AndrÃ© G Uitterlinden

List of Publications by Year
in descending order

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. Human Molecular Genetics, 2022, 31, 1171-1182.	2.9	4
2	Serum Phosphate, BMI, and Body Composition of Middle-Aged and Older Adults: A Cross-Sectional Association Analysis and Bidirectional Mendelian Randomization Study. Journal of Nutrition, 2022, 152, 276-285.	2.9	6
3	Skin Autofluorescence, a Noninvasive Biomarker for Advanced Glycation End-products, Is Associated With Sarcopenia. Journal of Clinical Endocrinology and Metabolism, 2022, 107, e793-e803.	3.6	13
4	Impact of SNP microarray analysis of compromised DNA on kinship classification success in the context of investigative genetic genealogy. Forensic Science International: Genetics, 2022, 56, 102625.	3.1	32
5	Obesity Partially Mediates the Diabetogenic Effect of Lowering LDL Cholesterol. Diabetes Care, 2022, 45, 232-240.	8.6	10
6	Genome-wide analysis of mitochondrial DNA copy number reveals loci implicated in nucleotide metabolism, platelet activation, and megakaryocyte proliferation. Human Genetics, 2022, 141, 127-146.	3.8	30
7	Skin Autofluorescence, a Noninvasive Biomarker of Advanced Glycation End-products, Is Associated With Frailty: The Rotterdam Study. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2022, 77, 2032-2039.	3.6	5
8	Elucidating the relationship between migraine risk and brain structure using genetic data. Brain, 2022, 145, 3214-3224.	7.6	7
9	Genome-wide study of DNA methylation shows alterations in metabolic, inflammatory, and cholesterol pathways in ALS. Science Translational Medicine, 2022, 14, eabj0264.	12.4	38
10	Genetic and clinical determinants of abdominal aortic diameter: genome-wide association studies, exome array data and Mendelian randomization study. Human Molecular Genetics, 2022, 31, 3566-3579.	2.9	5
11	Diversity in human genetics studies accelerates discovery and improves health care. Nature Reviews Cardiology, 2022, 19, 289-290.	13.7	4
12	Development of the ADFICE_IT Models for Predicting Falls and Recurrent Falls in Community-Dwelling Older Adults: Pooled Analyses of European Cohorts With Special Attention to Medication. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2022, 77, 1446-1454.	3.6	8
13	DNA methylation in peripheral tissues and left-handedness. Scientific Reports, 2022, 12, 5606.	3.3	12
14	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	21.4	700
15	Role of the Microbiome in Regulating Bone Metabolism and Susceptibility to Osteoporosis. Calcified Tissue International, 2022, 110, 273-284.	3.1	22
16	OUP accepted manuscript. Human Reproduction, 2022, , .	0.9	2
17	Candidate genetic variants and antidepressant-related fall risk in middle-aged and older adults. PLoS ONE, 2022, 17, e0266590.	2.5	1
18	Whole-exome sequencing of 14â€‰389 individuals from the ESP and CHARGE consortia identifies novel rare variation associated with hemostatic factors. Human Molecular Genetics, 2022, 31, 3120-3132.	2.9	3

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19	Genomic analysis of diet composition finds novel loci and associations with health and lifestyle. Molecular Psychiatry, 2021, 26, 2056-2069.	7.9	79
20	Microbiomics, Metabolomics, Predicted Metagenomics, and Hepatic Steatosis in a Populationâ€Based Study of 1,355 Adults. Hepatology, 2021, 73, 968-982.	7.3	43
21	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	12.0	79
22	Genome-wide association of phenotypes based on clustering patterns of hand osteoarthritis identifyWNT9Aas novel osteoarthritis gene. Annals of the Rheumatic Diseases, 2021, 80, 367-375.	0.9	26
23	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. Human Genetics and Genomics Advances, 2021, 2, 100013.	1.7	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. Clinical Nutrition, 2021, 40, 1199-1206.	5.0	9
25	Assessment of Advanced Glycation End Products and Receptors and the Risk of Dementia. JAMA Network Open, 2021, 4, e2033012.	5.9	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. Nature Communications, 2021, 12, 654.	12.8	75
28	DNA methylation signatures of aggression and closely related constructs: A meta-analysis of epigenome-wide studies across the lifespan. Molecular Psychiatry, 2021, 26, 2148-2162.	7.9	21
29	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	21.4	676
30	Age-dependent sex differences in calcium and phosphate homeostasis. Endocrine Connections, 2021, 10, 273-282.	1.9	19
31	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
32	Vitamin K antagonist anticoagulant usage is associated with increased incidence and progression of osteoarthritis. Annals of the Rheumatic Diseases, 2021, 80, 598-604.	0.9	21
33	Plasma amyloid Î² levels are driven by genetic variants near APOE, BACE1, APP, PSEN2: A genomeâ€wide association study in over 12,000 nonâ€demented participants. Alzheimer's and Dementia, 2021, 17, 1663-1674.	0.8	20
34	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. Nature Communications, 2021, 12, 2830.	12.8	35
35	Genetic analysis in European ancestry individuals identifies 517 loci associated with liver enzymes. Nature Communications, 2021, 12, 2579.	12.8	51
36	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341

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37	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	8.8	90
38	A comparison of genotyping arrays. European Journal of Human Genetics, 2021, 29, 1611-1624.	2.8	43
39	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. Nature Communications, 2021, 12, 3987.	12.8	18
40	Genetic association study of childhood aggression across raters, instruments, and age. Translational Psychiatry, 2021, 11, 413.	4.8	31
41	TCERG1L allelic variation is associated with cisplatin-induced hearing loss in childhood cancer, a PanCareLIFE study. Npj Precision Oncology, 2021, 5, 64.	5.4	8
42	Association of Insulin Resistance and Type 2 Diabetes With Gut Microbial Diversity. JAMA Network Open, 2021, 4, e2118811.	5.9	119
43	Multiethnic Genome-Wide Association Study of Subclinical Atherosclerosis in Individuals With Type 2 Diabetes. Circulation Genomic and Precision Medicine, 2021, 14, e003258.	3.6	4
44	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
45	Continuity of Genetic Risk for Aggressive Behavior Across the Life-Course. Behavior Genetics, 2021, 51, 592-606.	2.1	13
46	The genomics of heart failure: design and rationale of the HERMES consortium. ESC Heart Failure, 2021, 8, 5531-5541.	3.1	11
47	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	21.4	218
48	Prevalence of and risk factors for extended-spectrum beta-lactamase genes carriership in a population-based cohort of middle-aged and elderly. International Journal of Antimicrobial Agents, 2021, 58, 106388.	2.5	4
49	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. Cell, 2021, 184, 4784-4818.e17.	28.9	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. Translational Psychiatry, 2021, 11, 451.	4.8	6
51	Validating biomarkers and models for epigenetic inference of alcohol consumption from blood. Clinical Epigenetics, 2021, 13, 198.	4.1	7
52	CYP11B1 variants influence skeletal maturation via alternative splicing. Communications Biology, 2021, 4, 1274.	4.4	3
53	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. Nature Genetics, 2021, 53, 1636-1648.	21.4	223
54	B-vitamins and body composition: integrating observational and experimental evidence from the B-PROOF study. European Journal of Nutrition, 2020, 59, 1253-1262.	3.9	8

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55	Do Vitamin D Level and Dietary Calcium Intake Modify the Association Between Loop Diuretics and Bone Health?. Calcified Tissue International, 2020, 106, 104-114.	3.1	4
56	Maternal environmental risk factors and the development of internalizing and externalizing problems in childhood: The complex role of genetic factors. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2020, 183, 17-25.	1.7	18
57	Vertebral Fractures in Individuals With Type 2 Diabetes: More Than Skeletal Complications Alone. Diabetes Care, 2020, 43, 137-144.	8.6	82
58	Genetic variation of cisplatin-induced ototoxicity in non-cranial-irradiated pediatric patients using a candidate gene approach: The International PanCareLIFE Study. Pharmacogenomics Journal, 2020, 20, 294-305.	2.0	28
59	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	12.8	466
60	Genome-wide meta-analysis of variant-by-diuretic interactions as modulators of lipid traits in persons of European and African ancestry. Pharmacogenomics Journal, 2020, 20, 482-493.	2.0	4
61	Skeletal maturation in relation to ethnic background in children of school age: The Generation R Study. Bone, 2020, 132, 115180.	2.9	18
62	Genetic basis of falling risk susceptibility in the UK Biobank Study. Communications Biology, 2020, 3, 543.	4.4	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. European Journal of Cancer, 2020, 138, 212-224.	2.8	31
64	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. Nature Communications, 2020, 11, 4796.	12.8	61
65	Serum fatty acid chain length associates with prevalent symptomatic end-stage osteoarthritis, independent of BMI. Scientific Reports, 2020, 10, 15459.	3.3	7
66	Novel loci for childhood body mass index and shared heritability with adult cardiometabolic traits. PLoS Genetics, 2020, 16, e1008718.	3.5	95
67	Association of candidate pharmacogenetic markers with platinum-induced ototoxicity: PanCareLIFE dataset. Data in Brief, 2020, 32, 106227.	1.0	2
68	Long-term effects of antimicrobial drugs on the composition of the human gut microbiota. Gut Microbes, 2020, 12, 1791677.	9.8	31
69	SomaticTARDBPvariants as a cause of semantic dementia. Brain, 2020, 143, 3827-3841.	7.6	12
70	Reduced penetrance of pathogenic ACMG variants in a deeply phenotyped cohort study and evaluation of ClinVar classification over time. Genetics in Medicine, 2020, 22, 1812-1820.	2.4	24
71	Dietary Advanced Glycation End-Products (dAGEs) Intake and Bone Health: A Cross-Sectional Analysis in the Rotterdam Study. Nutrients, 2020, 12, 2377.	4.1	13
72	Smoking-related changes in DNA methylation and gene expression are associated with cardio-metabolic traits. Clinical Epigenetics, 2020, 12, 157.	4.1	31

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73	Genome-wide identification of genes regulating DNA methylation using genetic anchors for causal inference. Genome Biology, 2020, 21, 220.	8.8	27
74	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.6	26
75	The role of the gut microbiome in cognitive function and Alzheimerâ€™s disease. Alzheimer's and Dementia, 2020, 16, e043197.	0.8	1
76	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
77	Objectives, design and main findings until 2020 from the Rotterdam Study. European Journal of Epidemiology, 2020, 35, 483-517.	5.7	314
78	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. PLoS ONE, 2020, 15, e0230815.	2.5	10
79	Skin Autofluorescence, a Noninvasive Biomarker for Advanced Glycation Endâ€Products, Is Associated With Prevalent Vertebral and Major Osteoporotic Fractures: The Rotterdam Study. Journal of Bone and Mineral Research, 2020, 35, 1904-1913.	2.8	28
80	The association between dietary and skin advanced glycation end products: the Rotterdam Study. American Journal of Clinical Nutrition, 2020, 112, 129-137.	4.7	24
81	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
82	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
83	The impact of thiazide diuretics on bone mineral density and the trabecular bone score: the Rotterdam Study. Bone, 2020, 138, 115475.	2.9	13
84	Translation of mouse model to human gives insights into periodontitis etiology. Scientific Reports, 2020, 10, 4892.	3.3	12
85	Validation of the BOADICEA model and a 313-variant polygenic risk score for breast cancer risk prediction in a Dutch prospective cohort. Genetics in Medicine, 2020, 22, 1803-1811.	2.4	49
86	Exercise with food withdrawal at thermoneutrality impacts fuel use, the microbiome, AMPK phosphorylation, muscle fibers, and thyroid hormone levels in rats. Physiological Reports, 2020, 8, e14354.	1.7	15
87	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. American Journal of Human Genetics, 2020, 106, 389-404.	6.2	118
88	Integration of epidemiologic, pharmacologic, genetic and gut microbiome data in a drugâ€“metabolite atlas. Nature Medicine, 2020, 26, 110-117.	30.7	54
89	Diversity, compositional and functional differences between gut microbiota of children and adults. Scientific Reports, 2020, 10, 1040.	3.3	89
90	Rapid Low-Cost Microarray-Based Genotyping for Genetic Screening in Primary Immunodeficiency. Frontiers in Immunology, 2020, 11, 614.	4.8	21

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91	Genome-wide meta-analysis identifies eight new susceptibility loci for cutaneous squamous cell carcinoma. Nature Communications, 2020, 11, 820.	12.8	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. PLoS ONE, 2020, 15, e0230035.	2.5	5
93	Advanced glycation end products, their receptor and the risk of dementia in the general population: A prospective cohort study. Alzheimer's and Dementia, 2020, 16, e043005.	0.8	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. Multiple Sclerosis Journal, 2019, 25, 909-917.	3.0	19
99	Interaction between plasma homocysteine and the MTHFR C.677C > T polymorphism is associated with siteâ€specific changes in DNA methylation in humans. FASEB Journal, 2019, 33, 833-843.	0.5	14
100	Genome-wide meta-analysis of SNP-by9-ACEI/ARB and SNP-by-thiazide diuretic and effect on serum potassium in cohorts of European and African ancestry. Pharmacogenomics Journal, 2019, 19, 97-108.	2.0	3
101	EIF2AK3 variants in Dutch patients with Alzheimer's disease. Neurobiology of Aging, 2019, 73, 229.e11-229.e18.	3.1	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. Molecular Psychiatry, 2019, 24, 1920-1932.	7.9	44
103	A meta-analysis of genome-wide association studies identifies multiple longevity genes. Nature Communications, 2019, 10, 3669.	12.8	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 Metaâ€Analysis of 19Â005 Individuals. Molecular Nutrition and Food Research, 2019, 63, e1900226.	3.3	12
105	A trans-ancestral meta-analysis of genome-wide association studies reveals loci associated with childhood obesity. Human Molecular Genetics, 2019, 28, 3327-3338.	2.9	76
106	Intestinal microbiome composition and its relation to joint pain and inflammation. Nature Communications, 2019, 10, 4881.	12.8	176
107	Genome-wide association meta-analysis identifies five novel loci for age-related hearing impairment. Scientific Reports, 2019, 9, 15192.	3.3	32
108	Disentangling the genetics of lean mass. American Journal of Clinical Nutrition, 2019, 109, 276-287.	4.7	38

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109	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. BMC Cardiovascular Disorders, 2019, 19, 240.	1.7	22
110	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
111	Î²2-Adrenergic Receptor (ADRB2) Gene Polymorphisms and Risk of COPD Exacerbations: The Rotterdam Study. Journal of Clinical Medicine, 2019, 8, 1835.	2.4	12
112	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
113	GWAS on longitudinal growth traits reveals different genetic factors influencing infant, child, and adult BMI. Science Advances, 2019, 5, eaaw3095.	10.3	86
114	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
115	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	12.8	133
116	Association of Birth Weight With Type 2 Diabetes and Glycemic Traits. JAMA Network Open, 2019, 2, e1910915.	5.9	41
117	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
118	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
119	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
120	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
121	Fractures in school age children in relation to sex and ethnic background: The Generation R Study. Bone, 2019, 121, 227-231.	2.9	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. American Journal of Clinical Nutrition, 2019, 110, 437-450.	4.7	46
123	Update on the predictability of tall stature from DNA markers in Europeans. Forensic Science International: Genetics, 2019, 42, 8-13.	3.1	18
124	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
125	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. Nature Communications, 2019, 10, 2581.	12.8	62
126	Molecular Alterations in Dog Pheochromocytomas and Paragangliomas. Cancers, 2019, 11, 607.	3.7	13

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127	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. PLoS ONE, 2019, 14, e0216222.	2.5	17
128	GWAS of bone size yields twelve loci that also affect height, BMD, osteoarthritis or fractures. Nature Communications, 2019, 10, 2054.	12.8	74
129	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	21.4	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.	2.8	27
131	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
132	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
133	Femoral stress is prominently associated with fracture risk in children: The Generation R Study. Bone, 2019, 122, 150-155.	2.9	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.	6.7	48
135	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
136	Relationship between gut microbiota and circulating metabolites in population-based cohorts. Nature Communications, 2019, 10, 5813.	12.8	168
137	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	21.4	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.	2.8	58
139	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. American Journal of Human Genetics, 2019, 104, 112-138.	6.2	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.	21.4	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.	1.4	34
143	The effect of antimicrobial drug use on the composition of the genitourinary microbiota in an elderly population. BMC Microbiology, 2019, 19, 9.	3.3	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.	2.5	56

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145	Hippocampal transcriptome profiling combined with protein-protein interaction analysis elucidates Alzheimer's disease pathways and genes. Neurobiology of Aging, 2019, 74, 225-233.	3.1	30
146	Response to VilariÃ±o-GÃ¼ell et al.. Multiple Sclerosis Journal, 2019, 25, 1013-1015.	3.0	0
147	Serum 25-hydroxyvitamin D3 is associated with advanced glycation end products (AGEs) measured as skin autofluorescence: The Rotterdam Study. European Journal of Epidemiology, 2019, 34, 67-77.	5.7	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. Arthritis and Rheumatology, 2019, 71, 361-369.	5.6	22
149	Candidate CSPG4 mutations and induced pluripotent stem cell modeling implicate oligodendrocyte progenitor cell dysfunction in familial schizophrenia. Molecular Psychiatry, 2019, 24, 757-771.	7.9	51
150	KCND3 potassium channel gene variant confers susceptibility to electrocardiographic early repolarization pattern. JCI Insight, 2019, 4, .	5.0	15
151	Genetic Determinants of Ototoxicity During and After Childhood Cancer Treatment: Protocol for the PanCareLIFE Study. JMIR Research Protocols, 2019, 8, e11868.	1.0	10
152	MON-208 Association Study of AMH Promoter Polymorphisms and Serum AMH Levels in PCOS Patients. Journal of the Endocrine Society, 2019, 3, .	0.2	0
153	Development of a prediction model for future risk of radiographic hip osteoarthritis. Osteoarthritis and Cartilage, 2018, 26, 540-546.	1.3	33
154	Sarcopenia and Its Clinical Correlates in the General Population: The Rotterdam Study. Journal of Bone and Mineral Research, 2018, 33, 1209-1218.	2.8	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. Nature Genetics, 2018, 50, 652-656.	21.4	86
156	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor Î±. JAMA Cardiology, 2018, 3, 463.	6.1	33
157	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	21.4	356
158	The Genetics of Seborrheic Dermatitis: AÂCandidate Gene Approach and Pilot Genome-Wide Association Study. Journal of Investigative Dermatology, 2018, 138, 991-993.	0.7	17
159	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
160	A systematic analysis highlights multiple long non-coding RNAs associated with cardiometabolic disorders. Journal of Human Genetics, 2018, 63, 431-446.	2.3	17
161	COPD GWAS variant at 19q13.2 in relation with DNA methylation and gene expression. Human Molecular Genetics, 2018, 27, 396-405.	2.9	24
162	Understanding the role of the chromosome 15q25.1 in COPD through epigenetics and transcriptomics. European Journal of Human Genetics, 2018, 26, 709-722.	2.8	21

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163	Meta-analysis of epigenome-wide association studies of cognitive abilities. Molecular Psychiatry, 2018, 23, 2133-2144.	7.9	68
164	Integration of Murine and Human Studies for Mapping Periodontitis Susceptibility. Journal of Dental Research, 2018, 97, 537-546.	5.2	21
165	Life-Course Genome-wide Association Study Meta-analysis of Total Body BMD and Assessment of Age-Specific Effects. American Journal of Human Genetics, 2018, 102, 88-102.	6.2	252
166	Meta-analysis of genome-wide association studies identifies 8 novel loci involved in shape variation of human head hair. Human Molecular Genetics, 2018, 27, 559-575.	2.9	51
167	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681.	21.4	2,224
168	Genetic Determinants of Circulating Estrogen Levels and Evidence of a Causal Effect of Estradiol on Bone Density in Men. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 991-1004.	3.6	60
169	Genome-wide analyses using UK Biobank data provide insights into the genetic architecture of osteoarthritis. Nature Genetics, 2018, 50, 549-558.	21.4	223
170	A DNA methylation biomarker of alcohol consumption. Molecular Psychiatry, 2018, 23, 422-433.	7.9	280
171	A rare missense variant in RCL1 segregates with depression in extended families. Molecular Psychiatry, 2018, 23, 1120-1126.	7.9	34
172	Heritability and genome-wide associations studies of cerebral blood flow in the general population. Journal of Cerebral Blood Flow and Metabolism, 2018, 38, 1598-1608.	4.3	14
173	Association between subclinical thyroid dysfunction and change in bone mineral density in prospective cohorts. Journal of Internal Medicine, 2018, 283, 56-72.	6.0	62
174	Genomeâ€Wide Interactions with Dairy Intake for Body Mass Index in Adults of European Descent. Molecular Nutrition and Food Research, 2018, 62, 1700347.	3.3	9
175	Identification of a novel locus on chromosome 2q13, which predisposes to clinical vertebral fractures independently of bone density. Annals of the Rheumatic Diseases, 2018, 77, 378-385.	0.9	21
176	Dairy Consumption and Body Mass Index Among Adults: Mendelian Randomization Analysis of 184802 Individuals from 25 Studies. Clinical Chemistry, 2018, 64, 183-191.	3.2	34
177	Genetic variants associated with earlier age at menopause increase the risk of cardiovascular events in women. Menopause, 2018, 25, 451-457.	2.0	22
178	Dietary patterns in an elderly population and their relation with bone mineral density: the Rotterdam Study. European Journal of Nutrition, 2018, 57, 61-73.	3.9	25
179	O5â€04â€05: GENETIC VARIATION UNDERLYING COGNITION AND ITS RELATION WITH NEUROLOGICAL OUTCOMES. Alzheimer's and Dementia, 2018, 14, P1652.	0.8	0
180	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. Nature Communications, 2018, 9, 4774.	12.8	87

#	Article	IF	Citations
181	Association of maternal prenatal smoking GFI1-locus and cardio-metabolic phenotypes in 18,212 adults. EBioMedicine, 2018, 38, 206-216.	6.1	43
182	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. PLoS Genetics, 2018, 14, e1007813.	3.5	341
183	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	12.8	119
184	Genetic variation in gonadal impairment in female survivors of childhood cancer: a PanCareLIFE study protocol. BMC Cancer, 2018, 18, 930.	2.6	13
185	Genome-wide meta-analysis of 158,000 individuals of European ancestry identifies three loci associated with chronic back pain. PLoS Genetics, 2018, 14, e1007601.	3.5	112
186	PanCareLIFE: The scientific basis for a European project to improve long-term care regarding fertility, ototoxicity and health-related quality of life after cancer occurring among children and adolescents. European Journal of Cancer, 2018, 103, 227-237.	2.8	41
187	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. Nature Communications, 2018, 9, 4455.	12.8	181
188	Large-scale whole-exome sequencing association studies identify rare functional variants influencing serum urate levels. Nature Communications, 2018, 9, 4228.	12.8	43
189	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
190	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
191	Genome-wide association meta-analysis of coronary artery disease and periodontitis reveals a novel shared risk locus. Scientific Reports, 2018, 8, 13678.	3.3	35
192	Rare gene deletions in genetic generalized and Rolandic epilepsies. PLoS ONE, 2018, 13, e0202022.	2.5	6
193	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. Nature Genetics, 2018, 50, 834-848.	21.4	239
194	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	3.6	19
195	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	12.8	484
196	Serum phosphate levels are related to all-cause, cardiovascular and COPD mortality in men. European Journal of Epidemiology, 2018, 33, 859-871.	5.7	39
197	The influence of genetic variation on late toxicities in childhood cancer survivors: A review. Critical Reviews in Oncology/Hematology, 2018, 126, 154-167.	4.4	31
198	Association of BRCA2 K3326* With Small Cell Lung Cancer and Squamous Cell Cancer of the Skin. Journal of the National Cancer Institute, 2018, 110, 967-974.	6.3	29

#	Article	IF	Citations
199	Cross-ancestry genome-wide association analysis of corneal thickness strengthens link between complex and Mendelian eye diseases. Nature Communications, 2018, 9, 1864.	12.8	63
200	An Epigenome-Wide Association Study of Obesity-Related Traits. American Journal of Epidemiology, 2018, 187, 1662-1669.	3.4	59
201	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
202	Genome-wide association study in 176,678 Europeans reveals genetic loci for tanning response to sun exposure. Nature Communications, 2018, 9, 1684.	12.8	80
203	A combined linkage, microarray and exome analysis suggests MAP3K11 as a candidate gene for left ventricular hypertrophy. BMC Medical Genomics, 2018, 11, 22.	1.5	4
204	Employed family-based genetic discovery combining linkage analysis and exome sequencing to identify RCL1 as a novel candidate gene for depression, with independent replication in a population-based cohort. Molecular Psychiatry, 2018, 23, 1093-1093.	7.9	0
205	Genetics of the Vitamin D Endocrine System. , 2018, , 151-165.		0
206	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. Nature Communications, 2018, 9, 2976.	12.8	85
207	Fracture incidence and secular trends between 1989 and 2013 in a population based cohort: The Rotterdam Study. Bone, 2018, 114, 116-124.	2.9	67
208	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	21.4	552
209	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
210	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
211	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 2018, 3, 4.	1.8	19
212	A genome-wide association study of corneal astigmatism: The CREAM Consortium. Molecular Vision, 2018, 24, 127-142.	1.1	10
213	Vitamin D and body composition in the elderly. Clinical Nutrition, 2017, 36, 585-592.	5.0	27
214	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	12.8	250
215	Genome-wide association scan of neuropathic pain symptoms post total joint replacement highlights a variant in the protein-kinase C gene. European Journal of Human Genetics, 2017, 25, 446-451.	2.8	39
216	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544

#	Article	IF	Citations
217	Genome-wide methylation analysis identifies novel CpG loci for perimembranous ventricular septal defects in human. Epigenomics, 2017, 9, 241-251.	2.1	10
218	New insights into the genetics of primary open-angle glaucoma based on meta-analyses of intraocular pressure and optic disc characteristics.. Human Molecular Genetics, 2017, 26, ddw399.	2.9	120
219	Genetic loci associated with chronic obstructive pulmonary disease overlap with loci for lung function and pulmonary fibrosis. Nature Genetics, 2017, 49, 426-432.	21.4	306
220	Epigenome-wide association study (EWAS) on lipids: the Rotterdam Study. Clinical Epigenetics, 2017, 9, 15.	4.1	104
221	Serum Phosphate Is Associated With Fracture Risk: The Rotterdam Study and MrOS. Journal of Bone and Mineral Research, 2017, 32, 1182-1193.	2.8	40
222	Dietary acid load, trabecular bone integrity, and mineral density in an ageing population: the Rotterdam study. Osteoporosis International, 2017, 28, 2357-2365.	3.1	20
223	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426
224	Thyroid Function Tests in the Reference Range and Fracture: Individual Participant Analysis of Prospective Cohorts. Journal of Clinical Endocrinology and Metabolism, 2017, 102, 2719-2728.	3.6	41
225	Haplotype reference consortium panel: Practical implications of imputations with large reference panels. Human Mutation, 2017, 38, 1025-1032.	2.5	43
226	A genome-wide association study identifies nucleotide variants at SIGLEC5 and DEFA1A3 as risk loci for periodontitis. Human Molecular Genetics, 2017, 26, 2577-2588.	2.9	87
227	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
228	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	3.3	98
229	Dietary patterns explaining differences in bone mineral density and hip structure in the elderly: the Rotterdam Study. American Journal of Clinical Nutrition, 2017, 105, 203-211.	4.7	32
230	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2017, 5, 97-105.	11.4	298
231	Disease variants alter transcription factor levels and methylation of their binding sites. Nature Genetics, 2017, 49, 131-138.	21.4	390
232	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	12.8	95
233	Epigenome-Wide Association Study Identifies Methylation Sites Associated With Liver Enzymes and Hepatic Steatosis. Gastroenterology, 2017, 153, 1096-1106.e2.	1.3	52
234	Betaâ€blocker use and fall risk in older individuals: Original results from two studies with metaâ€analysis. British Journal of Clinical Pharmacology, 2017, 83, 2292-2302.	2.4	27

#	Article	IF	Citations
235	Characterization of pathogenic SORL1 genetic variants for association with Alzheimerâ€™s disease: a clinical interpretation strategy. European Journal of Human Genetics, 2017, 25, 973-981.	2.8	102
236	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	6.2	131
237	A haplotype block downstream of plasminogen is associated with chronic and aggressive periodontitis. Journal of Clinical Periodontology, 2017, 44, 962-970.	4.9	16
238	Genetic variants associated with type 2 diabetes and adiposity and risk of intracranial and abdominal aortic aneurysms. European Journal of Human Genetics, 2017, 25, 758-762.	2.8	13
239	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
240	Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis. American Journal of Human Genetics, 2017, 100, 51-63.	6.2	45
241	CYP2C9 Genotypes Modify Benzodiazepine-Related Fall Risk: Original Results From Three Studies With Meta-Analysis. Journal of the American Medical Directors Association, 2017, 18, 88.e1-88.e15.	2.5	19
242	Evaluation of the Myocilin Mutation Gln368Stop Demonstrates Reduced Penetrance for Glaucoma in European Populations. Ophthalmology, 2017, 124, 547-553.	5.2	23
243	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. Nature, 2017, 541, 81-86.	27.8	743
244	Homocysteine levels associate with subtle changes in leukocyte DNA methylation: an epigenome-wide analysis. Epigenomics, 2017, 9, 1403-1422.	2.1	6
245	The Rotterdam Study: 2018 update on objectives, design and main results. European Journal of Epidemiology, 2017, 32, 807-850.	5.7	379
246	Scrutinizing the Genetic Underpinnings of Bone Strength. Journal of Bone and Mineral Research, 2017, 32, 2147-2150.	2.8	0
247	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. Nature Communications, 2017, 8, 910.	12.8	118
248	Genome-wide association and functional studies identify a role for matrix Gla protein in osteoarthritis of the hand. Annals of the Rheumatic Diseases, 2017, 76, 2046-2053.	0.9	64
249	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
250	Population-specific genetic variation in large sequencing data sets: why more data is still better. European Journal of Human Genetics, 2017, 25, 1173-1175.	2.8	22
251	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	21.4	783
252	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	12.8	147

#	Article	IF	Citations
253	Bivariate genome-wide association meta-analysis of pediatric musculoskeletal traits reveals pleiotropic effects at the SREBF1/TOM1L2 locus. Nature Communications, 2017, 8, 121.	12.8	82
254	Establishing the role of rare coding variants in known Parkinson's disease risk loci. Neurobiology of Aging, 2017, 59, 220.e11-220.e18.	3.1	15
255	Fifteen Genetic Loci Associated With the Electrocardiographic P Wave. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	38
256	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	6.2	154
257	Microbiome measurement: Possibilities and pitfalls. Bailliere's Best Practice and Research in Clinical Gastroenterology, 2017, 31, 619-623.	2.4	7
258	Lack of evidence for a role of genetic variation in TMEM230 in the risk for Parkinson's disease in the Caucasian population. Neurobiology of Aging, 2017, 50, 167.e11-167.e13.	3.1	24
259	Nonsynonymous Variation in NKPD1 Increases Depressive Symptoms in European Populations. Biological Psychiatry, 2017, 81, 702-707.	1.3	26
260	Pigmentation-Independent Susceptibility Loci for Actinic Keratosis Highlighted by Compound Heterozygosity Analysis. Journal of Investigative Dermatology, 2017, 137, 77-84.	0.7	10
261	Cam Deformity and Acetabular Dysplasia as Risk Factors for Hip Osteoarthritis. Arthritis and Rheumatology, 2017, 69, 86-93.	5.6	105
262	Exome-sequencing in a large population-based study reveals a rare Asn396Ser variant in the LIPG gene associated with depressive symptoms. Molecular Psychiatry, 2017, 22, 537-543.	7.9	49
263	An epigenome-wide association study meta-analysis of educational attainment. Molecular Psychiatry, 2017, 22, 1680-1690.	7.9	70
264	Excessive burden of lysosomal storage disorder gene variants in Parkinsonâ€™s disease. Brain, 2017, 140, 3191-3203.	7.6	323
265	Exome-Wide Meta-Analysis Identifies Rare 3â€²-UTR Variant in ERCC1/CD3EAP Associated with Symptoms of Sleep Apnea. Frontiers in Genetics, 2017, 8, 151.	2.3	7
266	Genetic Polymorphism of miR-196a-2 is Associated with Bone Mineral Density (BMD). International Journal of Molecular Sciences, 2017, 18, 2529.	4.1	14
267	Genome-wide association meta-analysis of fish and EPA+DHA consumption in 17 US and European cohorts. PLoS ONE, 2017, 12, e0186456.	2.5	18
268	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. Journal of Clinical Investigation, 2017, 127, 1798-1812.	8.2	106
269	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
270	Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study. PLoS ONE, 2017, 12, e0167742.	2.5	29

#	Article	IF	Citations
271	Genetically defined elevated homocysteine levels do not result in widespread changes of DNA methylation in leukocytes. PLoS ONE, 2017, 12, e0182472.	2.5	10
272	The complex genetics of gait speed: genome-wide meta-analysis approach. Aging, 2017, 9, 209-246.	3.1	21
273	Effects of Two-Year Vitamin B12 and Folic Acid Supplementation on Depressive Symptoms and Quality of Life in Older Adults with Elevated Homocysteine Concentrations: Additional Results from the B-PROOF Study, an RCT. Nutrients, 2016, 8, 748.	4.1	46
274	Genome-Wide Association Study for Incident Myocardial Infarction and Coronary Heart Disease in Prospective Cohort Studies: The CHARGE Consortium. PLoS ONE, 2016, 11, e0144997.	2.5	69
275	Novel Genetic Variants for Cartilage Thickness and Hip Osteoarthritis. PLoS Genetics, 2016, 12, e1006260.	3.5	76
276	Bivariate genome-wide association study identifies novel pleiotropic loci for lipids and inflammation. BMC Genomics, 2016, 17, 443.	2.8	67
277	Identification of IDUA and WNT16 Phosphorylation-Related Non-Synonymous Polymorphisms for Bone Mineral Density in Meta-Analyses of Genome-Wide Association Studies. Journal of Bone and Mineral Research, 2016, 31, 358-368.	2.8	24
278	Burden of genetic risk variants in multiple sclerosis families in the Netherlands. Multiple Sclerosis Journal - Experimental, Translational and Clinical, 2016, 2, 205521731664872.	1.0	6
279	Determinants for Quantitative Sensory Testing and the Association with Chronic Musculoskeletal Pain in the General Elderly Population. Pain Practice, 2016, 16, 831-841.	1.9	16
280	Meta-analysis of genome-wide association studies of HDL cholesterol response to statins. Journal of Medical Genetics, 2016, 53, 835-845.	3.2	28
281	The Generation R Study: design and cohort update 2017. European Journal of Epidemiology, 2016, 31, 1243-1264.	5.7	608
282	Meta-analysis of 49â€…549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant inANGPTL4determining fasting TG levels. Journal of Medical Genetics, 2016, 53, 441-449.	3.2	34
283	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. Genome Biology, 2016, 17, 255.	8.8	251
284	Heritability of the shape of subcortical brain structures in the general population. Nature Communications, 2016, 7, 13738.	12.8	78
285	Somatic, positive and negative domains of the Center for Epidemiological Studies Depression (CES-D) scale: a meta-analysis of genome-wide association studies. Psychological Medicine, 2016, 46, 1613-1623.	4.5	17
286	P1â€123: Differential Expression in Hippocampus of Alzheimer's Disease Patients. Alzheimer's and Dementia, 2016, 12, P451.	0.8	0
287	Evaluation of a Genetic Risk Score to Improve Risk Prediction for Alzheimerâ€™s Disease. Journal of Alzheimer's Disease, 2016, 53, 921-932.	2.6	77
288	Low serum vitamin D is associated with axial length and risk of myopia in young children. European Journal of Epidemiology, 2016, 31, 491-499.	5.7	78

#	Article	IF	Citations
289	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. Nature Genetics, 2016, 48, 624-633.	21.4	870
290	Genetic variants in RBFOX3 are associated with sleep latency. European Journal of Human Genetics, 2016, 24, 1488-1495.	2.8	27
291	Gene transcripts associated with muscle strength: a CHARGE meta-analysis of 7,781 persons. Physiological Genomics, 2016, 48, 1-11.	2.3	11
292	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. Cancer Research, 2016, 76, 5103-5114.	0.9	100
293	Four Susceptibility Loci for Gallstone Disease Identified in a Meta-analysis of Genome-Wide Association Studies. Gastroenterology, 2016, 151, 351-363.e28.	1.3	74
294	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
295	Uncompromised 10-year survival of oldest old carrying somatic mutations in DNMT3A and TET2. Blood, 2016, 127, 1512-1515.	1.4	38
296	Genetic variation and bone mineral density in longâ€term adult survivors of childhood cancer. Pediatric Blood and Cancer, 2016, 63, 2212-2220.	1.5	9
297	Cystatin C and Cardiovascular Disease. Journal of the American College of Cardiology, 2016, 68, 934-945.	2.8	109
298	Fine-mapping the effects of Alzheimer's disease risk loci on brain morphology. Neurobiology of Aging, 2016, 48, 204-211.	3.1	31
299	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	21.4	66
300	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. Genome Biology, 2016, 17, 191.	8.8	120
301	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	27.8	406
302	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	14.8	213
303	Blood lipids influence DNA methylation in circulating cells. Genome Biology, 2016, 17, 138.	8.8	154
304	<scp>GWAS</scp> analysis of handgrip and lower body strength in older adults in the <scp>CHARGE</scp> consortium. Aging Cell, 2016, 15, 792-800.	6.7	51
305	Thyroid Function Characteristics and Determinants: The Rotterdam Study. Thyroid, 2016, 26, 1195-1204.	4.5	78
306	Whole-Exome Sequencing Identifies Loci Associated with Blood Cell Traits and Reveals a Role for Alternative GFI1B Splice Variants in Human Hematopoiesis. American Journal of Human Genetics, 2016, 99, 481-488.	6.2	45

#	Article	IF	Citations
307	An Introduction to Genome-Wide Association Studies: GWAS for Dummies. Seminars in Reproductive Medicine, 2016, 34, 196-204.	1.1	27
308	A Whole-Blood Transcriptome Meta-Analysis Identifies Gene Expression Signatures of Cigarette Smoking. Human Molecular Genetics, 2016, 25, ddw288.	2.9	76
309	Menopause: Genome stability as new paradigm. Maturitas, 2016, 92, 15-23.	2.4	57
310	KLB is associated with alcohol drinking, and its gene product Î²-Klotho is necessary for FGF21 regulation of alcohol preference. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14372-14377.	7.1	208
311	Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. Circulation: Cardiovascular Genetics, 2016, 9, 511-520.	5.1	54
312	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
313	Epigenetic Signatures of Cigarette Smoking. Circulation: Cardiovascular Genetics, 2016, 9, 436-447.	5.1	678
314	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113
315	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	21.4	223
316	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
317	Targeted sequencing of genome wide significant loci associated with bone mineral density (BMD) reveals significant novel and rare variants: the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) targeted sequencing study. Human Molecular Genetics, 2016, 25, ddw289.	2.9	7
318	Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis. Nature Genetics, 2016, 48, 1043-1048.	21.4	494
319	Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. Journal of the American Heart Association, 2016, 5, .	3.7	45
320	Meta-analysis of geneâ€“environment-wide association scans accounting for education level identifies additional loci for refractive error. Nature Communications, 2016, 7, 11008.	12.8	104
321	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. Nature Communications, 2016, 7, 12989.	12.8	99
322	Genome-wide association study for acute otitis media in children identifies FNDC1 as disease contributing gene. Nature Communications, 2016, 7, 12792.	12.8	50
323	Structural Brain Alterations in Community Dwelling Individuals with Chronic Joint Pain. American Journal of Neuroradiology, 2016, 37, 430-438.	2.4	17
324	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	21.4	520

#	Article	IF	Citations
325	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	6.2	82
326	Association between biomarkers of tissue inflammation and progression of osteoarthritis: evidence from the Rotterdam study cohort. Arthritis Research and Therapy, 2016, 18, 81.	3.5	85
327	Bone Mass and Strength in School-Age Children Exhibit Sexual Dimorphism Related to Differences in Lean Mass: The Generation R Study. Journal of Bone and Mineral Research, 2016, 31, 1099-1106.	2.8	19
328	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. American Journal of Human Genetics, 2016, 99, 22-39.	6.2	50
329	Genetic loci for serum lipid fractions and intracerebral hemorrhage. Atherosclerosis, 2016, 246, 287-292.	0.8	11
330	Meta-analysis of genome-wide association studies of anxiety disorders. Molecular Psychiatry, 2016, 21, 1391-1399.	7.9	373
331	Quantifying prion disease penetrance using large population control cohorts. Science Translational Medicine, 2016, 8, 322ra9.	12.4	289
332	Effect of vitamin B12 and folic acid supplementation on biomarkers of endothelial function and inflammation among elderly individuals with hyperhomocysteinemia. Vascular Medicine, 2016, 21, 91-98.	1.5	30
333	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	12.8	245
334	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	12.8	153
335	Maternal plasma folate impacts differential DNA methylation in an epigenome-wide meta-analysis of newborns. Nature Communications, 2016, 7, 10577.	12.8	219
336	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
337	Tobacco smoking is associated with DNA methylation of diabetes susceptibility genes. Diabetologia, 2016, 59, 998-1006.	6.3	43
338	Heritability and Genome-Wide Association Analyses of Intracranial Carotid Artery Calcification. Stroke, 2016, 47, 912-917.	2.0	15
339	The Influence of Serum Uric Acid on Bone Mineral Density, Hip Geometry, and Fracture Risk: The Rotterdam Study. Journal of Clinical Endocrinology and Metabolism, 2016, 101, 1113-1122.	3.6	41
340	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. Human Molecular Genetics, 2016, 25, 389-403.	2.9	275
341	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	2.9	73
342	A Randomized Controlled Trial to Examine the Effect of 2-Year Vitamin B12 and Folic Acid Supplementation on Physical Performance, Strength, and Falling: Additional Findings from the B-PROOF Study. Calcified Tissue International, 2016, 98, 18-27.	3.1	33

#	Article	IF	Citations
343	Risk of Frailty in Elderly With COPD: A Population-Based Study. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2016, 71, 689-695.	3.6	130
344	Low vitamin D status is associated with more depressive symptoms in Dutch older adults. European Journal of Nutrition, 2016, 55, 1525-1534.	3.9	43
345	25-Hydroxyvitamin D and osteoarthritis: A meta-analysis including new data. Seminars in Arthritis and Rheumatism, 2016, 45, 539-546.	3.4	36
346	Rare, low frequency and common coding variants in CHRNA5 and their contribution to nicotine dependence in European and African Americans. Molecular Psychiatry, 2016, 21, 601-607.	7.9	32
347	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. Molecular Psychiatry, 2016, 21, 189-197.	7.9	134
348	Arterial stiffness is not associated with bone parameters in an elderly hyperhomocysteinemic population. Journal of Bone and Mineral Metabolism, 2016, 34, 99-108.	2.7	4
349	Associations between joint effusion in the knee and gene expression levels in the circulation: a meta-analysis. F1000Research, 2016, 5, 109.	1.6	6
350	Discovery of Genetic Variation on Chromosome 5q22 Associated with Mortality in Heart Failure. PLoS Genetics, 2016, 12, e1006034.	3.5	34
351	Rare Functional Variant in TM2D3 is Associated with Late-Onset Alzheimer's Disease. PLoS Genetics, 2016, 12, e1006327.	3.5	47
352	Evaluation of Presumably Disease Causing SCN1A Variants in a Cohort of Common Epilepsy Syndromes. PLoS ONE, 2016, 11, e0150426.	2.5	22
353	Blood RNA expression profiles undergo major changes during the seventh decade. Oncotarget, 2016, 7, 71353-71361.	1.8	1
354	Incremental predictive value of 152 single nucleotide polymorphisms in the 10-year risk prediction of incident coronary heart disease: the Rotterdam Study. International Journal of Epidemiology, 2015, 44, 682-688.	1.9	44
355	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
356	Fine mapping the CETP region reveals a common intronic insertion associated to HDL-C. Npj Aging and Mechanisms of Disease, 2015, 1, 15011.	4.5	8
357	Prenatal parental tobacco smoking, gene specific DNA methylation, and newborns size: the Generation R study. Clinical Epigenetics, 2015, 7, 83.	4.1	51
358	The effects of long-term daily folic acid and vitamin B12 supplementation on genome-wide DNA methylation in elderly subjects. Clinical Epigenetics, 2015, 7, 121.	4.1	106
359	Rare variants in Î³â€aminobutyric acid type <scp>A</scp> receptor genes in rolandic epilepsy and related syndromes. Annals of Neurology, 2015, 77, 972-986.	5.3	51
360	Development of a Food Group-Based Diet Score and Its Association with Bone Mineral Density in the Elderly: The Rotterdam Study. Nutrients, 2015, 7, 6974-6990.	4.1	22

#	Article	IF	Citations
361	Pleiotropy among Common Genetic Loci Identified for Cardiometabolic Disorders and C-Reactive Protein. PLoS ONE, 2015, 10, e0118859.	2.5	43
362	A Genome Wide Association Study Links Glutamate Receptor Pathway to Sporadic Creutzfeldt-Jakob Disease Risk. PLoS ONE, 2015, 10, e0123654.	2.5	28
363	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
364	Drug-Gene Interactions of Antihypertensive Medications and Risk of Incident Cardiovascular Disease: A Pharmacogenomics Study from the CHARGE Consortium. PLoS ONE, 2015, 10, e0140496.	2.5	15
365	Adiposity as a cause of cardiovascular disease: a Mendelian randomization study. International Journal of Epidemiology, 2015, 44, 578-586.	1.9	123
366	Subclinical Thyroid Dysfunction and Fracture Risk. JAMA - Journal of the American Medical Association, 2015, 313, 2055.	7.4	264
367	Gene Ã— dietary pattern interactions in obesity: analysis of up to 68 317 adults of European ancestry. Human Molecular Genetics, 2015, 24, 4728-4738.	2.9	84
368	BMD Loci Contribute to Ethnic and Developmental Differences in Skeletal Fragility across Populations: Assessment of Evolutionary Selection Pressures. Molecular Biology and Evolution, 2015, 32, 2961-2972.	8.9	29
369	Bidirectional associations between circulating vitamin D and cholesterol levels: The Rotterdam Study. Maturitas, 2015, 82, 411-417.	2.4	21
370	Rare coding variants and X-linked loci associated with age at menarche. Nature Communications, 2015, 6, 7756.	12.8	32
371	P2-024: Whole-exome sequencing in dutch families with Alzheimer's disease. , 2015, 11, P490-P490.		0
372	ARHGEF12 influences the risk of glaucoma by increasing intraocular pressure. Human Molecular Genetics, 2015, 24, 2689-2699.	2.9	79
373	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
374	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
375	The dystrophin gene and cognitive function in the general population. European Journal of Human Genetics, 2015, 23, 837-843.	2.8	6
376	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
377	Non-linear associations between serum 25-OH vitamin D and indices of arterial stiffness and arteriosclerosis in an older population. Age and Ageing, 2015, 44, 136-142.	1.6	26
378	Age- and Sex-Specific Causal Effects of Adiposity on Cardiovascular Risk Factors. Diabetes, 2015, 64, 1841-1852.	0.6	63

#	Article	IF	Citations
379	GWAS with longitudinal phenotypes: performance of approximate procedures. European Journal of Human Genetics, 2015, 23, 1384-1391.	2.8	18
380	Genetic contributions to variation in general cognitive function: a meta-analysis of genome-wide association studies in the CHARGE consortium (N=53â€‰949). Molecular Psychiatry, 2015, 20, 183-192.	7.9	344
381	Identifying genetic loci associated with antidepressant drug response with drugâ€“gene interaction models in a population-based study. Journal of Psychiatric Research, 2015, 62, 31-37.	3.1	13
382	Tobacco smoking is associated with methylation of genes related to coronary artery disease. Clinical Epigenetics, 2015, 7, 54.	4.1	58
383	Bone health and coronary artery calcification: The Rotterdam Study. Atherosclerosis, 2015, 241, 278-283.	0.8	37
384	Identification of a novelFGFRL1MicroRNA target site polymorphism for bone mineral density in meta-analyses of genome-wide association studies. Human Molecular Genetics, 2015, 24, 4710-4727.	2.9	22
385	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
386	Cognitive Performance: A Cross-Sectional Study on Serum Vitamin D and Its Interplay With Glucose Homeostasis in Dutch Older Adults. Journal of the American Medical Directors Association, 2015, 16, 621-627.	2.5	21
387	Genetic risk of neurodegenerative diseases is associated with mild cognitive impairment and conversion to dementia. Alzheimer's and Dementia, 2015, 11, 1277-1285.	0.8	76
388	Characteristics of de novo structural changes in the human genome. Genome Research, 2015, 25, 792-801.	5.5	115
389	Multiethnic Genome-Wide Association Study of Cerebral White Matter Hyperintensities on MRI. Circulation: Cardiovascular Genetics, 2015, 8, 398-409.	5.1	162
390	GWAS of Longevity in CHARGE Consortium Confirms APOE and FOXO3 Candidacy. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2015, 70, 110-118.	3.6	250
391	PLD3 variants in population studies. Nature, 2015, 520, E2-E3.	27.8	49
392	Expression and Gene Variation Studies Deny Association of Human HSD3B1 Gene With Aldosterone Production or Blood Pressure. American Journal of Hypertension, 2015, 28, 113-120.	2.0	7
393	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
394	Causal mechanisms and balancing selection inferred from genetic associations with polycystic ovary syndrome. Nature Communications, 2015, 6, 8464.	12.8	304
395	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
396	Dietary vitamin A intake and bone health in the elderly: the Rotterdam Study. European Journal of Clinical Nutrition, 2015, 69, 1360-1368.	2.9	19

#	Article	IF	Citations
397	Common Variants Affecting Susceptibility to Develop Multiple Basal Cell Carcinomas. Journal of Investigative Dermatology, 2015, 135, 2135-2138.	0.7	7
398	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. Nature Genetics, 2015, 47, 1449-1456.	21.4	529
399	Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. Nature Communications, 2015, 6, 6065.	12.8	45
400	Genetic Determinants of Unruptured Intracranial Aneurysms in the General Population. Stroke, 2015, 46, 2961-2964.	2.0	13
401	Association of Rare Loss-Of-Function Alleles in HAL , Serum Histidine. Circulation: Cardiovascular Genetics, 2015, 8, 351-355.	5.1	41
402	Wholeâ€genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	27.8	483
403	A comprehensive 1000 Genomesâ€“based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	21.4	2,054
404	WNT10A exonic variant increases the risk of keratoconus by decreasing corneal thickness. Human Molecular Genetics, 2015, 24, 5060-5068.	2.9	58
405	Genome-wide association and functional studies identify a role forIGFBP3in hip osteoarthritis. Annals of the Rheumatic Diseases, 2015, 74, 1861-1867.	0.9	47
406	Consumption of meat is associated with higher fasting glucose and insulin concentrations regardless of glucose and insulin genetic risk scores: a meta-analysis of 50,345 Caucasians. American Journal of Clinical Nutrition, 2015, 102, 1266-1278.	4.7	69
407	The Rotterdam Study: 2016 objectives and design update. European Journal of Epidemiology, 2015, 30, 661-708.	5.7	358
408	A novel common variant in DCST2 is associated with length in early life and height in adulthood. Human Molecular Genetics, 2015, 24, 1155-1168.	2.9	109
409	Genome-wide association study of kidney function decline in individuals of European descent. Kidney International, 2015, 87, 1017-1029.	5.2	113
410	Novel loci associated with usual sleep duration: the CHARGE Consortium Genome-Wide Association Study. Molecular Psychiatry, 2015, 20, 1232-1239.	7.9	112
411	Identifying genetic risk variants for coronary heart disease in familial hypercholesterolemia: an extreme genetics approach. European Journal of Human Genetics, 2015, 23, 381-387.	2.8	15
412	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	7.9	235
413	Improving accuracy of rare variant imputation with a two-step imputation approach. European Journal of Human Genetics, 2015, 23, 395-400.	2.8	32
414	Genome-Wide Association Study in an Admixed Case Series Reveals IL12A as a New Candidate in BehÃ§et Disease. PLoS ONE, 2015, 10, e0119085.	2.5	61

#	Article	IF	Citations
415	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	2.5	64
416	The Association between Metabolic Syndrome, Bone Mineral Density, Hip Bone Geometry and Fracture Risk: The Rotterdam Study. PLoS ONE, 2015, 10, e0129116.	2.5	58
417	Vitamin D and C-Reactive Protein: A Mendelian Randomization Study. PLoS ONE, 2015, 10, e0131740.	2.5	61
418	Single nucleotide polymorphisms in CRTC1 and BARX1 are associated with esophageal adenocarcinoma. Journal of Carcinogenesis, 2015, 14, 5.	2.5	14
419	Methylation of Migraine-Related Genes in Different Tissues of the Rat. PLoS ONE, 2014, 9, e87616.	2.5	22
420	Large-Scale Genome-Wide Association Studies and Meta-Analyses of Longitudinal Change in Adult Lung Function. PLoS ONE, 2014, 9, e100776.	2.5	52
421	Genome-Wide Meta-Analysis of Myopia and Hyperopia Provides Evidence for Replication of 11 Loci. PLoS ONE, 2014, 9, e107110.	2.5	40
422	No Evidence for Genome-Wide Interactions on Plasma Fibrinogen by Smoking, Alcohol Consumption and Body Mass Index: Results from Meta-Analyses of 80,607 Subjects. PLoS ONE, 2014, 9, e111156.	2.5	8
423	The Generation R Study: Biobank update 2015. European Journal of Epidemiology, 2014, 29, 911-927.	5.7	189
424	Meta-analysis identifies loci affecting levels of the potential osteoarthritis biomarkers sCOMP and uCTX-II with genome wide significance. Journal of Medical Genetics, 2014, 51, 596-604.	3.2	18
425	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. Nature Communications, 2014, 5, 5068.	12.8	216
426	Phenotypic Dissection of Bone Mineral Density Reveals Skeletal Site Specificity and Facilitates the Identification of Novel Loci in the Genetic Regulation of Bone Mass Attainment. PLoS Genetics, 2014, 10, e1004423.	3.5	134
427	Genome Wide Association Identifies Common Variants at the SERPINA6/SERPINA1 Locus Influencing Plasma Cortisol and Corticosteroid Binding Globulin. PLoS Genetics, 2014, 10, e1004474.	3.5	105
428	Meta-analysis of genome-wide association studies identifies novel loci that influence cupping and the glaucomatous process. Nature Communications, 2014, 5, 4883.	12.8	89
429	A meta-analysis of genome-wide association studies identifies novel variants associated with osteoarthritis of the hip. Annals of the Rheumatic Diseases, 2014, 73, 2130-2136.	0.9	108
430	Effect of daily vitamin B-12 and folic acid supplementation on fracture incidence in elderly individuals with an elevated plasma homocysteine concentration: B-PROOF, a randomized controlled trial. American Journal of Clinical Nutrition, 2014, 100, 1578-1586.	4.7	76
431	FTO genetic variants, dietary intake and body mass index: insights from 177 330 individuals. Human Molecular Genetics, 2014, 23, 6961-6972.	2.9	143
432	Results of 2-year vitamin B treatment on cognitive performance. Neurology, 2014, 83, 2158-2166.	1.1	67

#	ARTICLE	IF	CITATIONS
433	Genetic diversity is a predictor of mortality in humans. BMC Genetics, 2014, 15, 159.	2.7	12
434	Leukocyte telomere length associates with prospective mortality independent of immune-related parameters and known genetic markers. International Journal of Epidemiology, 2014, 43, 878-886.	1.9	95
435	Intrinsic and Extrinsic Risk Factors for Sagging Eyelids. JAMA Dermatology, 2014, 150, 836.	4.1	64
436	Association of Uric Acid Genetic Risk Score With Blood Pressure. Hypertension, 2014, 64, 1061-1066.	2.7	38
437	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	6.2	158
438	Fraction of exhaled nitric oxide values in childhood are associated with 17q11.2-q12 and 17q12-q21 variants. Journal of Allergy and Clinical Immunology, 2014, 134, 46-55.	2.9	33
439	Genome-wide association study for radiographic vertebral fractures: A potential role for the 16q24 BMD locus. Bone, 2014, 59, 20-27.	2.9	32
440	B-vitamin levels and genetics of hyperhomocysteinemia are not associated with arterial stiffness. Nutrition, Metabolism and Cardiovascular Diseases, 2014, 24, 760-766.	2.6	5
441	Pleiotropic genes for metabolic syndrome and inflammation. Molecular Genetics and Metabolism, 2014, 112, 317-338.	1.1	107
442	Novel Genetic Markers Associate With Atrial Fibrillation Risk in Europeans and Japanese. Journal of the American College of Cardiology, 2014, 63, 1200-1210.	2.8	127
443	Association of Low-Frequency and Rare Coding-Sequence Variants with Blood Lipids and Coronary Heart Disease in 56,000 Whites and Blacks. American Journal of Human Genetics, 2014, 94, 223-232.	6.2	287
444	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
445	The Genome of the Netherlands: design, and project goals. European Journal of Human Genetics, 2014, 22, 221-227.	2.8	246
446	Common DNA variants predict tall stature in Europeans. Human Genetics, 2014, 133, 587-597.	3.8	48
447	Prediction model for knee osteoarthritis incidence, including clinical, genetic and biochemical risk factors. Annals of the Rheumatic Diseases, 2014, 73, 2116-2121.	0.9	111
448	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	21.4	131
449	Gene-Age Interactions in Blood Pressure Regulation: A Large-Scale Investigation with the CHARGE, Global BPgen, and ICBP Consortia. American Journal of Human Genetics, 2014, 95, 24-38.	6.2	109
450	Effects of Long-Term Averaging of Quantitative Blood Pressure Traits on the Detection of Genetic Associations. American Journal of Human Genetics, 2014, 95, 49-65.	6.2	73

#	Article	IF	Citations
451	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
452	Genome-wide analysis of multi-ancestry cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma. Nature Genetics, 2014, 46, 1126-1130.	21.4	212
453	Annotation of loci from genome-wide association studies using tissue-specific quantitative interaction proteomics. Nature Methods, 2014, 11, 868-874.	19.0	70
454	Genome-wide association meta-analysis of human longevity identifies a novel locus conferring survival beyond 90 years of age. Human Molecular Genetics, 2014, 23, 4420-4432.	2.9	227
455	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
456	<scp>C9orf72</scp> and <scp>UNC13A</scp> are shared risk loci for amyotrophic lateral sclerosis and frontotemporal dementia: A genomeâ€wide metaâ€analysis. Annals of Neurology, 2014, 76, 120-133.	5.3	91
457	DNA methylation profiles at birth and child ADHD symptoms. Journal of Psychiatric Research, 2014, 49, 51-59.	3.1	93
458	Severe osteoarthritis of the hand associates with common variants within the ALDH1A2 gene and with rare variants at 1p31. Nature Genetics, 2014, 46, 498-502.	21.4	136
459	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	6.0	528
460	Common genes underlying asthma and COPD? Genome-wide analysis on the Dutch hypothesis. European Respiratory Journal, 2014, 44, 860-872.	6.7	49
461	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	21.4	959
462	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
463	Trans-ethnic meta-analysis of white blood cell phenotypes. Human Molecular Genetics, 2014, 23, 6944-6960.	2.9	60
464	The association between plasma homocysteine levels and bone quality and bone mineral density parameters in older persons. Bone, 2014, 63, 141-146.	2.9	32
465	Large scale meta-analysis of urinary C-terminal telopeptide, serum cartilage oligomeric protein and matrix metalloprotease degraded type II collagen and their role in prevalence, incidence and progression of osteoarthritis. Osteoarthritis and Cartilage, 2014, 22, 683-689.	1.3	72
466	TMEM106B Influences Volume of Left-Sided Temporal Lobe and Interhemispheric Structures in the General Population. Biological Psychiatry, 2014, 76, 503-508.	1.3	21
467	Drugâ€“gene interactions and the search for missing heritability: a cross-sectional pharmacogenomics study of the QT interval. Pharmacogenomics Journal, 2014, 14, 6-13.	2.0	28
468	Susceptibility to Chronic Mucus Hypersecretion, a Genome Wide Association Study. PLoS ONE, 2014, 9, e91621.	2.5	25

#	Article	IF	Citations
469	Analysis of Rare Variants in the C3 Gene in Patients with Age-Related Macular Degeneration. PLoS ONE, 2014, 9, e94165.	2.5	34
470	Inhibin Alpha-Subunit (INHA) Expression in Adrenocortical Cancer Is Linked to Genetic and Epigenetic INHA Promoter Variation. PLoS ONE, 2014, 9, e104944.	2.5	10
471	The Challenges of Genome-Wide Interaction Studies: Lessons to Learn from the Analysis of HDL Blood Levels. PLoS ONE, 2014, 9, e109290.	2.5	13
472	Genome-wide association study for radiographic vertebral fractures: a potential role for the 16q24 BMD locus. Bone, 2014, 59, 20-7.	2.9	17
473	Genetic Determinants of Osteoporosis. , 2013, , 563-604.		1
474	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
475	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	21.4	754
476	Secretory Phospholipase A2-IIA and Cardiovascular Disease. Journal of the American College of Cardiology, 2013, 62, 1966-1976.	2.8	115
477	A Genomeâ€Wide Association Study for Venous Thromboembolism: The Extended Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. Genetic Epidemiology, 2013, 37, 512-521.	1.3	99
478	The Rotterdam Study: 2014 objectives and design update. European Journal of Epidemiology, 2013, 28, 889-926.	5.7	282
479	Systematic identification of trans eQTLs as putative drivers of known disease associations. Nature Genetics, 2013, 45, 1238-1243.	21.4	1,544
480	Review of radiological scoring methods of osteoporotic vertebral fractures for clinical and research settings. European Radiology, 2013, 23, 476-486.	4.5	67
481	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
482	Common genetic loci influencing plasma homocysteine concentrations and their effect on risk of coronary artery disease. American Journal of Clinical Nutrition, 2013, 98, 668-676.	4.7	161
483	Prediction of Age-related Macular Degeneration in the General Population. Ophthalmology, 2013, 120, 2644-2655.	5.2	84
484	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	21.4	578
485	A Genome-Wide Association Study of Depressive Symptoms. Biological Psychiatry, 2013, 73, 667-678.	1.3	149
486	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	12.6	750

#	Article	IF	Citations
487	Genome-wide meta-analysis identifies new susceptibility loci for migraine. Nature Genetics, 2013, 45, 912-917.	21.4	338
488	Genome-wide meta-analysis of observational studies shows common genetic variants associated with macronutrient intake. American Journal of Clinical Nutrition, 2013, 97, 1395-1402.	4.7	210
489	Meta-Analysis of Genome-Wide Association Studies Identifies Six New Loci for Serum Calcium Concentrations. PLoS Genetics, 2013, 9, e1003796.	3.5	142
490	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. PLoS Medicine, 2013, 10, e1001474.	8.4	178
491	Scheuermann Disease. Spine, 2013, 38, 1690-1694.	2.0	38
492	Polymorphisms in genes within the IGF-axis influence antenatal and postnatal growth. Journal of Developmental Origins of Health and Disease, 2013, 4, 157-169.	1.4	2
493	The Molecular Genetic Architecture of Self-Employment. PLoS ONE, 2013, 8, e60542.	2.5	41
494	A Genetic Deconstruction of Neurocognitive Traits in Schizophrenia and Bipolar Disorder. PLoS ONE, 2013, 8, e81052.	2.5	20
495	Multi-functionality of computer-aided quantitative vertebral fracture morphometry analyses. Quantitative Imaging in Medicine and Surgery, 2013, 3, 249-55.	2.0	9
496	Evidence of Inbreeding Depression on Human Height. PLoS Genetics, 2012, 8, e1002655.	3.5	79
497	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. PLoS Genetics, 2012, 8, e1002490.	3.5	181
498	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	3.5	419
499	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	21.4	746
500	Common variants at 6q22 and 17q21 are associated with intracranial volume. Nature Genetics, 2012, 44, 539-544.	21.4	126
501	Common variants at 12q15 and 12q24 are associated with infant head circumference. Nature Genetics, 2012, 44, 532-538.	21.4	130
502	A Genome-Wide Association Study Identifies Five Loci Influencing Facial Morphology in Europeans. PLoS Genetics, 2012, 8, e1002932.	3.5	274
503	Genome-wide association and functional studies identify the DOT1L gene to be involved in cartilage thickness and hip osteoarthritis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8218-8223.	7.1	154
504	Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. Lancet, The, 2012, 380, 815-823.	13.7	373

#	Article	IF	Citations
505	Genome-wide association study for circulating levels of PAI-1 provides novel insights into its regulation. Blood, 2012, 120, 4873-4881.	1.4	90
506	Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture. Nature Genetics, 2012, 44, 491-501.	21.4	1,100
507	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	21.4	1,748
508	The association between plasma homocysteine levels, methylation capacity and incident osteoporotic fractures. Bone, 2012, 50, 1401-1405.	2.9	25
509	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. Nature Genetics, 2012, 44, 260-268.	21.4	303
510	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669.	21.4	762
511	Meta-Analysis of Genome-Wide Association Studies in >80 000 Subjects Identifies Multiple Loci for C-Reactive Protein Levels. Circulation, 2011, 123, 731-738.	1.6	461
512	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. Nature Genetics, 2011, 43, 753-760.	21.4	289
513	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	21.4	501
514	Genomeâ€wide association study identifies a single major locus contributing to survival into old age; the APOE locus revisited. Aging Cell, 2011, 10, 686-698.	6.7	249
515	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. Nature Genetics, 2011, 43, 333-338.	21.4	1,685
516	Genome-Wide Association Study for Coronary Artery Calcification With Follow-Up in Myocardial Infarction. Circulation, 2011, 124, 2855-2864.	1.6	269
517	The Rotterdam Study: 2012 objectives and design update. European Journal of Epidemiology, 2011, 26, 657-686.	5.7	273
518	Candidate gene studies and the quest for the entrepreneurial gene. Small Business Economics, 2011, 37, 269-275.	6.7	22
519	Rationale and design of the B-PROOF study, a randomized controlled trial on the effect of supplemental intake of vitamin B12and folic acid on fracture incidence. BMC Geriatrics, 2011, 11, 80.	2.7	83
520	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
521	Meta-analysis of genome-wide association studies from the CHARGE consortium identifies common variants associated with carotid intima media thickness and plaque. Nature Genetics, 2011, 43, 940-947.	21.4	191
522	Multiple Loci Are Associated with White Blood Cell Phenotypes. PLoS Genetics, 2011, 7, e1002113.	3.5	106

#	ARTICLE	IF	CITATIONS
523	Genetic Loci Associated with Plasma Phospholipid n-3 Fatty Acids: A Meta-Analysis of Genome-Wide Association Studies from the CHARGE Consortium. PLoS Genetics, 2011, 7, e1002193.	3.5	324
524	Genetics of the Vitamin D Endocrine System. , 2011, , 1025-1039.		0
525	Genome-Wide Association Studies of MRI-Defined Brain Infarcts. Stroke, 2010, 41, 210-217.	2.0	82
526	Pharmacogenetic risk factors for altered bone mineral density and body composition in pediatric acute lymphoblastic leukemia. Haematologica, 2010, 95, 752-759.	3.5	38
527	Vitamin D receptor: a new risk marker for clinical restenosis after percutaneous coronary intervention. Expert Opinion on Therapeutic Targets, 2010, 14, 243-251.	3.4	23
528	The Role of Body Mass Index, Insulin, and Adiponectin in the Relation Between Fat Distribution and Bone Mineral Density. Calcified Tissue International, 2010, 86, 116-125.	3.1	68
529	Genome-wide association studies in economics and entrepreneurship research: promises and limitations. Small Business Economics, 2010, 35, 1-18.	6.7	41
530	Common genetic variation in the Estrogen Receptor Beta (ESR2) gene and osteoarthritis: results of a meta-analysis. BMC Medical Genetics, 2010, 11, 164.	2.1	8
531	Vitamin Dâ€binding protein polymorphisms are not associated with development of (multiple) basal cell carcinomas. Experimental Dermatology, 2010, 19, 1103-1105.	2.9	16
532	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	27.8	3,249
533	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
534	Genome-wide association study of PR interval. Nature Genetics, 2010, 42, 153-159.	21.4	400
535	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	21.4	1,631
536	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	21.4	2,634
537	Genome-wide Analysis of Genetic Loci Associated With Alzheimer Disease. JAMA - Journal of the American Medical Association, 2010, 303, 1832.	7.4	1,064
538	Association of Genome-Wide Variation With the Risk of Incident Heart Failure in Adults of European and African Ancestry. Circulation: Cardiovascular Genetics, 2010, 3, 256-266.	5.1	176
539	Common Genetic Variants Associate with Serum Phosphorus Concentration. Journal of the American Society of Nephrology: JASN, 2010, 21, 1223-1232.	6.1	123
540	Multiple Genetic Loci Influence Serum Urate Levels and Their Relationship With Gout and Cardiovascular Disease Risk Factors. Circulation: Cardiovascular Genetics, 2010, 3, 523-530.	5.1	285

#	ARTICLE	IF	CITATIONS
541	Genetics of Osteoporosis. Endocrine Reviews, 2010, 31, 629-662.	20.1	316
542	A Meta-analysis of Four Genome-Wide Association Studies of Survival to Age 90 Years or Older: The Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2010, 65A, 478-487.	3.6	117
543	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	21.4	1,982
544	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	3.5	453
545	GRIMP: a web- and grid-based tool for high-speed analysis of large-scale genome-wide association using imputed data. Bioinformatics, 2009, 25, 2750-2752.	4.1	45
546	NRXN3 Is a Novel Locus for Waist Circumference: A Genome-Wide Association Study from the CHARGE Consortium. PLoS Genetics, 2009, 5, e1000539.	3.5	230
547	Genetic variation in the GDF5 region is associated with osteoarthritis, height, hip axis length and fracture risk: the Rotterdam study. Annals of the Rheumatic Diseases, 2009, 68, 1754-1760.	0.9	61
548	Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. Circulation: Cardiovascular Genetics, 2009, 2, 73-80.	5.1	519
549	Eye color and the prediction of complex phenotypes from genotypes. Current Biology, 2009, 19, R192-R193.	3.9	226
550	The Rotterdam Study: 2010 objectives and design update. European Journal of Epidemiology, 2009, 24, 553-572.	5.7	235
551	Genotypes Associated With Reduced Activity of VKORC1 and CYP2C9 and Their Modification of Acenocoumarol Anticoagulation During the Initial Treatment Period. Clinical Pharmacology and Therapeutics, 2009, 85, 379-386.	4.7	32
552	Predicting human height by Victorian and genomic methods. European Journal of Human Genetics, 2009, 17, 1070-1075.	2.8	108
553	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. Nature Genetics, 2009, 41, 47-55.	21.4	776
554	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	21.4	1,572
555	Genome-wide association study of blood pressure and hypertension. Nature Genetics, 2009, 41, 677-687.	21.4	1,224
556	Genome-wide association study identifies 19p13.3 (UNC13A) and 9p21.2 as susceptibility loci for sporadic amyotrophic lateral sclerosis. Nature Genetics, 2009, 41, 1083-1087.	21.4	344
557	Twenty bone-mineral-density loci identified by large-scale meta-analysis of genome-wide association studies. Nature Genetics, 2009, 41, 1199-1206.	21.4	660
558	Collaborative Meta-analysis: Associations of 150 Candidate Genes With Osteoporosis and Osteoporotic Fracture. Annals of Internal Medicine, 2009, 151, 528.	3.9	250

#	Article	IF	Citations
559	A genome-wide association study of acenocoumarol maintenance dosage. Human Molecular Genetics, 2009, 18, 3758-3768.	2.9	133
560	Vitamin D Binding Protein Genotype and Osteoporosis. Calcified Tissue International, 2009, 85, 85-93.	3.1	97
561	Genetic Determinants of Osteoporosis. , 2008, , 759-798.		0
562	The RIZ Pro704 insertionâ€“deletion polymorphism, bone mineral density and fracture risk: The Rotterdam study. Bone, 2008, 42, 286-293.	2.9	14
563	Bone mineral density, osteoporosis, and osteoporotic fractures: a genome-wide association study. Lancet, The, 2008, 371, 1505-1512.	13.7	612
564	Estrogen Receptor Î± Gene Polymorphisms Associated with Incident Aging Macula Disorder. , 2007, 48, 1012.		27
565	Genome-wide association study identifies novel breast cancer susceptibility loci. Nature, 2007, 447, 1087-1093.	27.8	2,165
566	The -1997 G/T and Sp1 Polymorphisms in the Collagen Type I alpha1 (COLIA1) Gene in Relation to Changes in Femoral Neck Bone Mineral Density and the Risk of Fracture in the Elderly: The Rotterdam Study. Calcified Tissue International, 2007, 81, 18-25.	3.1	32
567	Large-Scale Evidence for the Effect of the COLIA1 Sp1 Polymorphism on Osteoporosis Outcomes: The GENOMOS Study. PLoS Medicine, 2006, 3, e90.	8.4	160
568	BMP-2 Gene Polymorphisms and Osteoporosis: The Rotterdam Study. Journal of Bone and Mineral Research, 2006, 21, 845-854.	2.8	41
569	Estrogen Receptor Î² (ESR2) Polymorphisms in Interaction With Estrogen Receptor Î± (ESR1) and Insulin-Like Growth Factor I (IGF1) Variants Influence the Risk of Fracture in Postmenopausal Women. Journal of Bone and Mineral Research, 2006, 21, 1443-1456.	2.8	73
570	Evidence for auto/paracrine actions of vitamin D in bone: 1aâ€hydroxylase expression and activity in human bone cells. FASEB Journal, 2006, 20, 2417-2419.	0.5	184
571	The Role of Genetic Variation in Osteoporosis. , 2006, , 471-485.		0
572	Identifying genetic risk factors for osteoporosis. Journal of Musculoskeletal Neuronal Interactions, 2006, 6, 16-26.	0.1	17
573	Staphylococcus aureusnasal carriage is not associated with known polymorphism in the Vitamin D receptor gene. FEMS Immunology and Medical Microbiology, 2005, 43, 173-176.	2.7	22
574	Estrogen receptor alpha gene polymorphisms are associated with estradiol levels in postmenopausal women. European Journal of Endocrinology, 2005, 153, 327-334.	3.7	102
575	Loci for regulation of bone mineral density in men and women identified by genome wide linkage scan: the FAMOS study. Human Molecular Genetics, 2005, 14, 943-951.	2.9	124
576	Promoter and 3â€²-Untranslated-Region Haplotypes in the Vitamin D Receptor Gene Predispose to Osteoporotic Fracture: The Rotterdam Study. American Journal of Human Genetics, 2005, 77, 807-823.	6.2	282

#	Article	IF	Citations
577	Bone mineral density and vertebral fracture history are associated with incident and progressive radiographic knee osteoarthritis in elderly men and women: The Rotterdam Study. Bone, 2005, 37, 446-456.	2.9	76
578	Genetic Vitamin D Receptor Polymorphisms and Risk of Disease. , 2005, , 1121-1157.		9
579	Estrogen Receptor Î± Gene Polymorphisms and Risk of Myocardial Infarction. JAMA - Journal of the American Medical Association, 2004, 291, 2969.	7.4	208
580	Differential Genetic Effects of <EMPH TYPE="ITAL">ESR1</EMPH> Gene Polymorphisms on Osteoporosis Outcomes. JAMA - Journal of the American Medical Association, 2004, 292, 2105.	7.4	265
581	Collagen type I Â1 Sp1 polymorphism, osteoporosis, and intervertebral disc degeneration in older men and women. Annals of the Rheumatic Diseases, 2004, 63, 71-77.	0.9	104
582	ApoE Gene Polymorphisms, BMD, and Fracture Risk in Elderly Men and Women: The Rotterdam Study. Journal of Bone and Mineral Research, 2004, 19, 1490-1496.	2.8	31
583	Estrogen Receptor Î± Gene Polymorphisms and Bone Mineral Density in Healthy Children and Young Adults. Calcified Tissue International, 2004, 74, 495-500.	3.1	56
584	A new marker for osteoarthritis: Cross-sectional and longitudinal approach. Arthritis and Rheumatism, 2004, 50, 2471-2478.	6.7	235
585	Polymorphisms in the Sclerosteosis/van Buchem Disease Gene (SOST) Region Are Associated with Bone-Mineral Density in Elderly Whites. American Journal of Human Genetics, 2004, 75, 1032-1045.	6.2	121
586	Homocysteine Levels and the Risk of Osteoporotic Fracture. New England Journal of Medicine, 2004, 350, 2033-2041.	27.0	673
587	Genetics and biology of vitamin D receptor polymorphisms. Gene, 2004, 338, 143-156.	2.2	1,249
588	Fracture incidence and association with bone mineral density in elderly men and women: the Rotterdam Study. Bone, 2004, 34, 195-202.	2.9	1,324
589	Vitamin D receptor gene polymorphisms in relation to Vitamin D related disease states. Journal of Steroid Biochemistry and Molecular Biology, 2004, 89-90, 187-193.	2.5	194
590	Cdx-2 Polymorphism in the Promoter Region of the Human Vitamin D Receptor Gene Determines Susceptibility to Fracture in the Elderly. Journal of Bone and Mineral Research, 2003, 18, 1632-1641.	2.8	120
591	Estrogen receptor ? gene haplotype is associated with radiographic osteoarthritis of the knee in elderly men and women. Arthritis and Rheumatism, 2003, 48, 1913-1922.	6.7	125
592	Association of 5' estrogen receptor alpha gene polymorphisms with bone mineral density, vertebral bone area and fracture risk. Human Molecular Genetics, 2003, 12, 1745-1754.	2.9	170
593	Genetic approaches to the study of complex diseases: osteoporosis. , 2002, , 159-164.		0
594	The role of vitamin D receptor gene polymorphisms in bone biology. Molecular and Cellular Endocrinology, 2002, 197, 15-21.	3.2	79

#	Article	IF	Citations
595	Interaction Between the Vitamin D Receptor Gene and Collagen Type IÎ±1 Gene in Susceptibility for Fracture. Journal of Bone and Mineral Research, 2001, 16, 379-385.	2.8	111
596	Genetics and Genomics of Osteoporosis. , 2001, , 639-667.		20
597	Detection of sequence variability of the collagen type IIÎ± 1 3â€² variable number of tandem repeat. Electrophoresis, 2000, 21, 3571-3577.	2.4	3
598	Adjacent genes, for COL2A1 and the vitamin D receptor, are associated with separate features of radiographic osteoarthritis of the knee. Arthritis and Rheumatism, 2000, 43, 1456-1464.	6.7	80
599	Consequences of vitamin D receptor gene polymorphisms for growth inhibition of cultured human peripheral blood mononuclear cells by 1,25-dihydroxyvitamin D3. Clinical Endocrinology, 2000, 52, 211-216.	2.4	168
600	Estrogen Receptor Polymorphism Predicts the Onset of Natural and Surgical Menopause¹. Journal of Clinical Endocrinology and Metabolism, 1999, 84, 3146-3150.	3.6	209
601	Relation of Alleles of the Collagen Type IÎ±1 Gene to Bone Density and the Risk of Osteoporotic Fractures in Postmenopausal Women. New England Journal of Medicine, 1998, 338, 1016-1021.	27.0	428
602	Direct Haplotyping at the Vitamin D Receptor Locus Improves Genetic Resolution. Journal of Bone and Mineral Research, 1997, 12, 494-495.	2.8	8
603	The Effect of Vitamin D Supplementation on the Bone Mineral Density of the Femoral Neck Is Associated with Vitamin D Receptor Genotype. Journal of Bone and Mineral Research, 1997, 12, 1241-1245.	2.8	130
604	Vitamin D receptor genotype is associated with radiographic osteoarthritis at the knee.. Journal of Clinical Investigation, 1997, 100, 259-263.	8.2	129
605	A large-scale population-based study of the association of vitamin D receptor gene polymorphisms with bone mineral density. Journal of Bone and Mineral Research, 1996, 11, 1241-1248.	2.8	200
606	Gene and genome scanning by two-dimensional DNA typing. Electrophoresis, 1995, 16, 186-196.	2.4	6