of lipid traits in persons of European and African ancestry. <i>Pharmacogenomics Journal</i> , 2020, 20, 482-493.	0.9	4
61	Skeletal maturation in relation to ethnic background in children of school age: The Generation R Study. <i>Bone</i> , 2020, 132, 115180.	1.4	18
62	Genetic basis of falling risk susceptibility in the UK Biobank Study. <i>Communications Biology</i> , 2020, 3, 543.	2.0	17
63	Usefulness of current candidate genetic markers to identify childhood cancer patients at risk for platinum-induced ototoxicity: Results of the European PanCareLIFE cohort study. <i>European Journal of Cancer</i> , 2020, 138, 212-224.	1.3	31
64	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. <i>Nature Communications</i> , 2020, 11, 4796.	5.8	61
65	Serum fatty acid chain length associates with prevalent symptomatic end-stage osteoarthritis, independent of BMI. <i>Scientific Reports</i> , 2020, 10, 15459.	1.6	7
66	Novel loci for childhood body mass index and shared heritability with adult cardiometabolic traits. <i>PLoS Genetics</i> , 2020, 16, e1008718.	1.5	95
67	Association of candidate pharmacogenetic markers with platinum-induced ototoxicity: PanCareLIFE dataset. <i>Data in Brief</i> , 2020, 32, 106227.	0.5	2
68	Long-term effects of antimicrobial drugs on the composition of the human gut microbiota. <i>Gut Microbes</i> , 2020, 12, 1791677.	4.3	31
69	Somatic <i>TARDBP</i> variants as a cause of semantic dementia. <i>Brain</i> , 2020, 143, 3827-3841.	3.7	12
70	Reduced penetrance of pathogenic ACMG variants in a deeply phenotyped cohort study and evaluation of ClinVar classification over time. <i>Genetics in Medicine</i> , 2020, 22, 1812-1820.	1.1	24
71	Dietary Advanced Glycation End-Products (dAGEs) Intake and Bone Health: A Cross-Sectional Analysis in the Rotterdam Study. <i>Nutrients</i> , 2020, 12, 2377.	1.7	13
72	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

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73	Genome-wide identification of genes regulating DNA methylation using genetic anchors for causal inference. <i>Genome Biology</i> , 2020, 21, 220.	3.8	27
74	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. <i>Diabetes</i> , 2020, 69, 2806-2818.	0.3	26
75	The role of the gut microbiome in cognitive function and Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2020, 16, e043197.	0.4	1
76	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
77	Objectives, design and main findings until 2020 from the Rotterdam Study. <i>European Journal of Epidemiology</i> , 2020, 35, 483-517.	2.5	314
78	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. <i>PLoS ONE</i> , 2020, 15, e0230815.	1.1	10
79	Skin Autofluorescence, a Noninvasive Biomarker for Advanced Glycation End Products, Is Associated With Prevalent Vertebral and Major Osteoporotic Fractures: The Rotterdam Study. <i>Journal of Bone and Mineral Research</i> , 2020, 35, 1904-1913.	3.1	28
80	The association between dietary and skin advanced glycation end products: the Rotterdam Study. <i>American Journal of Clinical Nutrition</i> , 2020, 112, 129-137.	2.2	24
81	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020, 11, 2542.	5.8	59
82	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
83	The impact of thiazide diuretics on bone mineral density and the trabecular bone score: the Rotterdam Study. <i>Bone</i> , 2020, 138, 115475.	1.4	13
84	Translation of mouse model to human gives insights into periodontitis etiology. <i>Scientific Reports</i> , 2020, 10, 4892.	1.6	12
85	Validation of the BOADICEA model and a 313-variant polygenic risk score for breast cancer risk prediction in a Dutch prospective cohort. <i>Genetics in Medicine</i> , 2020, 22, 1803-1811.	1.1	49
86	Exercise with food withdrawal at thermoneutrality impacts fuel use, the microbiome, AMPK phosphorylation, muscle fibers, and thyroid hormone levels in rats. <i>Physiological Reports</i> , 2020, 8, e14354.	0.7	15
87	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. <i>American Journal of Human Genetics</i> , 2020, 106, 389-404.	2.6	118
88	Integration of epidemiologic, pharmacologic, genetic and gut microbiome data in a drug metabolite atlas. <i>Nature Medicine</i> , 2020, 26, 110-117.	15.2	54
89	Diversity, compositional and functional differences between gut microbiota of children and adults. <i>Scientific Reports</i> , 2020, 10, 1040.	1.6	89
90	Rapid Low-Cost Microarray-Based Genotyping for Genetic Screening in Primary Immunodeficiency. <i>Frontiers in Immunology</i> , 2020, 11, 614.	2.2	21

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91	Genome-wide meta-analysis identifies eight new susceptibility loci for cutaneous squamous cell carcinoma. <i>Nature Communications</i> , 2020, 11, 820.	5.8	30
92	Genetic loci associated with prevalent and incident myocardial infarction and coronary heart disease in the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. <i>PLoS ONE</i> , 2020, 15, e0230035.	1.1	5
93	Advanced glycation end products, their receptor and the risk of dementia in the general population: A prospective cohort study. <i>Alzheimer's and Dementia</i> , 2020, 16, e043005.	0.4	1
94	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
95	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
96	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
97	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
98	Linkage analysis and whole exome sequencing identify a novel candidate gene in a Dutch multiple sclerosis family. <i>Multiple Sclerosis Journal</i> , 2019, 25, 909-917.	1.4	19
99	Interaction between plasma homocysteine and the <i>MTHFR C.677C &gt; T</i> polymorphism is associated with site-specific changes in DNA methylation in humans. <i>FASEB Journal</i> , 2019, 33, 833-843.	0.2	14
100	Genome-wide meta-analysis of SNP-by-ACEI/ARB and SNP-by-thiazide diuretic and effect on serum potassium in cohorts of European and African ancestry. <i>Pharmacogenomics Journal</i> , 2019, 19, 97-108.	0.9	3
101	EIF2AK3 variants in Dutch patients with Alzheimer's disease. <i>Neurobiology of Aging</i> , 2019, 73, 229.e11-229.e18.	1.5	25
102	Genome-wide meta-analysis of macronutrient intake of 91,114 European ancestry participants from the cohorts for heart and aging research in genomic epidemiology consortium. <i>Molecular Psychiatry</i> , 2019, 24, 1920-1932.	4.1	44
103	A meta-analysis of genome-wide association studies identifies multiple longevity genes. <i>Nature Communications</i> , 2019, 10, 3669.	5.8	214
104	Potential Interplay between Dietary Saturated Fats and Genetic Variants of the NLRP3 Inflammasome to Modulate Insulin Resistance and Diabetes Risk: Insights from a Meta-Analysis of 19,005 Individuals. <i>Molecular Nutrition and Food Research</i> , 2019, 63, e1900226.	1.5	12
105	A trans-ancestral meta-analysis of genome-wide association studies reveals loci associated with childhood obesity. <i>Human Molecular Genetics</i> , 2019, 28, 3327-3338.	1.4	76
106	Intestinal microbiome composition and its relation to joint pain and inflammation. <i>Nature Communications</i> , 2019, 10, 4881.	5.8	176
107	Genome-wide association meta-analysis identifies five novel loci for age-related hearing impairment. <i>Scientific Reports</i> , 2019, 9, 15192.	1.6	32
108	Disentangling the genetics of lean mass. <i>American Journal of Clinical Nutrition</i> , 2019, 109, 276-287.	2.2	38



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109	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. <i>BMC Cardiovascular Disorders</i> , 2019, 19, 240.	0.7	22
110	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	5.8	84
111	β2-Adrenergic Receptor (ADRB2) Gene Polymorphisms and Risk of COPD Exacerbations: The Rotterdam Study. <i>Journal of Clinical Medicine</i> , 2019, 8, 1835.	1.0	12
112	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
113	GWAS on longitudinal growth traits reveals different genetic factors influencing infant, child, and adult BMI. <i>Science Advances</i> , 2019, 5, eaaw3095.	4.7	86
114	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
115	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019, 10, 4130.	5.8	133
116	Association of Birth Weight With Type 2 Diabetes and Glycemic Traits. <i>JAMA Network Open</i> , 2019, 2, e1910915.	2.8	41
117	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	9.4	251
118	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
119	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
120	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376.	5.8	64
121	Fractures in school age children in relation to sex and ethnic background: The Generation R Study. <i>Bone</i> , 2019, 121, 227-231.	1.4	7
122	Association of dietary folate and vitamin B-12 intake with genome-wide DNA methylation in blood: a large-scale epigenome-wide association analysis in 5841 individuals. <i>American Journal of Clinical Nutrition</i> , 2019, 110, 437-450.	2.2	46
123	Update on the predictability of tall stature from DNA markers in Europeans. <i>Forensic Science International: Genetics</i> , 2019, 42, 8-13.	1.6	18
124	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
125	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. <i>Nature Communications</i> , 2019, 10, 2581.	5.8	62
126	Molecular Alterations in Dog Pheochromocytomas and Paragangliomas. <i>Cancers</i> , 2019, 11, 607.	1.7	13



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127	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. PLoS ONE, 2019, 14, e0216222.	1.1	17
128	GWAS of bone size yields twelve loci that also affect height, BMD, osteoarthritis or fractures. Nature Communications, 2019, 10, 2054.	5.8	74
129	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	9.4	402
130	Meta-Analysis of Genomewide Association Studies Reveals Genetic Variants for Hip Bone Geometry. Journal of Bone and Mineral Research, 2019, 34, 1284-1296.	3.1	27
131	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.	1.4	31
132	Multi-ancestry genome-wide gene€smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	9.4	112
133	Femoral stress is prominently associated with fracture risk in children: The Generation R Study. Bone, 2019, 122, 150-155.	1.4	5
134	Newborn DNA-methylation, childhood lung function, and the risks of asthma and COPD across the life course. European Respiratory Journal, 2019, 53, 1801795.	3.1	48
135	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
136	Relationship between gut microbiota and circulating metabolites in population-based cohorts. Nature Communications, 2019, 10, 5813.	5.8	168
137	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	9.4	192
138	Meta-analysis of genome-wide association studies of aggressive and chronic periodontitis identifies two novel risk loci. European Journal of Human Genetics, 2019, 27, 102-113.	1.4	58
139	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. American Journal of Human Genetics, 2019, 104, 112-138.	2.6	106
140	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. Circulation, 2019, 139, 620-635.	1.6	102
141	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. Nature Genetics, 2019, 51, 245-257.	9.4	536
142	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. Blood, 2019, 133, 967-977.	0.6	34
143	The effect of antimicrobial drug use on the composition of the genitourinary microbiota in an elderly population. BMC Microbiology, 2019, 19, 9.	1.3	21
144	Folic Acid and Vitamin B12 Supplementation and the Risk of Cancer: Long-term Follow-up of the B Vitamins for the Prevention of Osteoporotic Fractures (B-PROOF) Trial. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 275-282.	1.1	56

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145	Hippocampal transcriptome profiling combined with protein-protein interaction analysis elucidates Alzheimer's disease pathways and genes. <i>Neurobiology of Aging</i> , 2019, 74, 225-233.	1.5	30
146	Response to VilariÄ±o-GÄ¼ell et al.. <i>Multiple Sclerosis Journal</i> , 2019, 25, 1013-1015.	1.4	0
147	Serum 25-hydroxyvitamin D3 is associated with advanced glycation end products (AGEs) measured as skin autofluorescence: The Rotterdam Study. <i>European Journal of Epidemiology</i> , 2019, 34, 67-77.	2.5	14
148	Are Bone Mineral Density and Fractures Related to the Incidence and Progression of Radiographic Osteoarthritis of the Knee, Hip, and Hand in Elderly Men and Women? The Rotterdam Study. <i>Arthritis and Rheumatology</i> , 2019, 71, 361-369.	2.9	22
149	Candidate CSPG4 mutations and induced pluripotent stem cell modeling implicate oligodendrocyte progenitor cell dysfunction in familial schizophrenia. <i>Molecular Psychiatry</i> , 2019, 24, 757-771.	4.1	51
150	KCND3 potassium channel gene variant confers susceptibility to electrocardiographic early repolarization pattern. <i>JCI Insight</i> , 2019, 4, .	2.3	15
151	Genetic Determinants of Ototoxicity During and After Childhood Cancer Treatment: Protocol for the PanCareLIFE Study. <i>JMIR Research Protocols</i> , 2019, 8, e11868.	0.5	10
152	MON-208 Association Study of AMH Promoter Polymorphisms and Serum AMH Levels in PCOS Patients. <i>Journal of the Endocrine Society</i> , 2019, 3, .	0.1	0
153	Development of a prediction model for future risk of radiographic hip osteoarthritis. <i>Osteoarthritis and Cartilage</i> , 2018, 26, 540-546.	0.6	33
154	Sarcopenia and Its Clinical Correlates in the General Population: The Rotterdam Study. <i>Journal of Bone and Mineral Research</i> , 2018, 33, 1209-1218.	3.1	51
155	Genome-wide association meta-analysis of individuals of European ancestry identifies new loci explaining a substantial fraction of hair color variation and heritability. <i>Nature Genetics</i> , 2018, 50, 652-656.	9.4	86
156	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor Î±. <i>JAMA Cardiology</i> , 2018, 3, 463.	3.0	33
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