Cornelia M Van Duijn

List of Publications by Year
in descending order

854	144,871	57 177	127 336
papers	citations	h-index	g-index

942	942	942	102670
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
2	Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. Nature Genetics, 2013, 45, 1452-1458.	9.4	3,741
3	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
4	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	9.4	2,641
5	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
6	Mutations in the DJ-1 Gene Associated with Autosomal Recessive Early-Onset Parkinsonism. Science, 2003, 299, 256-259.	6.0	2,467
7	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	9.4	2,421
8	Variant ofTREM2Associated with the Risk of Alzheimer's Disease. New England Journal of Medicine, 2013, 368, 107-116.	13.9	2,085
9	Genetic meta-analysis of diagnosed Alzheimerâ€™s disease identifies new risk loci and implicates AÎ², tau, immunity and lipid processing. Nature Genetics, 2019, 51, 414-430.	9.4	1,962
10	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
11	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
12	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	9.4	1,748
13	GenABEL: an R library for genome-wide association analysis. Bioinformatics, 2007, 23, 1294-1296.	1.8	1,711
14	Common variants at ABCA7, MS4A6A/MS4A4E, EPHA1, CD33 and CD2AP are associated with Alzheimer's disease. Nature Genetics, 2011, 43, 429-435.	9.4	1,708
15	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	9.4	1,631
16	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	9.4	1,572
17	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
18	Genome-wide association study of blood pressure and hypertension. Nature Genetics, 2009, 41, 677-687.	9.4	1,224

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19	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
20	A large genome-wide association study of age-related macular degeneration highlights contributions of rare and common variants. Nature Genetics, 2016, 48, 134-143.	9.4	1,167
21	Nonsteroidal Antiinflammatory Drugs and the Risk of Alzheimer's Disease. New England Journal of Medicine, 2001, 345, 1515-1521.	13.9	1,148
22	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	9.4	1,124
23	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.	9.4	1,100
24	Genome-wide Analysis of Genetic Loci Associated With Alzheimer Disease. JAMA - Journal of the American Medical Association, 2010, 303, 1832.	3.8	1,064
25	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959
26	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
27	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
28	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
29	Identification of seven loci affecting mean telomere length and their association with disease. Nature Genetics, 2013, 45, 422-427.	9.4	808
30	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	9.4	783
31	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. Nature Genetics, 2009, 41, 47-55.	9.4	776
32	Common genetic variants influence human subcortical brain structures. Nature, 2015, 520, 224-229.	13.7	772
33	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
34	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	9.4	754
35	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	6.0	750
36	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

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37	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. Nature, 2017, 541, 81-86.	13.7	743
38	Diagnostic Yield and Clinical Utility of Sequencing Familial Hypercholesterolemia Genes in Patients With Severe Hypercholesterolemia. Journal of the American College of Cardiology, 2016, 67, 2578-2589.	1.2	723
39	Presenile dementia and cerebral haemorrhage linked to a mutation at codon 692 of the Î²â€“amyloid precursor protein gene. Nature Genetics, 1992, 1, 218-221.	9.4	715
40	New loci associated with kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 376-384.	9.4	710
41	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	9.4	700
42	Seven new loci associated with age-related macular degeneration. Nature Genetics, 2013, 45, 433-439.	9.4	687
43	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	9.4	676
44	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	9.4	675
45	Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81.	9.4	662
46	Twenty bone-mineral-density loci identified by large-scale meta-analysis of genome-wide association studies. Nature Genetics, 2009, 41, 1199-1206.	9.4	660
47	Sequence variants at CHRNB3â€“CHRNA6 and CYP2A6 affect smoking behavior. Nature Genetics, 2010, 42, 448-453.	9.4	649
48	The Rotterdam Study: objectives and design update. European Journal of Epidemiology, 2007, 22, 819-829.	2.5	644
49	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
50	Association of three genetic loci with uric acid concentration and risk of gout: a genome-wide association study. Lancet, The, 2008, 372, 1953-1961.	6.3	610
51	The Generation R Study: design and cohort update 2017. European Journal of Epidemiology, 2016, 31, 1243-1264.	2.5	608
52	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
53	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. Nature Communications, 2016, 7, 11122.	5.8	576
54	Multiple loci associated with indices of renal function and chronic kidney disease. Nature Genetics, 2009, 41, 712-717.	9.4	553

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55	Meta-analyses of genome-wide association studies identify multiple loci associated with pulmonary function. Nature Genetics, 2010, 42, 45-52.	9.4	549
56	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
57	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	13.7	548
58	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
59	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	9.4	520
60	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	9.4	501
61	Alcohol consumption and risk of dementia: the Rotterdam Study. Lancet, The, 2002, 359, 281-286.	6.3	499
62	The Generation R Study: design and cohort update 2012. European Journal of Epidemiology, 2012, 27, 739-756.	2.5	486
63	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	5.8	484
64	Wholeâ€genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	13.7	483
65	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
66	Apolipoprotein E4 allele in a populationâ€“based study of earlyâ€“onset Alzheimer's disease. Nature Genetics, 1994, 7, 74-78.	9.4	460
67	A mutation in SLC11A3 is associated with autosomal dominant hemochromatosis. Nature Genetics, 2001, 28, 213-214.	9.4	458
68	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	1.5	453
69	Physical Activity Attenuates the Influence of FTO Variants on Obesity Risk: A Meta-Analysis of 218,166 Adults and 19,268 Children. PLoS Medicine, 2011, 8, e1001116.	3.9	446
70	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. Nature Genetics, 2010, 42, 1077-1085.	9.4	445
71	Genetic Association of Apolipoprotein E with Age-Related Macular Degeneration. American Journal of Human Genetics, 1998, 63, 200-206.	2.6	425
72	Genome-wide association meta-analysis of 78,308 individuals identifies new loci and genes influencing human intelligence. Nature Genetics, 2017, 49, 1107-1112.	9.4	425

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73	Frontotemporal dementia in The Netherlands: patient characteristics and prevalence estimates from a population-based study. Brain, 2003, 126, 2016-2022.	3.7	423
74	Genomewide Association Studies of Stroke. New England Journal of Medicine, 2009, 360, 1718-1728.	13.9	420
75	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.	1.5	419
76	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	5.8	412
77	High Prevalence of Mutations in the Microtubule-Associated Protein Tau in a Population Study of Frontotemporal Dementia in the Netherlands. American Journal of Human Genetics, 1999, 64, 414-421.	2.6	410
78	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	13.7	406
79	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	9.4	403
80	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	9.4	402
81	Genome-wide association study of PR interval. Nature Genetics, 2010, 42, 153-159.	9.4	400
82	Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. Nature Genetics, 2013, 45, 314-318.	9.4	398
83	Altered bile acid profile associates with cognitive impairment in Alzheimer's diseaseâ€"An emerging role for gut microbiome. Alzheimer's and Dementia, 2019, 15, 76-92.	0.4	396
84	Disease variants alter transcription factor levels and methylation of their binding sites. Nature Genetics, 2017, 49, 131-138.	9.4	390
85	Genome-wide patterns and properties of de novo mutations in humans. Nature Genetics, 2015, 47, 822-826.	9.4	384
86	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	13.7	383
87	Meta-analysis of telomere length in 19â€‰713 subjects reveals high heritability, stronger maternal inheritance and a paternal age effect. European Journal of Human Genetics, 2013, 21, 1163-1168.	1.4	380
88	The Rotterdam Study: 2018 update on objectives, design and main results. European Journal of Epidemiology, 2017, 32, 807-850.	2.5	379
89	Risk Estimates of Dementia by Apolipoprotein E Genotypes From a Population-Based Incidence Study: The Rotterdam Study. Archives of Neurology, 1998, 55, 964.	4.9	378
90	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	1.5	371

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91	Genetic Variants Influencing Circulating Lipid Levels and Risk of Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 2264-2276.	1.1	369
92	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365
93	Variants in ZFHX3 are associated with atrial fibrillation in individuals of European ancestry. Nature Genetics, 2009, 41, 879-881.	9.4	363
94	Identification of context-dependent expression quantitative trait loci in whole blood. Nature Genetics, 2017, 49, 139-145.	9.4	363
95	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	9.4	362
96	Metabolic network failures in Alzheimer's disease: A biochemical roadÂmap. Alzheimer's and Dementia, 2017, 13, 965-984.	0.4	362
97	Common polygenic variation enhances risk prediction for Alzheimerâ€™s disease. Brain, 2015, 138, 3673-3684.	3.7	359
98	The Rotterdam Study: 2016 objectives and design update. European Journal of Epidemiology, 2015, 30, 661-708.	2.5	358
99	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	9.4	357
100	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	9.4	356
101	ProbABEL package for genome-wide association analysis of imputed data. BMC Bioinformatics, 2010, 11, 134.	1.2	354
102	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
103	A genome-wide association meta-analysis identifies new childhood obesity loci. Nature Genetics, 2012, 44, 526-531.	9.4	352
104	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
105	Genome-wide meta-analysis identifies new susceptibility loci for migraine. Nature Genetics, 2013, 45, 912-917.	9.4	338
106	Genome-wide association study of migraine implicates a common susceptibility variant on 8q22.1. Nature Genetics, 2010, 42, 869-873.	9.4	332
107	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.	1.5	331
108	A common haplotype lowers PU.1 expression in myeloid cells and delays onset of Alzheimer's disease. Nature Neuroscience, 2017, 20, 1052-1061.	7.1	330

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109	Increasing Prevalence of Myopia in Europe and the Impact of Education. Ophthalmology, 2015, 122, 1489-1497.	2.5	329
110	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. Nature Genetics, 2009, 41, 1191-1198.	9.4	324
111	Novel Associations of Multiple Genetic Loci With Plasma Levels of Factor VII, Factor VIII, and von Willebrand Factor. Circulation, 2010, 121, 1382-1392.	1.6	311
112	Meta-analysis of genome-wide association studies identifies three new risk loci for atopic dermatitis. Nature Genetics, 2012, 44, 187-192.	9.4	311
113	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	9.4	310
114	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	9.4	308
115	Complement Factor H Polymorphism, Complement Activators, and Risk of Age-Related Macular Degeneration. JAMA - Journal of the American Medical Association, 2006, 296, 301.	3.8	306
116	Prevalence of refractive error in Europe: the European Eye Epidemiology (E3) Consortium. European Journal of Epidemiology, 2015, 30, 305-315.	2.5	306
117	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. Nature Genetics, 2012, 44, 260-268.	9.4	303
118	Genome-wide association analysis identifies susceptibility loci for migraine without aura. Nature Genetics, 2012, 44, 777-782.	9.4	294
119	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. Nature Genetics, 2013, 45, 76-82.	9.4	293
120	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. Nature Genetics, 2011, 43, 753-760.	9.4	289
121	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. JAMA Psychiatry, 2015, 72, 642.	6.0	289
122	Quantifying prion disease penetrance using large population control cohorts. Science Translational Medicine, 2016, 8, 322ra9.	5.8	289
123	Genome-based prediction of common diseases: advances and prospects. Human Molecular Genetics, 2008, 17, R166-R173.	1.4	287
124	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.	2.6	287
125	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
126	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	9.4	284

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127	The Rotterdam Study: 2014 objectives and design update. European Journal of Epidemiology, 2013, 28, 889-926.	2.5	282
128	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
129	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
130	Antiepileptic drug regimens and major congenital abnormalities in the offspring. Annals of Neurology, 1999, 46, 739-746.	2.8	276
131	The Rotterdam Study: 2012 objectives and design update. European Journal of Epidemiology, 2011, 26, 657-686.	2.5	273
132	Genome-Wide Association Study for Coronary Artery Calcification With Follow-Up in Myocardial Infarction. Circulation, 2011, 124, 2855-2864.	1.6	269
133	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. Nature Genetics, 2013, 45, 155-163.	9.4	269
134	Predicting Type 2 Diabetes Based on Polymorphisms From Genome-Wide Association Studies. Diabetes, 2008, 57, 3122-3128.	0.3	265
135	Genome-wide association study of intracranial aneurysm identifies three new risk loci. Nature Genetics, 2010, 42, 420-425.	9.4	262
136	Epidemiology of Alzheimer's Disease. Epidemiologic Reviews, 1992, 14, 59-82.	1.3	261
137	A Critical Appraisal of the Scientific Basis of Commercial Genomic Profiles Used to Assess Health Risks and Personalize Health Interventions. American Journal of Human Genetics, 2008, 82, 593-599.	2.6	258
138	Genome-wide association and genetic functional studies identify autism susceptibility candidate 2 gene (AUTS2) in the regulation of alcohol consumption. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7119-7124.	3.3	258
139	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.	2.6	252
140	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	9.4	251
141	Collaborative Meta-analysis: Associations of 150 Candidate Genes With Osteoporosis and Osteoporotic Fracture. Annals of Internal Medicine, 2009, 151, 528.	2.0	250
142	Fine-Mapping the Genetic Association of the Major Histocompatibility Complex in Multiple Sclerosis: HLA and Non-HLA Effects. PLoS Genetics, 2013, 9, e1003926.	1.5	250
143	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.	1.7	250
144	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	5.8	250

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145	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.	3.0	249
146	Susceptibility loci for intracranial aneurysm in European and Japanese populations. Nature Genetics, 2008, 40, 1472-1477.	9.4	247
147	The Genome of the Netherlands: design, and project goals. European Journal of Human Genetics, 2014, 22, 221-227.	1.4	246
148	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
149	Common genetic variants associated with cognitive performance identified using the proxy-phenotype method. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13790-13794.	3.3	244
150	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. Nature Genetics, 2018, 50, 834-848.	9.4	239
151	The Rotterdam Study: 2010 objectives and design update. European Journal of Epidemiology, 2009, 24, 553-572.	2.5	235
152	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	4.1	235
153	A Genomic Background Based Method for Association Analysis in Related Individuals. PLoS ONE, 2007, 2, e1274.	1.1	233
154	Common variants near FRK/COL10A1 and VEGFA are associated with advanced age-related macular degeneration. Human Molecular Genetics, 2011, 20, 3699-3709.	1.4	232
155	PredictABEL: an R package for the assessment of risk prediction models. European Journal of Epidemiology, 2011, 26, 261-264.	2.5	231
156	NRXN3 Is a Novel Locus for Waist Circumference: A Genome-Wide Association Study from the CHARGE Consortium. PLoS Genetics, 2009, 5, e1000539.	1.5	230
157	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.	1.4	227
158	Variants in ADCY5 and near CCNL1 are associated with fetal growth and birth weight. Nature Genetics, 2010, 42, 430-435.	9.4	223
159	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	9.4	223
160	Three Genome-wide Association Studies and a Linkage Analysis Identify HERC2 as a Human Iris Color Gene. American Journal of Human Genetics, 2008, 82, 411-423.	2.6	220
161	Best Practices and Joint Calling of the HumanExome BeadChip: The CHARGE Consortium. PLoS ONE, 2013, 8, e68095.	1.1	219
162	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. Nature Genetics, 2022, 54, 437-449.	9.4	215

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163	Genome-wide association meta-analysis for total serum bilirubin levels. Human Molecular Genetics, 2009, 18, 2700-2710.	1.4	214
164	A meta-analysis of genome-wide association studies identifies multiple longevity genes. Nature Communications, 2019, 10, 3669.	5.8	214
165	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	7.1	213
166	Common variants at 12q14 and 12q24 are associated with hippocampal volume. Nature Genetics, 2012, 44, 545-551.	9.4	212
167	Genome-wide analysis of multi-ancestry cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma. Nature Genetics, 2014, 46, 1126-1130.	9.4	212
168	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.	3.3	208
169	A genome-wide association study for myopia and refractive error identifies a susceptibility locus at 15q25. Nature Genetics, 2010, 42, 902-905.	9.4	204
170	Shared Constitutional Risks for Maternal Vascular-Related Pregnancy Complications and Future Cardiovascular Disease. Hypertension, 2008, 51, 1034-1041.	1.3	203
171	The probabilistic model of Alzheimer disease: the amyloid hypothesis revised. Nature Reviews Neuroscience, 2022, 23, 53-66.	4.9	203
172	Predictive testing for complex diseases using multiple genes: Fact or fiction?. Genetics in Medicine, 2006, 8, 395-400.	1.1	202
173	Genetic Variants Associated With Cardiac Structure and Function. JAMA - Journal of the American Medical Association, 2009, 302, 168.	3.8	202
174	Genomeâ€wide association studies of cerebral white matter lesion burden. Annals of Neurology, 2011, 69, 928-939.	2.8	201
175	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.	3.1	200
176	A genome-wide association study identifies a susceptibility locus for refractive errors and myopia at 15q14. Nature Genetics, 2010, 42, 897-901.	9.4	200
177	Altered bile acid profile in mild cognitive impairment and Alzheimer's disease: Relationship to neuroimaging and CSF biomarkers. Alzheimer's and Dementia, 2019, 15, 232-244.	0.4	198
178	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
179	Genome-wide meta-analysis identifies 127 open-angle glaucoma loci with consistent effect across ancestries. Nature Communications, 2021, 12, 1258.	5.8	196
180	Rapid variance componentsâ€“based method for whole-genome association analysis. Nature Genetics, 2012, 44, 1166-1170.	9.4	193

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181	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	2.6	193
182	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	5.8	192
183	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	9.4	192
184	Multitrait analysis of glaucoma identifies new risk loci and enables polygenic prediction of disease susceptibility and progression. Nature Genetics, 2020, 52, 160-166.	9.4	192
185	Association between genetic variation in the gene for insulin-like growth factor-I and low birthweight. Lancet, The, 2002, 359, 1036-1037.	6.3	191
186	Whole exome sequencing study identifies novel rare and common Alzheimerâ€™s-Associated variants involved in immune response and transcriptional regulation. Molecular Psychiatry, 2020, 25, 1859-1875.	4.1	191
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