

Albert V. Smith

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8111052/publications.pdf>

Version: 2024-02-01

316
papers

88,845
citations

729

120
h-index

407

277
g-index

359
all docs

359
docs citations

359
times ranked

75315
citing authors

#	ARTICLE	IF	CITATIONS
1	A haplotype map of the human genome. <i>Nature</i> , 2005, 437, 1299-1320.	13.7	5,440
2	A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , 2007, 449, 851-861.	13.7	4,137
3	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
4	Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. <i>Nature Genetics</i> , 2013, 45, 1452-1458.	9.4	3,741
5	Biological, clinical and population relevance of 95 loci for blood lipids. <i>Nature</i> , 2010, 466, 707-713.	13.7	3,249
6	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	9.4	2,634
7	A comprehensive 1000 Genomesâ€‘based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , 2015, 47, 1121-1130.	9.4	2,054
8	Genetic meta-analysis of diagnosed Alzheimerâ€™s disease identifies new risk loci and implicates AÎ², tau, immunity and lipid processing. <i>Nature Genetics</i> , 2019, 51, 414-430.	9.4	1,962
9	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011, 478, 103-109.	13.7	1,855
10	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	9.4	1,818
11	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	13.7	1,789
12	Genome-wide detection and characterization of positive selection in human populations. <i>Nature</i> , 2007, 449, 913-918.	13.7	1,788
13	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. <i>Nature Genetics</i> , 2011, 43, 333-338.	9.4	1,685
14	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	13.7	1,328
15	Genome-wide association study of blood pressure and hypertension. <i>Nature Genetics</i> , 2009, 41, 677-687.	9.4	1,224
16	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	13.7	1,204
17	Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture. <i>Nature Genetics</i> , 2012, 44, 491-501.	9.4	1,100
18	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021, 590, 290-299.	13.7	1,069

#	ARTICLE	IF	CITATIONS
19	Genome-wide Analysis of Genetic Loci Associated With Alzheimer Disease. JAMA - Journal of the American Medical Association, 2010, 303, 1832.	3.8	1,064
20	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	9.4	924
21	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. Nature Genetics, 2016, 48, 624-633.	9.4	870
22	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	9.4	836
23	Genome-Wide Association Analysis Identifies Variants Associated with Nonalcoholic Fatty Liver Disease That Have Distinct Effects on Metabolic Traits. PLoS Genetics, 2011, 7, e1001324.	1.5	796
24	Rare coding variants in PLCC2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	9.4	783
25	Genetic Associations with Valvular Calcification and Aortic Stenosis. New England Journal of Medicine, 2013, 368, 503-512.	13.9	767
26	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.	9.4	762
27	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	6.0	750
28	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	9.4	746
29	New loci associated with kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 376-384.	9.4	710
30	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	9.4	675
31	Identification of common variants associated with human hippocampal and intracranial volumes. Nature Genetics, 2012, 44, 552-561.	9.4	594
32	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
33	Multiple loci associated with indices of renal function and chronic kidney disease. Nature Genetics, 2009, 41, 712-717.	9.4	553
34	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	9.4	552
35	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
36	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	13.7	548

#	ARTICLE	IF	CITATIONS
37	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	13.7	544
38	Meta-analysis identifies six new susceptibility loci for atrial fibrillation. <i>Nature Genetics</i> , 2012, 44, 670-675.	9.4	533
39	The International HapMap Project Web site. <i>Genome Research</i> , 2005, 15, 1592-1593.	2.4	497
40	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. <i>Nature Communications</i> , 2018, 9, 2098.	5.8	484
41	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. <i>Nature</i> , 2015, 526, 112-117.	13.7	483
42	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766.	9.4	470
43	Meta-Analysis of Genome-Wide Association Studies in >80 000 Subjects Identifies Multiple Loci for C-Reactive Protein Levels. <i>Circulation</i> , 2011, 123, 731-738.	1.6	461
44	Genomic inflation factors under polygenic inheritance. <i>European Journal of Human Genetics</i> , 2011, 19, 807-812.	1.4	460
45	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 1077-1085.	9.4	445
46	Common variants in KCNN3 are associated with lone atrial fibrillation. <i>Nature Genetics</i> , 2010, 42, 240-244.	9.4	438
47	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	9.4	426
48	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016, 7, 10023.	5.8	412
49	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011, 43, 1005-1011.	9.4	403
50	Genome-wide association study of PR interval. <i>Nature Genetics</i> , 2010, 42, 153-159.	9.4	400
51	Quality control and conduct of genome-wide association meta-analyses. <i>Nature Protocols</i> , 2014, 9, 1192-1212.	5.5	398
52	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012, 490, 267-272.	13.7	383
53	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020, 586, 763-768.	13.7	376
54	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. <i>PLoS Genetics</i> , 2013, 9, e1003500.	1.5	371

#	ARTICLE	IF	CITATIONS
55	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. <i>Nature Genetics</i> , 2011, 43, 1082-1090.	9.4	367
56	Variants in ZFHX3 are associated with atrial fibrillation in individuals of European ancestry. <i>Nature Genetics</i> , 2009, 41, 879-881.	9.4	363
57	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016, 48, 1171-1184.	9.4	362
58	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015, 47, 1294-1303.	9.4	357
59	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018, 50, 559-571.	9.4	356
60	Genetic contributions to variation in general cognitive function: a meta-analysis of genome-wide association studies in the CHARGE consortium (N=53,949). <i>Molecular Psychiatry</i> , 2015, 20, 183-192.	4.1	344
61	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	9.4	341
62	The Yeast Red1 Protein Localizes to the Cores of Meiotic Chromosomes. <i>Journal of Cell Biology</i> , 1997, 136, 957-967.	2.3	336
63	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	1.5	331
64	A common haplotype lowers PU.1 expression in myeloid cells and delays onset of Alzheimer's disease. <i>Nature Neuroscience</i> , 2017, 20, 1052-1061.	7.1	330
65	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , 2018, 103, 691-706.	2.6	326
66	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. <i>Nature Genetics</i> , 2009, 41, 1191-1198.	9.4	324
67	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. <i>Nature Genetics</i> , 2010, 42, 1068-1076.	9.4	308
68	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. <i>Nature Genetics</i> , 2012, 44, 260-268.	9.4	303
69	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. <i>Nature Genetics</i> , 2011, 43, 753-760.	9.4	289
70	Association of Low-Frequency and Rare Coding-Sequence Variants with Blood Lipids and Coronary Heart Disease in 56,000 Whites and Blacks. <i>American Journal of Human Genetics</i> , 2014, 94, 223-232.	2.6	287
71	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018, 50, 26-41.	9.4	286
72	Multiple Genetic Loci Influence Serum Urate Levels and Their Relationship With Gout and Cardiovascular Disease Risk Factors. <i>Circulation: Cardiovascular Genetics</i> , 2010, 3, 523-530.	5.1	285

#	ARTICLE	IF	CITATIONS
73	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013, 45, 621-631.	9.4	282
74	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. <i>Nature Genetics</i> , 2014, 46, 826-836.	9.4	281
75	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. <i>Nature Genetics</i> , 2017, 49, 946-952.	9.4	279
76	Genome-Wide Association Study for Coronary Artery Calcification With Follow-Up in Myocardial Infarction. <i>Circulation</i> , 2011, 124, 2855-2864.	1.6	269
77	Meta-analysis of genome-wide association data identifies two loci influencing age at menarche. <i>Nature Genetics</i> , 2009, 41, 648-650.	9.4	266
78	A novel Alzheimer disease locus located near the gene encoding tau protein. <i>Molecular Psychiatry</i> , 2016, 21, 108-117.	4.1	260
79	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	9.4	251
80	GWAS of Longevity in CHARGE Consortium Confirms APOE and FOXO3 Candidacy. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2015, 70, 110-118.	1.7	250
81	Novel genetic loci associated with hippocampal volume. <i>Nature Communications</i> , 2017, 8, 13624.	5.8	250
82	Genome-Wide Association for Abdominal Subcutaneous and Visceral Adipose Reveals a Novel Locus for Visceral Fat in Women. <i>PLoS Genetics</i> , 2012, 8, e1002695.	1.5	245
83	NRXN3 Is a Novel Locus for Waist Circumference: A Genome-Wide Association Study from the CHARGE Consortium. <i>PLoS Genetics</i> , 2009, 5, e1000539.	1.5	230
84	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. <i>Nature Genetics</i> , 2016, 48, 1162-1170.	9.4	223
85	Best Practices and Joint Calling of the HumanExome BeadChip: The CHARGE Consortium. <i>PLoS ONE</i> , 2013, 8, e68095.	1.1	219
86	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. <i>Nature Communications</i> , 2014, 5, 5068.	5.8	216
87	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. <i>Nature Genetics</i> , 2022, 54, 437-449.	9.4	215
88	Genome-wide association meta-analysis for total serum bilirubin levels. <i>Human Molecular Genetics</i> , 2009, 18, 2700-2710.	1.4	214
89	A meta-analysis of genome-wide association studies identifies multiple longevity genes. <i>Nature Communications</i> , 2019, 10, 3669.	5.8	214
90	Novel genetic loci underlying human intracranial volume identified through genome-wide association. <i>Nature Neuroscience</i> , 2016, 19, 1569-1582.	7.1	213

#	ARTICLE	IF	CITATIONS
91	Omega-6 fatty acid biomarkers and incident type 2 diabetes: pooled analysis of individual-level data for 39â€740 adults from 20 prospective cohort studies. <i>Lancet Diabetes and Endocrinology</i> , 2017, 5, 965-974.	5.5	213
92	Common variants at 12q14 and 12q24 are associated with hippocampal volume. <i>Nature Genetics</i> , 2012, 44, 545-551.	9.4	212
93	CUBN Is a Gene Locus for Albuminuria. <i>Journal of the American Society of Nephrology: JASN</i> , 2011, 22, 555-570.	3.0	208
94	<i>KLB</i> is associated with alcohol drinking, and its gene product β -Klotho is necessary for FGF21 regulation of alcohol preference. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 14372-14377.	3.3	208
95	Assessing population differentiation and isolation from single-nucleotide polymorphism data. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2002, 64, 695-715.	1.1	201
96	Genome-wide association studies of cerebral white matter lesion burden. <i>Annals of Neurology</i> , 2011, 69, 928-939.	2.8	201
97	Biomarkers of Dietary Omega-6 Fatty Acids and Incident Cardiovascular Disease and Mortality. <i>Circulation</i> , 2019, 139, 2422-2436.	1.6	199
98	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. <i>American Journal of Human Genetics</i> , 2014, 94, 233-245.	2.6	193
99	Genetic architecture of subcortical brain structures in 38,851 individuals. <i>Nature Genetics</i> , 2019, 51, 1624-1636.	9.4	192
100	Meta-analysis of genome-wide association studies from the CHARGE consortium identifies common variants associated with carotid intima media thickness and plaque. <i>Nature Genetics</i> , 2011, 43, 940-947.	9.4	191
101	Genome-Wide Association Studies of Serum Magnesium, Potassium, and Sodium Concentrations Identify Six Loci Influencing Serum Magnesium Levels. <i>PLoS Genetics</i> , 2010, 6, e1001045.	1.5	185
102	Association of Low-Density Lipoprotein Cholesterol-Related Genetic Variants With Aortic Valve Calcium and Incident Aortic Stenosis. <i>JAMA - Journal of the American Medical Association</i> , 2014, 312, 1764.	3.8	184
103	Heterogeneity in White Blood Cells Has Potential to Confound DNA Methylation Measurements. <i>PLoS ONE</i> , 2012, 7, e46705.	1.1	183
104	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	13.7	183
105	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. <i>Nature Communications</i> , 2015, 6, 5897.	5.8	173
106	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	13.7	173
107	Convergent genetic and expression data implicate immunity in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2015, 11, 658-671.	0.4	173
108	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, 14977.	5.8	169

#	ARTICLE	IF	CITATIONS
109	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. <i>Human Molecular Genetics</i> , 2011, 20, 2273-2284.	1.4	168
110	The Promises and Pitfalls of Genoeconomics. <i>Annual Review of Economics</i> , 2012, 4, 627-662.	2.4	168
111	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. <i>PLoS Genetics</i> , 2012, 8, e1002584.	1.5	166
112	Genome-Wide Association Studies Identify <i>CHRNA5</i> and <i>HTR4</i> in the Development of Airflow Obstruction. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2012, 186, 622-632.	2.5	164
113	Multiethnic Genome-Wide Association Study of Cerebral White Matter Hyperintensities on MRI. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 398-409.	5.1	162
114	Genome-wide physical activity interactions in adiposity – A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	1.5	158
115	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. <i>PLoS ONE</i> , 2014, 9, e94661.	1.1	155
116	A Genome-Wide Association Study of Depressive Symptoms. <i>Biological Psychiatry</i> , 2013, 73, 667-678.	0.7	149
117	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 2017, 8, 80.	5.8	147
118	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. <i>Journal of the American College of Cardiology</i> , 2019, 73, 58-66.	1.2	147
119	Meta-Analysis of Genome-Wide Association Studies Identifies Six New Loci for Serum Calcium Concentrations. <i>PLoS Genetics</i> , 2013, 9, e1003796.	1.5	142
120	Four Novel Loci (19q13, 6q24, 12q24, and 5q14) Influence the Microcirculation In Vivo. <i>PLoS Genetics</i> , 2010, 6, e1001184.	1.5	134
121	GWAS for executive function and processing speed suggests involvement of the <i>CADM2</i> gene. <i>Molecular Psychiatry</i> , 2016, 21, 189-197.	4.1	134
122	Genome-wide association analysis identifies multiple loci related to resting heart rate. <i>Human Molecular Genetics</i> , 2010, 19, 3885-3894.	1.4	133
123	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019, 10, 4130.	5.8	133
124	Genome-wide association analysis identifies six new loci associated with forced vital capacity. <i>Nature Genetics</i> , 2014, 46, 669-677.	9.4	131
125	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. <i>Diabetes</i> , 2016, 65, 803-817.	0.3	131
126	A Genome-Wide Association Study Identifies <i>LIPA</i> as a Susceptibility Gene for Coronary Artery Disease. <i>Circulation: Cardiovascular Genetics</i> , 2011, 4, 403-412.	5.1	130

#	ARTICLE	IF	CITATIONS
127	Genome-Wide Joint Meta-Analysis of SNP and SNP-by-Smoking Interaction Identifies Novel Loci for Pulmonary Function. <i>PLoS Genetics</i> , 2012, 8, e1003098.	1.5	130
128	Common variants at 12q15 and 12q24 are associated with infant head circumference. <i>Nature Genetics</i> , 2012, 44, 532-538.	9.4	130
129	Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. <i>Lancet Neurology</i> , The, 2016, 15, 695-707.	4.9	130
130	Interactions of Dietary Whole-Grain Intake With Fasting Glucose- and Insulin-Related Genetic Loci in Individuals of European Descent: A meta-analysis of 14 cohort studies. <i>Diabetes Care</i> , 2010, 33, 2684-2691.	4.3	127
131	A genome-wide association study of aging. <i>Neurobiology of Aging</i> , 2011, 32, 2109.e15-2109.e28.	1.5	127
132	Novel Genetic Markers Associate With Atrial Fibrillation Risk in Europeans and Japanese. <i>Journal of the American College of Cardiology</i> , 2014, 63, 1200-1210.	1.2	127
133	Common variants at 6q22 and 17q21 are associated with intracranial volume. <i>Nature Genetics</i> , 2012, 44, 539-544.	9.4	126
134	Characterization of european ancestry nonalcoholic fatty liver disease-associated variants in individuals of african and hispanic descent. <i>Hepatology</i> , 2013, 58, 966-975.	3.6	126
135	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. <i>Hypertension</i> , 2017, 70, .	1.3	123
136	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018, 102, 375-400.	2.6	123
137	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. <i>Nature Communications</i> , 2018, 9, 5141.	5.8	119
138	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. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2010, 65A, 478-487.	1.7	117
139	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. <i>Nature Genetics</i> , 2017, 49, 125-130.	9.4	116
140	Cardiometabolic effects of genetic upregulation of the interleukin 1 receptor antagonist: a Mendelian randomisation analysis. <i>Lancet Diabetes and Endocrinology</i> , the, 2015, 3, 243-253.	5.5	115
141	Genome-wide association study of kidney function decline in individuals of European descent. <i>Kidney International</i> , 2015, 87, 1017-1029.	2.6	113
142	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1435-1448.	1.2	113
143	Genome-wide association study meta-analysis of chronic widespread pain: evidence for involvement of the 5p15.2 region. <i>Annals of the Rheumatic Diseases</i> , 2013, 72, 427-436.	0.5	112
144	Novel loci associated with usual sleep duration: the CHARGE Consortium Genome-Wide Association Study. <i>Molecular Psychiatry</i> , 2015, 20, 1232-1239.	4.1	112

#	ARTICLE	IF	CITATIONS
145	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019, 51, 636-648.	9.4	112
146	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13366-13371.	3.3	110
147	Gene-Age Interactions in Blood Pressure Regulation: A Large-Scale Investigation with the CHARGE, Global BPgen, and ICBP Consortia. <i>American Journal of Human Genetics</i> , 2014, 95, 24-38.	2.6	109
148	Insights into the Genetic Architecture of Early Stage Age-Related Macular Degeneration: A Genome-Wide Association Study Meta-Analysis. <i>PLoS ONE</i> , 2013, 8, e53830.	1.1	108
149	Multiple Loci Are Associated with White Blood Cell Phenotypes. <i>PLoS Genetics</i> , 2011, 7, e1002113.	1.5	106
150	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. <i>Journal of Clinical Investigation</i> , 2017, 127, 1798-1812.	3.9	106
151	A genome-wide association study of early menopause and the combined impact of identified variants. <i>Human Molecular Genetics</i> , 2013, 22, 1465-1472.	1.4	104
152	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. <i>Circulation</i> , 2019, 139, 620-635.	1.6	102
153	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. <i>Scientific Reports</i> , 2017, 7, 45040.	1.6	98
154	Genetic Obesity and the Risk of Atrial Fibrillation. <i>Circulation</i> , 2017, 135, 741-754.	1.6	96
155	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018, 13, e0198166.	1.1	94
156	GA4GH: International policies and standards for data sharing across genomic research and healthcare. <i>Cell Genomics</i> , 2021, 1, 100029.	3.0	94
157	HDAC9 is implicated in atherosclerotic aortic calcification and affects vascular smooth muscle cell phenotype. <i>Nature Genetics</i> , 2019, 51, 1580-1587.	9.4	92
158	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. <i>Nature Genetics</i> , 2020, 52, 1314-1332.	9.4	91
159	Common Genetic Variation in the <i>BCL11B</i> Gene Desert Is Associated With Carotid-Femoral Pulse Wave Velocity and Excess Cardiovascular Disease Risk. <i>Circulation: Cardiovascular Genetics</i> , 2012, 5, 81-90.	5.1	90
160	Genetic determinants of heel bone properties: genome-wide association meta-analysis and replication in the GEFOs/GENOMOS consortium. <i>Human Molecular Genetics</i> , 2014, 23, 3054-3068.	1.4	90
161	Sequence features in regions of weak and strong linkage disequilibrium. <i>Genome Research</i> , 2005, 15, 1519-1534.	2.4	89
162	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. <i>Journal of the American Heart Association</i> , 2017, 6, .	1.6	89

#	ARTICLE	IF	CITATIONS
163	Cerebral small vessel disease genomics and its implications across the lifespan. <i>Nature Communications</i> , 2020, 11, 6285.	5.8	89
164	Meta-analysis of genome-wide association for migraine in six population-based European cohorts. <i>European Journal of Human Genetics</i> , 2011, 19, 901-907.	1.4	87
165	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021, 12, 24.	5.8	87
166	Common variants in the calcium-sensing receptor gene are associated with total serum calcium levels. <i>Human Molecular Genetics</i> , 2010, 19, 4296-4303.	1.4	86
167	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. <i>Nature Communications</i> , 2018, 9, 2976.	5.8	85
168	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019, 188, 1033-1054.	1.6	85
169	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	5.8	84
170	Genome-Wide Association Studies of MRI-Defined Brain Infarcts. <i>Stroke</i> , 2010, 41, 210-217.	1.0	82
171	Candidate Gene Association Study for Diabetic Retinopathy in Persons with Type 2 Diabetes: The Candidate Gene Association Resource (CARE)., 2011, 52, 7593.		82
172	Association of Alzheimer's disease GWAS loci with MRI markers of brain aging. <i>Neurobiology of Aging</i> , 2015, 36, 1765.e7-1765.e16.	1.5	82
173	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. <i>American Journal of Human Genetics</i> , 2016, 99, 40-55.	2.6	82
174	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. <i>PLoS Genetics</i> , 2014, 10, e1004508.	1.5	80
175	rs641738C>T near MBOAT7 is associated with liver fat, ALT and fibrosis in NAFLD: A meta-analysis. <i>Journal of Hepatology</i> , 2021, 74, 20-30.	1.8	77
176	Effects of Long-Term Averaging of Quantitative Blood Pressure Traits on the Detection of Genetic Associations. <i>American Journal of Human Genetics</i> , 2014, 95, 49-65.	2.6	73
177	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. <i>Nature Communications</i> , 2018, 9, 2904.	5.8	71
178	Common Genetic Variation Indicates Separate Causes for Periventricular and Deep White Matter Hyperintensities. <i>Stroke</i> , 2020, 51, 2111-2121.	1.0	71
179	Isolation and characterization of a thermostable RNA ligase 1 from a <i>Thermus scotoductus</i> bacteriophage TS2126 with good single-stranded DNA ligation properties. <i>Nucleic Acids Research</i> , 2005, 33, 135-142.	6.5	70
180	Identification of Nine Novel Loci Associated with White Blood Cell Subtypes in a Japanese Population. <i>PLoS Genetics</i> , 2011, 7, e1002067.	1.5	69

#	ARTICLE	IF	CITATIONS
181	Discovery and Fine Mapping of Serum Protein Loci through Transethnic Meta-analysis. <i>American Journal of Human Genetics</i> , 2012, 91, 744-753.	2.6	69
182	Genome-Wide Association Study for Incident Myocardial Infarction and Coronary Heart Disease in Prospective Cohort Studies: The CHARGE Consortium. <i>PLoS ONE</i> , 2016, 11, e0144997.	1.1	69
183	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. <i>Nature Genetics</i> , 2021, 53, 1504-1516.	9.4	69
184	Large scale international replication and meta-analysis study confirms association of the 15q14 locus with myopia. The CREAM consortium. <i>Human Genetics</i> , 2012, 131, 1467-1480.	1.8	67
185	Genome-wide Studies of Verbal Declarative Memory in Nondemented Older People: The Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. <i>Biological Psychiatry</i> , 2015, 77, 749-763.	0.7	67
186	Molecular mechanisms underlying variations in lung function: a systems genetics analysis. <i>Lancet Respiratory Medicine</i> , 2015, 3, 782-795.	5.2	66
187	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. <i>Human Molecular Genetics</i> , 2012, 21, 5329-5343.	1.4	64
188	Assessment of the Relationship Between Genetic Determinants of Thyroid Function and Atrial Fibrillation. <i>JAMA Cardiology</i> , 2019, 4, 144.	3.0	64
189	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376.	5.8	64
190	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. <i>PLoS ONE</i> , 2015, 10, e0119752.	1.1	64
191	<i>PCSK9</i> Loss-of-Function Variants, Low-Density Lipoprotein Cholesterol, and Risk of Coronary Heart Disease and Stroke. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, e001632.	5.1	63
192	Trans-ethnic meta-analysis of white blood cell phenotypes. <i>Human Molecular Genetics</i> , 2014, 23, 6944-6960.	1.4	60
193	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. <i>American Journal of Human Genetics</i> , 2016, 99, 8-21.	2.6	60
194	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25% subjects. <i>Molecular Psychiatry</i> , 2015, 20, 735-743.	4.1	59
195	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020, 11, 2542.	5.8	59
196	HapMap methylation-associated SNPs, markers of germline DNA methylation, positively correlate with regional levels of human meiotic recombination. <i>Genome Research</i> , 2009, 19, 581-589.	2.4	57
197	A novel cyclin gene from <i>Drosophila</i> complements CLN function in yeast.. <i>Genes and Development</i> , 1991, 5, 2166-2175.	2.7	56
198	Genetic variation associated with circulating monocyte count in the eMERGE Network. <i>Human Molecular Genetics</i> , 2013, 22, 2119-2127.	1.4	56

#	ARTICLE	IF	CITATIONS
199	Shared genetic contribution to ischemic stroke and Alzheimer's disease. <i>Annals of Neurology</i> , 2016, 79, 739-747.	2.8	56
200	Six Novel Loci Associated with Circulating VEGF Levels Identified by a Meta-analysis of Genome-Wide Association Studies. <i>PLoS Genetics</i> , 2016, 12, e1005874.	1.5	56
201	Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 511-520.	5.1	54
202	Multiethnic Genome-Wide Association Study of Diabetic Retinopathy Using Liability Threshold Modeling of Duration of Diabetes and Glycemic Control. <i>Diabetes</i> , 2019, 68, 441-456.	0.3	54
203	Large-Scale Genome-Wide Association Studies and Meta-Analyses of Longitudinal Change in Adult Lung Function. <i>PLoS ONE</i> , 2014, 9, e100776.	1.1	52
204	Association of Adiposity Genetic Variants With Menarche Timing in 92,105 Women of European Descent. <i>American Journal of Epidemiology</i> , 2013, 178, 451-460.	1.6	51
205	<scp>GWAS</scp> analysis of handgrip and lower body strength in older adults in the <scp>CHARGE</scp> consortium. <i>Aging Cell</i> , 2016, 15, 792-800.	3.0	51
206	Loss of Cardioprotective Effects at the <i>ADAMTS7</i> Locus as a Result of Gene-Smoking Interactions. <i>Circulation</i> , 2017, 135, 2336-2353.	1.6	51
207	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. <i>American Journal of Human Genetics</i> , 2016, 99, 22-39.	2.6	50
208	PLD3 variants in population studies. <i>Nature</i> , 2015, 520, E2-E3.	13.7	49
209	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475,000 Individuals. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	48
210	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. <i>Genome Biology</i> , 2018, 19, 87.	3.8	47
211	Rare Functional Variant in TM2D3 is Associated with Late-Onset Alzheimer's Disease. <i>PLoS Genetics</i> , 2016, 12, e1006327.	1.5	47
212	Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis. <i>American Journal of Human Genetics</i> , 2017, 100, 51-63.	2.6	45
213	Novel Genetic Variants Associated With Increased Vertebral Volumetric BMD, Reduced Vertebral Fracture Risk, and Increased Expression of <i>SLC1A3</i> and <i>EPHB2</i>. <i>Journal of Bone and Mineral Research</i> , 2016, 31, 2085-2097.	3.1	42
214	The Molecular Genetic Architecture of Self-Employment. <i>PLoS ONE</i> , 2013, 8, e60542.	1.1	41
215	Insulin Resistance Exacerbates Genetic Predisposition to Nonalcoholic Fatty Liver Disease in Individuals Without Diabetes. <i>Hepatology Communications</i> , 2019, 3, 894-907.	2.0	41
216	Association of common genetic variants with brain microbleeds. <i>Neurology</i> , 2020, 95, e3331-e3343.	1.5	40

#	ARTICLE	IF	CITATIONS
217	Circadian clock genes and risk of fatal prostate cancer. <i>Cancer Causes and Control</i> , 2015, 26, 25-33.	0.8	39
218	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 981-994.	3.0	39
219	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. <i>Nature Communications</i> , 2020, 11, 6417.	5.8	39
220	Disentangling the genetics of lean mass. <i>American Journal of Clinical Nutrition</i> , 2019, 109, 276-287.	2.2	38
221	Discovery and characterization of a thermostable bacteriophage RNA ligase homologous to T4 RNA ligase 1. <i>Nucleic Acids Research</i> , 2003, 31, 7247-7254.	6.5	36
222	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. <i>International Journal of Epidemiology</i> , 2017, 46, dyw318.	0.9	36
223	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. <i>Science Advances</i> , 2022, 8, eabl6579.	4.7	36
224	Meta-analysis of 49â€¦549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant in <i>ANGPTL4</i> determining fasting TG levels. <i>Journal of Medical Genetics</i> , 2016, 53, 441-449.	1.5	34
225	The interaction of adiposity with the CRP gene affects CRP levels: Age, Gene/Environment Susceptibility-Reykjavik Study. <i>International Journal of Obesity</i> , 2009, 33, 267-272.	1.6	33
226	Genome-wide meta-analysis of common variant differences between men and women. <i>Human Molecular Genetics</i> , 2012, 21, 4805-4815.	1.4	33
227	Common Variants in Mendelian Kidney Disease Genes and Their Association with Renal Function. <i>Journal of the American Society of Nephrology: JASN</i> , 2013, 24, 2105-2117.	3.0	33
228	Genome-Wide Profiling of Blood Pressure in Adults and Children. <i>Hypertension</i> , 2012, 59, 241-247.	1.3	31
229	Genome-wide association study of 23,500 individuals identifies 7 loci associated with brain ventricular volume. <i>Nature Communications</i> , 2018, 9, 3945.	5.8	31
230	A multi-ancestry genome-wide study incorporating geneâ€¦smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. <i>Human Molecular Genetics</i> , 2019, 28, 2615-2633.	1.4	31
231	Genetic overlap between vascular pathologies and Alzheimer's dementia and potential causal mechanisms. <i>Alzheimer's and Dementia</i> , 2019, 15, 65-75.	0.4	31
232	Bypass of a Meiotic Checkpoint by Overproduction of Meiotic Chromosomal Proteins. <i>Molecular and Cellular Biology</i> , 2000, 20, 4838-4848.	1.1	30
233	Effect of Genetically Low 25-Hydroxyvitamin D on Mortality Risk: Mendelian Randomization Analysis in 3 Large European Cohorts. <i>Nutrients</i> , 2019, 11, 74.	1.7	30
234	Genetic and lifestyle risk factors for MRI-defined brain infarcts in a population-based setting. <i>Neurology</i> , 2019, 92, .	1.5	30

#	ARTICLE	IF	CITATIONS
235	Discovery of novel heart rate-associated loci using the Exome Chip. <i>Human Molecular Genetics</i> , 2017, 26, 2346-2363.	1.4	29
236	Genome-wide association meta-analysis of 30,000 samples identifies seven novel loci for quantitative ECG traits. <i>European Journal of Human Genetics</i> , 2019, 27, 952-962.	1.4	29
237	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. <i>Cell Genomics</i> , 2022, 2, 100084.	3.0	29
238	Drug-gene interactions and the search for missing heritability: a cross-sectional pharmacogenomics study of the QT interval. <i>Pharmacogenomics Journal</i> , 2014, 14, 6-13.	0.9	28
239	Integrative pathway genomics of lung function and airflow obstruction. <i>Human Molecular Genetics</i> , 2015, 24, 6836-6848.	1.4	28
240	Meta-analysis of genome-wide association studies of HDL cholesterol response to statins. <i>Journal of Medical Genetics</i> , 2016, 53, 835-845.	1.5	28
241	Novel Genetic Loci Associated With Retinal Microvascular Diameter. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 45-54.	5.1	28
242	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2021, 108, 874-893.	2.6	28
243	Genetic Loci for Retinal Arteriolar Microcirculation. <i>PLoS ONE</i> , 2013, 8, e65804.	1.1	27
244	White Matter Lesion Progression. <i>Stroke</i> , 2015, 46, 3048-3057.	1.0	27
245	ExomeChip-Wide Analysis of 95 626 Individuals Identifies 10 Novel Loci Associated With QT and JT Intervals. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e001758.	1.6	27
246	A genome-wide association study identifies genetic loci associated with specific lobar brain volumes. <i>Communications Biology</i> , 2019, 2, 285.	2.0	27
247	Characterization of a 5'-Polynucleotide Kinase/3'-Phosphatase from Bacteriophage RM378. <i>Journal of Biological Chemistry</i> , 2005, 280, 5188-5194.	1.6	26
248	Association of Triglyceride-Related Genetic Variants With Mitral Annular Calcification. <i>Journal of the American College of Cardiology</i> , 2017, 69, 2941-2948.	1.2	25
249	TOP-LD: A tool to explore linkage disequilibrium with TOPMed whole-genome sequence data. <i>American Journal of Human Genetics</i> , 2022, 109, 1175-1181.	2.6	25
250	A novel MALDI-TOF based methodology for genotyping single nucleotide polymorphisms. <i>Nucleic Acids Research</i> , 2003, 31, 155e-155.	6.5	23
251	Are C-Reactive Protein Associated Genetic Variants Associated with Serum Levels and Retinal Markers of Microvascular Pathology in Asian Populations from Singapore?. <i>PLoS ONE</i> , 2013, 8, e67650.	1.1	23
252	Genome-Wide Association Study of Retinopathy in Individuals without Diabetes. <i>PLoS ONE</i> , 2013, 8, e54232.	1.1	22

#	ARTICLE	IF	CITATIONS
253	The complex genetics of gait speed: genome-wide meta-analysis approach. <i>Aging</i> , 2017, 9, 209-246.	1.4	21
254	Allele-specific variation at <i>APOE</i> increases nonalcoholic fatty liver disease and obesity but decreases risk of Alzheimer's disease and myocardial infarction. <i>Human Molecular Genetics</i> , 2021, 30, 1443-1456.	1.4	20
255	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002037.	1.6	19
256	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , 2018, 3, 4.	0.9	19
257	The phenotype and genotype experiment object model (PaGE-OM): a robust data structure for information related to DNA variation. <i>Human Mutation</i> , 2009, 30, 968-977.	1.1	18
258	An Empirical Comparison of Joint and Stratified Frameworks for Studying G × E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Gene-Lifestyle Interactions Working Group. <i>Genetic Epidemiology</i> , 2016, 40, 404-415.	0.6	18
259	Genetically Determined Plasma Lipid Levels and Risk of Diabetic Retinopathy: A Mendelian Randomization Study. <i>Diabetes</i> , 2017, 66, 3130-3141.	0.3	17
260	Exome Chip Analysis Identifies Low-Frequency and Rare Variants in <i>MRPL38</i> for White Matter Hyperintensities on Brain Magnetic Resonance Imaging. <i>Stroke</i> , 2018, 49, 1812-1819.	1.0	17
261	Reversal of Aging-Induced Increases in Aortic Stiffness by Targeting Cytoskeletal Protein-Protein Interfaces. <i>Journal of the American Heart Association</i> , 2018, 7, .	1.6	17
262	Genome-Wide Association Study of Apparent Treatment-Resistant Hypertension in the CHARGE Consortium: The CHARGE Pharmacogenetics Working Group. <i>American Journal of Hypertension</i> , 2019, 32, 1146-1153.	1.0	17
263	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. <i>Molecular Psychiatry</i> , 2020, 26, 2111-2125.	4.1	17
264	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. <i>Nature Communications</i> , 2021, 12, 2182.	5.8	17
265	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022, 5, .	2.0	17
266	Association of Lipid-Related Genetic Variants with the Incidence of Atrial Fibrillation: The AFGen Consortium. <i>PLoS ONE</i> , 2016, 11, e0151932.	1.1	16
267	Genetic improvement of runtime and its fitness landscape in a bioinformatics application. , 2017, , .		16
268	Cloning and characterization of the <i>Kluyveromyces lactis</i> homologs of the <i>Saccharomyces cerevisiae</i> RED1 and HOP1 genes. <i>Chromosoma</i> , 2000, 109, 50-61.	1.0	15
269	The distribution of a germline methylation marker suggests a regional mechanism of LINE-1 silencing by the piRNA-PIWI system. <i>BMC Genetics</i> , 2012, 13, 31.	2.7	15
270	Lack of association between the MTHFR C677T variant and migraine with aura in an older population: Could selective survival play a role?. <i>Cephalalgia</i> , 2013, 33, 308-315.	1.8	15

#	ARTICLE	IF	CITATIONS
271	Drug-Gene Interactions of Antihypertensive Medications and Risk of Incident Cardiovascular Disease: A Pharmacogenomics Study from the CHARGE Consortium. <i>PLoS ONE</i> , 2015, 10, e0140496.	1.1	15
272	Gene-gene Interaction Analyses for Atrial Fibrillation. <i>Scientific Reports</i> , 2016, 6, 35371.	1.6	15
273	Genetic Interactions with Age, Sex, Body Mass Index, and Hypertension in Relation to Atrial Fibrillation: The AFGen Consortium. <i>Scientific Reports</i> , 2017, 7, 11303.	1.6	15
274	Meta-imputation: An efficient method to combine genotype data after imputation with multiple reference panels. <i>American Journal of Human Genetics</i> , 2022, 109, 1007-1015.	2.6	15
275	Heritability and genome-wide associations studies of cerebral blood flow in the general population. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2018, 38, 1598-1608.	2.4	14
276	Omega-3 Fatty Acids and Genome-Wide Interaction Analyses Reveal <i>DPP10</i> Pulmonary Function Association. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 199, 631-642.	2.5	14
277	Copy Number Variations in Alternative Splicing Gene Networks Impact Lifespan. <i>PLoS ONE</i> , 2013, 8, e53846.	1.1	13
278	The Challenges of Genome-Wide Interaction Studies: Lessons to Learn from the Analysis of HDL Blood Levels. <i>PLoS ONE</i> , 2014, 9, e109290.	1.1	13
279	Genetic diversity is a predictor of mortality in humans. <i>BMC Genetics</i> , 2014, 15, 159.	2.7	12
280	Large-scale pharmacogenomic study of sulfonylureas and the QT, JT and QRS intervals: CHARGE Pharmacogenomics Working Group. <i>Pharmacogenomics Journal</i> , 2018, 18, 127-135.	0.9	12
281	A Noncoding Variant Near <i>PPP1R3B</i> Promotes Liver Glycogen Storage and MetS, but Protects Against Myocardial Infarction. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021, 106, 372-387.	1.8	12
282	Haplotype analysis of the folate-related genes <i>MTHFR</i> , <i>MTRR</i> , and <i>MTR</i> and migraine with aura. <i>Cephalalgia</i> , 2013, 33, 469-482.	1.8	11
283	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , 0, 3, 4.	0.9	11
284	Manipulating HapMap Data Using HaploView. <i>Cold Spring Harbor Protocols</i> , 2008, 2008, pdb.prot5025.	0.2	10
285	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. <i>PLoS ONE</i> , 2020, 15, e0230815.	1.1	10
286	A genome-wide interaction analysis of tricyclic/tetracyclic antidepressants and RR and QT intervals: a pharmacogenomics study from the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium. <i>Journal of Medical Genetics</i> , 2017, 54, 313-323.	1.5	9
287	Pharmacogenomics study of thiazide diuretics and QT interval in multi-ethnic populations: the cohorts for heart and aging research in genomic epidemiology. <i>Pharmacogenomics Journal</i> , 2018, 18, 215-226.	0.9	9
288	Meta-analysis across Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium provides evidence for an association of serum vitamin D with pulmonary function. <i>British Journal of Nutrition</i> , 2018, 120, 1159-1170.	1.2	9

#	ARTICLE	IF	CITATIONS
289	Retrieving HapMap Data Using HapMart: Figure 1.. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5026.	0.2	8
290	Browsing HapMap Data Using the Genome Browser. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5023-pdb.prot5023.	0.2	8
291	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
292	Is the adiposity-associated <i>FTO</i> gene variant related to all-cause mortality independent of adiposity? Meta-analysis of data from 169,551 Caucasian adults. Obesity Reviews, 2015, 16, 327-340.	3.1	8
293	Gene Set Enrichment Analyses Identify Pathways Involved in Genetic Risk for Diabetic Retinopathy. American Journal of Ophthalmology, 2022, 233, 111-123.	1.7	7
294	Genetic Analysis: Moving between Linkage and Association. Cold Spring Harbor Protocols, 2012, 2012, pdb.top067819.	0.2	6
295	Robust, flexible, and scalable tests for Hardy-Weinberg equilibrium across diverse ancestries. Genetics, 2021, 218, .	1.2	6
296	Distribution of a marker of germline methylation differs between major families of transposon-derived repeats in the human genome. Gene, 2012, 492, 104-109.	1.0	5
297	Association of heat shock proteins with all-cause mortality. Age, 2013, 35, 1367-1376.	3.0	5
298	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.	1.1	5
299	Retrieving HapMap Data via Bulk Download. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5027-pdb.prot5027.	0.2	4
300	Generating HapMap Data Text Reports Using the Genome Browser. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5024-pdb.prot5024.	0.2	4
301	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.	0.9	4
302	Identification of novel and rare variants associated with handgrip strength using whole genome sequence data from the NHLBI Trans-Omics in Precision Medicine (TOPMed) Program. PLoS ONE, 2021, 16, e0253611.	1.1	4
303	Multiethnic Genome-Wide Association Study of Subclinical Atherosclerosis in Individuals With Type 2 Diabetes. Circulation Genomic and Precision Medicine, 2021, 14, e003258.	1.6	4
304	Genome-wide meta-analysis of SNP-by-ACEI/ARB and SNP-by-thiazide diuretic and effect on serum potassium in cohorts of European and African ancestry. Pharmacogenomics Journal, 2019, 19, 97-108.	0.9	3
305	Sparse allele vectors and the savvy software suite. Bioinformatics, 2021, 37, 4248-4250.	1.8	3
306	STRATEGY: Optimal Selection of Individuals for Sequencing in Genetic Association Studies. Genetic Epidemiology, 2016, 40, 446-460.	0.6	2

#	ARTICLE	IF	CITATIONS
307	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100013.	1.0	2
308	Rare and low-frequency exonic variants and gene-by-smoking interactions in pulmonary function. <i>Scientific Reports</i> , 2021, 11, 19365.	1.6	2
309	Association of low-frequency and rare coding variants with information processing speed. <i>Translational Psychiatry</i> , 2021, 11, 613.	2.4	2
310	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , 0, 3, 4.	0.9	1
311	Accounting for population structure in genetic studies of cystic fibrosis. <i>Human Genetics and Genomics Advances</i> , 2022, 3, 100117.	1.0	1
312	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. <i>Obstetrical and Gynecological Survey</i> , 2015, 70, 758-762.	0.2	0
313	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
314	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
315	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
316	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0