

Caroline Hayward

List of Publications by Year in descending order

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Version: 2024-02-01

512
papers

88,046
citations

613

124
h-index

547

264
g-index

610
all docs

610
docs citations

610
times ranked

74170
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
2	Biological, clinical and population relevance of 95 loci for blood lipids. <i>Nature</i> , 2010, 466, 707-713.	13.7	3,249
3	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013, 45, 1274-1283.	9.4	2,641
4	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
5	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	9.4	2,224
6	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010, 42, 105-116.	9.4	1,982
7	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011, 478, 103-109.	13.7	1,855
8	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. <i>Nature Genetics</i> , 2018, 50, 1112-1121.	9.4	1,835
9	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
10	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	13.7	1,789
11	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. <i>Nature Genetics</i> , 2018, 50, 381-389.	9.4	1,332
12	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	13.7	1,328
13	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	13.7	1,204
14	A large genome-wide association study of age-related macular degeneration highlights contributions of rare and common variants. <i>Nature Genetics</i> , 2016, 48, 134-143.	9.4	1,167
15	Genetic mechanisms of critical illness in COVID-19. <i>Nature</i> , 2021, 591, 92-98.	13.7	1,014
16	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014, 46, 234-244.	9.4	959
17	Runs of Homozygosity in European Populations. <i>American Journal of Human Genetics</i> , 2008, 83, 359-372.	2.6	958
18	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022, 604, 502-508.	13.7	929

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19	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	9.4	924
20	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. <i>Nature Genetics</i> , 2016, 48, 624-633.	9.4	870
21	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010, 42, 949-960.	9.4	836
22	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. <i>Nature Genetics</i> , 2009, 41, 47-55.	9.4	776
23	Complement C3 Variant and the Risk of Age-Related Macular Degeneration. <i>New England Journal of Medicine</i> , 2007, 357, 553-561.	13.9	762
24	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. <i>Nature Genetics</i> , 2012, 44, 659-669.	9.4	762
25	Common variants associated with plasma triglycerides and risk for coronary artery disease. <i>Nature Genetics</i> , 2013, 45, 1345-1352.	9.4	754
26	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. <i>Science</i> , 2013, 340, 1467-1471.	6.0	750
27	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , 2012, 44, 991-1005.	9.4	746
28	New loci associated with kidney function and chronic kidney disease. <i>Nature Genetics</i> , 2010, 42, 376-384.	9.4	710
29	SLC2A9 is a newly identified urate transporter influencing serum urate concentration, urate excretion and gout. <i>Nature Genetics</i> , 2008, 40, 437-442.	9.4	678
30	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2013, 45, 145-154.	9.4	675
31	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. <i>Nature Genetics</i> , 2010, 42, 436-440.	9.4	581
32	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013, 45, 501-512.	9.4	578
33	A General Approach for Haplotype Phasing across the Full Spectrum of Relatedness. <i>PLoS Genetics</i> , 2014, 10, e1004234.	1.5	553
34	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018, 50, 1225-1233.	9.4	552
35	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	9.4	549
36	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	13.7	544

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37	Genome-wide association study identifies five loci associated with lung function. <i>Nature Genetics</i> , 2010, 42, 36-44.	9.4	518
38	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , 2017, 49, 403-415.	9.4	492
39	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. <i>Nature Neuroscience</i> , 2018, 21, 1656-1669.	7.1	490
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	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766.	9.4	470
42	Mutations in SOX2 cause anophthalmia. <i>Nature Genetics</i> , 2003, 33, 462-463.	9.4	466
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	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
45	Ultra-High-Throughput Clinical Proteomics Reveals Classifiers of COVID-19 Infection. <i>Cell Systems</i> , 2020, 11, 11-24.e4.	2.9	439
46	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. <i>Science</i> , 2016, 351, 1166-1171.	6.0	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	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. <i>PLoS Genetics</i> , 2012, 8, e1002607.	1.5	419
49	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
50	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
51	Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. <i>Nature Genetics</i> , 2013, 45, 314-318.	9.4	398
52	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. <i>Diabetes</i> , 2010, 59, 3229-3239.	0.3	387
53	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012, 490, 267-272.	13.7	383
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

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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	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
57	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
58	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
59	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	13.7	353
60	Genome-wide association study of alcohol consumption and genetic overlap with other health-related traits in UK Biobank (N=112,117). <i>Molecular Psychiatry</i> , 2017, 22, 1376-1384.	4.1	351
61	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. <i>Nature Genetics</i> , 2019, 51, 481-493.	9.4	350
62	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
63	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. <i>PLoS Medicine</i> , 2017, 14, e1002383.	3.9	341
64	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	9.4	341
65	Genome-Wide Association Identifies Nine Common Variants Associated With Fasting Proinsulin Levels and Provides New Insights Into the Pathophysiology of Type 2 Diabetes. <i>Diabetes</i> , 2011, 60, 2624-2634.	0.3	335
66	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
67	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. <i>Nature Genetics</i> , 2019, 51, 51-62.	9.4	328
68	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. <i>Nature Metabolism</i> , 2020, 2, 1135-1148.	5.1	327
69	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
70	Loci Associated with N-Glycosylation of Human Immunoglobulin G Show Pleiotropy with Autoimmune Diseases and Haematological Cancers. <i>PLoS Genetics</i> , 2013, 9, e1003225.	1.5	323
71	Genome-wide association study of cognitive functions and educational attainment in UK Biobank (N=112,151). <i>Molecular Psychiatry</i> , 2016, 21, 758-767.	4.1	317
72	Novel Associations of Multiple Genetic Loci With Plasma Levels of Factor VII, Factor VIII, and von Willebrand Factor. <i>Circulation</i> , 2010, 121, 1382-1392.	1.6	311

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73	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
74	Genome-Wide Association Analyses in 128,266 Individuals Identifies New Morningness and Sleep Duration Loci. <i>PLoS Genetics</i> , 2016, 12, e1006125.	1.5	308
75	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
76	Glycans Are a Novel Biomarker of Chronological and Biological Ages. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2014, 69, 779-789.	1.7	297
77	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. <i>Nature Communications</i> , 2018, 9, 260.	5.8	295
78	Genetic variation near <i>IRS1</i> associates with reduced adiposity and an impaired metabolic profile. <i>Nature Genetics</i> , 2011, 43, 753-760.	9.4	289
79	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. <i>JAMA Psychiatry</i> , 2015, 72, 642.	6.0	289
80	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
81	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
82	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016, 48, 1462-1472.	9.4	284
83	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
84	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
85	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
86	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. <i>Nature Genetics</i> , 2013, 45, 155-163.	9.4	269
87	Cognitive change and the <i>APOE</i> ϵ 4 allele. <i>Nature</i> , 2002, 418, 932-932.	13.7	267
88	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016, 48, 1151-1161.	9.4	261
89	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. <i>Nature Genetics</i> , 2017, 49, 416-425.	9.4	257
90	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	9.4	251

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91	Identification of SATB2 as the cleft palate gene on 2q32-q33. <i>Human Molecular Genetics</i> , 2003, 12, 2491-2501.	1.4	248
92	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016, 7, 10495.	5.8	245
93	Common genetic variants associated with cognitive performance identified using the proxy-phenotype method. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 13790-13794.	3.3	244
94	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. <i>Nature Genetics</i> , 2018, 50, 834-848.	9.4	239
95	Application of high-dimensional feature selection: evaluation for genomic prediction in man. <i>Scientific Reports</i> , 2015, 5, 10312.	1.6	233
96	Genome-wide analysis of over 106â€™000 individuals identifies 9 neuroticism-associated loci. <i>Molecular Psychiatry</i> , 2016, 21, 749-757.	4.1	220
97	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
98	Genomics Meets Glycomicsâ€™ The First GWAS Study of Human N-Glycome Identifies HNF1Î± as a Master Regulator of Plasma Protein Fucosylation. <i>PLoS Genetics</i> , 2010, 6, e1001256.	1.5	213
99	Variability, Heritability and Environmental Determinants of Human Plasma N-Glycome. <i>Journal of Proteome Research</i> , 2009, 8, 694-701.	1.8	212
100	CUBN Is a Gene Locus for Albuminuria. <i>Journal of the American Society of Nephrology: JASN</i> , 2011, 22, 555-570.	3.0	208
101	Cardiac Troponin T and Troponin I in the General Population. <i>Circulation</i> , 2019, 139, 2754-2764.	1.6	200
102	A large-scale genome-wide association study meta-analysis of cannabis use disorder. <i>Lancet Psychiatry</i> , 2020, 7, 1032-1045.	3.7	200
103	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. <i>PLoS ONE</i> , 2012, 7, e29202.	1.1	197
104	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
105	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
106	Genetic Determinants of Circulating Sphingolipid Concentrations in European Populations. <i>PLoS Genetics</i> , 2009, 5, e1000672.	1.5	184
107	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	13.7	183
108	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. <i>PLoS Genetics</i> , 2012, 8, e1002490.	1.5	181

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109	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. <i>Behavior Genetics</i> , 2016, 46, 170-182.	1.4	178
110	Effects of genome-wide heterozygosity on a range of biomedically relevant human quantitative traits. <i>Human Molecular Genetics</i> , 2007, 16, 233-241.	1.4	176
111	Genome-wide Association for Major Depression Through Age at Onset Stratification: Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. <i>Biological Psychiatry</i> , 2017, 81, 325-335.	0.7	175
112	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
113	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	13.7	173
114	Mutation in a short-chain collagen gene, <i>CTRP5</i> , results in extracellular deposit formation in late-onset retinal degeneration: a genetic model for age-related macular degeneration. <i>Human Molecular Genetics</i> , 2003, 12, 2657-2667.	1.4	172
115	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. <i>Nature Communications</i> , 2019, 10, 2154.	5.8	172
116	Comparative Performance of Four Methods for High-throughput Glycosylation Analysis of Immunoglobulin G in Genetic and Epidemiological Research. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1598-1610.	2.5	169
117	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
118	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. <i>PLoS Genetics</i> , 2012, 8, e1002584.	1.5	166
119	Genome-wide physical activity interactions in adiposity – A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	1.5	158
120	Molecular genetic contributions to socioeconomic status and intelligence. <i>Intelligence</i> , 2014, 44, 26-32.	1.6	156
121	Investigating the possible causal association of smoking with depression and anxiety using Mendelian randomisation meta-analysis: the CARTA consortium. <i>BMJ Open</i> , 2014, 4, e006141.	0.8	150
122	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
123	The brain-derived neurotrophic factor Val66Met polymorphism is associated with age-related change in reasoning skills. <i>Molecular Psychiatry</i> , 2006, 11, 505-513.	4.1	146
124	Common polygenic risk for autism spectrum disorder (ASD) is associated with cognitive ability in the general population. <i>Molecular Psychiatry</i> , 2016, 21, 419-425.	4.1	145
125	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
126	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. <i>Nature Genetics</i> , 2022, 54, 581-592.	9.4	142

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127	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. <i>Nature Genetics</i> , 2020, 52, 494-504.	9.4	138
128	New loci associated with central cornea thickness include COL5A1, AKAP13 and AVGR8. <i>Human Molecular Genetics</i> , 2010, 19, 4304-4311.	1.4	136
129	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. <i>Molecular Psychiatry</i> , 2016, 21, 189-197.	4.1	134
130	Evidence for a Familial Pregnancy-Induced Hypertension Locus in the eNOS-Gene Region. <i>American Journal of Human Genetics</i> , 1997, 61, 354-362.	2.6	132
131	A KATP channel gene effect on sleep duration: from genome-wide association studies to function in <i>Drosophila</i> . <i>Molecular Psychiatry</i> , 2013, 18, 122-132.	4.1	132
132	Genome-wide association analysis identifies six new loci associated with forced vital capacity. <i>Nature Genetics</i> , 2014, 46, 669-677.	9.4	131
133	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. <i>Diabetes</i> , 2016, 65, 803-817.	0.3	131
134	Systems genetics identifies a convergent gene network for cognition and neurodevelopmental disease. <i>Nature Neuroscience</i> , 2016, 19, 223-232.	7.1	131
135	Genomic analysis of family data reveals additional genetic effects on intelligence and personality. <i>Molecular Psychiatry</i> , 2018, 23, 2347-2362.	4.1	131
136	Evidence of association of <i>APOE</i> with age-related macular degeneration - a pooled analysis of 15 studies. <i>Human Mutation</i> , 2011, 32, 1407-1416.	1.1	130
137	Multiethnic Meta-Analysis of Genome-Wide Association Studies in >100 000 Subjects Identifies 23 Fibrinogen-Associated Loci but No Strong Evidence of a Causal Association Between Circulating Fibrinogen and Cardiovascular Disease. <i>Circulation</i> , 2013, 128, 1310-1324.	1.6	128
138	Identification of susceptibility loci for colorectal cancer in a genome-wide meta-analysis. <i>Human Molecular Genetics</i> , 2014, 23, 4729-4737.	1.4	128
139	A time-resolved proteomic and prognostic map of COVID-19. <i>Cell Systems</i> , 2021, 12, 780-794.e7.	2.9	125
140	Common Genetic Variants Associate with Serum Phosphorus Concentration. <i>Journal of the American Society of Nephrology: JASN</i> , 2010, 21, 1223-1232.	3.0	123
141	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
142	Genetic Evidence for a Link Between Favorable Adiposity and Lower Risk of Type 2 Diabetes, Hypertension, and Heart Disease. <i>Diabetes</i> , 2016, 65, 2448-2460.	0.3	122
143	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. <i>Nature Communications</i> , 2017, 8, 910.	5.8	118
144	An epigenome-wide association study of sex-specific chronological ageing. <i>Genome Medicine</i> , 2020, 12, 1.	3.6	117

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145	Genome-wide gene-environment analyses of major depressive disorder and reported lifetime traumatic experiences in UK Biobank. <i>Molecular Psychiatry</i> , 2020, 25, 1430-1446.	4.1	116
146	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1435-1448.	1.2	113
147	Genome-wide association uncovers shared genetic effects among personality traits and mood states. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2012, 159B, 684-695.	1.1	112
148	Genome-wide meta-analysis of 158,000 individuals of European ancestry identifies three loci associated with chronic back pain. <i>PLoS Genetics</i> , 2018, 14, e1007601.	1.5	112
149	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
150	Localising Loci underlying Complex Trait Variation Using Regional Genomic Relationship Mapping. <i>PLoS ONE</i> , 2012, 7, e46501.	1.1	111
151	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
152	Exploration of haplotype research consortium imputation for genome-wide association studies in 20,032 Generation Scotland participants. <i>Genome Medicine</i> , 2017, 9, 23.	3.6	110
153	Genome-wide analysis identifies molecular systems and 149 genetic loci associated with income. <i>Nature Communications</i> , 2019, 10, 5741.	5.8	110
154	Epigenetic measures of ageing predict the prevalence and incidence of leading causes of death and disease burden. <i>Clinical Epigenetics</i> , 2020, 12, 115.	1.8	109
155	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. <i>Nature Communications</i> , 2015, 6, 8658.	5.8	108
156	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. <i>American Journal of Human Genetics</i> , 2019, 104, 112-138.	2.6	106
157	Genome Wide Association Identifies Common Variants at the SERPINA6/SERPINA1 Locus Influencing Plasma Cortisol and Corticosteroid Binding Globulin. <i>PLoS Genetics</i> , 2014, 10, e1004474.	1.5	105
158	Meta-analysis of gene-environment-wide association scans accounting for education level identifies additional loci for refractive error. <i>Nature Communications</i> , 2016, 7, 11008.	5.8	104
159	Harmonization of Neuroticism and Extraversion phenotypes across inventories and cohorts in the Genetics of Personality Consortium: an application of Item Response Theory. <i>Behavior Genetics</i> , 2014, 44, 295-313.	1.4	103
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