Caroline Hayward

List of Publications by Year in Descending Order

533 papers	61,133 citations	113 h-index	238 g-index
610 ext. papers	77,045 ext. citations	12.5 avg, IF	6 L-index

#	Paper	IF	Citations
533	A multi-omics study of circulating phospholipid markers of blood pressure.. *Scientific Reports*, **2022**, 12, 574	4.9	0
532	A proteomic survival predictor for COVID-19 patients in intensive care **2022**, 1, e0000007		6
531	A catalogue of omics biological ageing clocks reveals substantial commonality and associations with disease risk.. *Aging*, **2022**, 14, 623-659	5.6	0
530	Epigenetic scores for the circulating proteome as tools for disease prediction.. *ELife*, **2022**, 11,	8.9	2
529	The association of dispositional optimism and handedness with pressure pain: A cross-sectional study in the general population. *Personality and Individual Differences*, **2022**, 185, 111265	3.3	
528	Meta-GWAS Reveals Novel Genetic Variants Associated with Urinary Excretion of Uromodulin.. *Journal of the American Society of Nephrology: JASN*, **2022**, 33, 511-529	12.7	2
527	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus.. *Nature Communications*, **2022**, 13, 1222	17.4	0
526	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals.. *Nature Genetics*, **2022**,	36.3	7
525	Genetic regulation of post-translational modification of two distinct proteins.. *Nature Communications*, **2022**, 13, 1586	17.4	0
524	Mapping genomic loci implicates genes and synaptic biology in schizophrenia.. *Nature*, **2022**,	50.4	35
523	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects.. *Nature Genetics*, **2022**, 54, 581-592	36.3	6
522	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. *Communications Biology*, **2022**, 5,	6.7	1
521	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. *Molecular Psychiatry*, **2021**, 26, 2111-2125	15.1	3
520	SNP and Haplotype Regional Heritability Mapping (SNHap-RHM): Joint Mapping of Common and Rare Variation Affecting Complex Traits.. *Frontiers in Genetics*, **2021**, 12, 791712	4.5	
519	Lifestyle and Genetic Factors Modify Parent-of-Origin Effects on the Human Methylome. *EBioMedicine*, **2021**, 74, 103730	8.8	1
518	Association of low-frequency and rare coding variants with information processing speed. *Translational Psychiatry*, **2021**, 11, 613	8.6	0
517	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24

516	Genome-wide interaction study with major depression identifies novel variants associated with cognitive function. *Molecular Psychiatry*, **2021**,	15.1	1
515	Association of Genetic Variant at Chromosome 12q23.1 With Neuropathic Pain Susceptibility. *JAMA Network Open*, **2021**, 4, e2136560	10.4	0
514	Mendelian randomization to assess causality between uromodulin, blood pressure and chronic kidney disease. *Kidney International*, **2021**, 100, 1282-1291	9.9	4
513	Genetic mechanisms of critical illness in COVID-19. *Nature*, **2021**, 591, 92-98	50.4	451
512	Sex- and age-specific genetic analysis of chronic back pain. *Pain*, **2021**, 162, 1176-1187	8	6
511	Multivariate genome-wide analysis of immunoglobulin G N-glycosylation identifies new loci pleiotropic with immune function. *Human Molecular Genetics*, **2021**, 30, 1259-1270	5.6	0
510	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. *Genome Medicine*, **2021**, 13, 74	14.4	3
509	Genome-wide association study of cardiac troponin I in the general population. *Human Molecular Genetics*, **2021**, 30, 2027-2039	5.6	5
508	The trans-ancestral genomic architecture of glycemic traits. *Nature Genetics*, **2021**, 53, 840-860	36.3	44
507	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. *Genome Biology*, **2021**, 22, 194	18.3	14
506	Contribution of common risk variants to multiple sclerosis in Orkney and Shetland. *European Journal of Human Genetics*, **2021**, 29, 1701-1709	5.3	1
505	Evaluation of Shared Genetic Susceptibility to High and Low Myopia and Hyperopia. *JAMA Ophthalmology*, **2021**, 139, 601-609	3.9	4
504	Utilizing Large Electronic Medical Record Data Sets to Identify Novel Drug-Gene Interactions for Commonly Used Drugs. *Clinical Pharmacology and Therapeutics*, **2021**, 110, 816-825	6.1	0
503	Genetic and shared couple environmental contributions to smoking and alcohol use in the UK population. *Molecular Psychiatry*, **2021**, 26, 4344-4354	15.1	4
502	Polygenic contributions to alcohol use and alcohol use disorders across population-based and clinically ascertained samples. *Psychological Medicine*, **2021**, 51, 1147-1156	6.9	5
501	The influence of X chromosome variants on trait neuroticism. *Molecular Psychiatry*, **2021**, 26, 483-491	15.1	5
500	Genome-wide association study identifies 48 common genetic variants associated with handedness. *Nature Human Behaviour*, **2021**, 5, 59-70	12.8	33
499	Distinguishing pedigree relationships via multi-way identity by descent sharing and sex-specific genetic maps. *American Journal of Human Genetics*, **2021**, 108, 68-83	11	1

498	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. *Nature Communications*, **2021**, 12, 24	17.4	30
497	Sex Differences in Cardiac Troponin I and T and the Prediction of Cardiovascular Events in the General Population. *Clinical Chemistry*, **2021**, 67, 1351-1360	5.5	2
496	Using symptom-based case predictions to identify host genetic factors that contribute to COVID-19 susceptibility. *PLoS ONE*, **2021**, 16, e0255402	3.7	3
495	A time-resolved proteomic and prognostic map of COVID-19. *Cell Systems*, **2021**, 12, 780-794.e7	10.6	32
494	Genetic insights into biological mechanisms governing human ovarian ageing. *Nature*, **2021**, 596, 393-397	50.4	28
493	Identifying the Common Genetic Basis of Antidepressant Response. *Biological Psychiatry Global Open Science*, **2021**,		4
492	The Genetic Architecture of Depression in Individuals of East Asian Ancestry: A Genome-Wide Association Study. *JAMA Psychiatry*, **2021**, 78, 1258-1269	14.5	7
491	Genome-Wide Association Study of NAFLD Using Electronic Health Records. *Hepatology Communications*, **2021**,	6	3
490	Genome-wide methylation data improves dissection of the effect of smoking on body mass index. *PLoS Genetics*, **2021**, 17, e1009750	6	1
489	The effect of food groups and nutrients on thyroid hormone levels in healthy individuals. *Nutrition*, **2021**, 91-92, 111394	4.8	1
488	Variation in the SERPINA6/SERPINA1 locus alters morning plasma cortisol, hepatic corticosteroid binding globulin expression, gene expression in peripheral tissues, and risk of cardiovascular disease. *Journal of Human Genetics*, **2021**, 66, 625-636	4.3	12
487	Identification of epigenome-wide DNA methylation differences between carriers of APOE 4 and APOE 2 alleles. *Genome Medicine*, **2021**, 13, 1	14.4	11
486	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. *PLoS ONE*, **2020**, 15, e0230815	3.7	4
485	Ultra-High-Throughput Clinical Proteomics Reveals Classifiers of COVID-19 Infection. *Cell Systems*, **2020**, 11, 11-24.e4	10.6	219
484	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. *Nature Communications*, **2020**, 11, 2542	17.4	16
483	Exome Sequencing Identifies Genes and Gene Sets Contributing to Severe Childhood Obesity, Linking PHIP Variants to Repressed POMC Transcription. *Cell Metabolism*, **2020**, 31, 1107-1119.e12	24.6	16
482	Genome-wide association meta-analysis of corneal curvature identifies novel loci and shared genetic influences across axial length and refractive error. *Communications Biology*, **2020**, 3, 133	6.7	9
481	Systematic Evaluation of Normalization Methods for Glycomics Data Based on Performance of Network Inference. *Metabolites*, **2020**, 10,	5.6	5

480	Linking protein to phenotype with Mendelian Randomization detects 38 proteins with causal roles in human diseases and traits. *PLoS Genetics*, **2020**, 16, e1008785	6	12
479	Glycosylation of immunoglobulin G is regulated by a large network of genes pleiotropic with inflammatory diseases. *Science Advances*, **2020**, 6, eaax0301	14.3	38
478	Genome-wide gene-environment analyses of major depressive disorder and reported lifetime traumatic experiences in UK Biobank. *Molecular Psychiatry*, **2020**, 25, 1430-1446	15.1	47
477	Molecular Genetic Risk for Psychosis Is Associated With Psychosis Risk Symptoms in a Population-Based UK Cohort: Findings From Generation Scotland. *Schizophrenia Bulletin*, **2020**,	1.3	4
476	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. *Nature Genetics*, **2020**, 52, 494-504	36.3	39
475	Global variability of the human IgG glycome. *Aging*, **2020**, 12, 15222-15259	5.6	15
474	Variants associated with HHIP expression have sex-differential effects on lung function. *Wellcome Open Research*, **2020**, 5, 111	4.8	0
473	Genome-Wide Analysis Identifies Two Susceptibility Loci for Positive Thyroid Peroxidase and Thyroglobulin Antibodies. *Journal of Clinical Endocrinology and Metabolism*, **2020**, 105,	5.6	3
472	Insights into the genetic basis of retinal detachment. *Human Molecular Genetics*, **2020**, 29, 689-702	5.6	9
471	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. *Nature Metabolism*, **2020**, 2, 1135-1148	14.6	61
470	Genome-Wide Association Study of Suicide Death and Polygenic Prediction of Clinical Antecedents. *American Journal of Psychiatry*, **2020**, 177, 917-927	11.9	24
469	A large-scale genome-wide association study meta-analysis of cannabis use disorder. *Lancet Psychiatry,the*, **2020**, 7, 1032-1045	23.3	43
468	A strategy to incorporate prior knowledge into correlation network cutoff selection. *Nature Communications*, **2020**, 11, 5153	17.4	5
467	Genetic comorbidity between major depression and cardio-metabolic traits, stratified by age at onset of major depression. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2020**, 183, 309-330	3.5	8
466	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. *Nature Genetics*, **2020**, 52, 1314-1332	36.3	26
465	Chronic obstructive pulmonary disease and related phenotypes: polygenic risk scores in population-based and case-control cohorts. *Lancet Respiratory Medicine,the*, **2020**, 8, 696-708	35.1	29
464	Characterisation of an inflammation-related epigenetic score and its association with cognitive ability. *Clinical Epigenetics*, **2020**, 12, 113	7.7	15
463	Epigenetic measures of ageing predict the prevalence and incidence of leading causes of death and disease burden. *Clinical Epigenetics*, **2020**, 12, 115	7.7	40

462	Epigenome-wide analyses identify DNA methylation signatures of dementia risk. *Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring*, **2020**, 12, e12078	5.2	1
461	Variants associated with expression have sex-differential effects on lung function. *Wellcome Open Research*, **2020**, 5, 111	4.8	0
460	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. *Molecular Psychiatry*, **2020**, 25, 2392-2409	15.1	45
459	Genome-wide association study of antidepressant treatment resistance in a population-based cohort using health service prescription data and meta-analysis with GENDEP. *Pharmacogenomics Journal*, **2020**, 20, 329-341	3.5	24
458	Genetic contributions to two special factors of neuroticism are associated with affluence, higher intelligence, better health, and longer life. *Molecular Psychiatry*, **2020**, 25, 3034-3052	15.1	27
457	Rare and common genetic variations in the Keap1/Nrf2 antioxidant response pathway impact thyroglobulin gene expression and circulating levels, respectively. *Biochemical Pharmacology*, **2020**, 173, 113605	6	11
456	Factors associated with sharing e-mail information and mental health survey participation in large population cohorts. *International Journal of Epidemiology*, **2020**, 49, 410-421	7.8	32
455	The Association between Salt Taste Perception, Mediterranean Diet and Metabolic Syndrome: A Cross-Sectional Study. *Nutrients*, **2020**, 12,	6.7	11
454	A genome-wide association study finds genetic variants associated with neck or shoulder pain in UK Biobank. *Human Molecular Genetics*, **2020**, 29, 1396-1404	5.6	10
453	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815		
452	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815		
451	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815		
450	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815		
449	The genetic landscape of Scotland and the Isles. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 19064-19070	11.5	10
448	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. *Nature Genetics*, **2019**, 51, 1459-1474	36.3	122
447	Low-frequency variation in TP53 has large effects on head circumference and intracranial volume. *Nature Communications*, **2019**, 10, 357	17.4	12
446	A validation of the diathesis-stress model for depression in Generation Scotland. *Translational Psychiatry*, **2019**, 9, 25	8.6	17
445	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. *American Journal of Epidemiology*, **2019**, 188, 1033-1054	3.8	39

444	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. *Nature Communications*, **2019**, 10, 376	17.4	41
443	Genome-wide by environment interaction studies of depressive symptoms and psychosocial stress in UK Biobank and Generation Scotland. *Translational Psychiatry*, **2019**, 9, 14	8.6	52
442	A catalog of genetic loci associated with kidney function from analyses of a million individuals. *Nature Genetics*, **2019**, 51, 957-972	36.3	217
441	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. *Nature Communications*, **2019**, 10, 2154	17.4	81
440	Cardiac Troponin T and Troponin I in the General Population. *Circulation*, **2019**, 139, 2754-2764	16.7	90
439	Genome-wide association meta-analysis for total thyroid hormone levels in Croatian population. *Journal of Human Genetics*, **2019**, 64, 473-480	4.3	3
438	Genome-wide meta-analysis identifies novel loci associated with free triiodothyronine and thyroid-stimulating hormone. *Journal of Endocrinological Investigation*, **2019**, 42, 1171-1180	5.2	6
437	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. *Nature Communications*, **2019**, 10, 1383	17.4	21
436	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. *Human Molecular Genetics*, **2019**, 28, 2615-2633	5.6	14
435	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. *Nature Genetics*, **2019**, 51, 636-648	36.3	59
434	Genetic Variants in the Gene Are Associated with Thyroglobulin Plasma Level in Healthy Individuals. *Thyroid*, **2019**, 29, 886-893	6.2	3
433	Identification of novel differentially methylated sites with potential as clinical predictors of impaired respiratory function and COPD. *EBioMedicine*, **2019**, 43, 576-586	8.8	13
432	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. *Nature Genetics*, **2019**, 51, 481-493	36.3	156
431	Using tree-based methods for detection of gene-gene interactions in the presence of a polygenic signal: simulation study with application to educational attainment in the Generation Scotland Cohort Study. *Bioinformatics*, **2019**, 35, 181-188	7.2	3
430	Late-onset retinal degeneration pathology due to mutations in CTRP5 is mediated through HTRA1. *Aging Cell*, **2019**, 18, e13011	9.9	9
429	An actionable KCNH2 Long QT Syndrome variant detected by sequence and haplotype analysis in a population research cohort. *Scientific Reports*, **2019**, 9, 10964	4.9	6
428	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. *Nature Human Behaviour*, **2019**, 3, 950-961	12.8	32
427	Novel Genetic Locus Influencing Retinal Venular Tortuosity Is Also Associated With Risk of Coronary Artery Disease. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2019**, 39, 2542-2552	9.4	11

426	Disentangling the genetics of lean mass. *American Journal of Clinical Nutrition*, **2019**, 109, 276-287	7	24
425	Associations of autozygosity with a broad range of human phenotypes. *Nature Communications*, **2019**, 10, 4957	17.4	40
424	An epigenome-wide association study of sex-specific chronological ageing. *Genome Medicine*, **2019**, 12, 1	14.4	43
423	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
422	A meta-analysis of genome-wide association studies of epigenetic age acceleration. *PLoS Genetics*, **2019**, 15, e1008104	6	38
421	Multi-trait genome-wide association study identifies new loci associated with optic disc parameters. *Communications Biology*, **2019**, 2, 435	6.7	10
420	Genome-wide analysis identifies molecular systems and 149 genetic loci associated with income. *Nature Communications*, **2019**, 10, 5741	17.4	42
419	Association of Whole-Genome and NETRIN1 Signaling Pathway-Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. *Biological Psychiatry: Cognitive Neuroscience and Neuroimaging*, **2019**, 4, 91-100	3.4	12
418	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. *American Journal of Human Genetics*, **2019**, 104, 112-138	11	54
417	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. *Nature Genetics*, **2019**, 51, 51-62	36.3	152
416	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. *Circulation*, **2019**, 139, 620-635	16.7	51
415	The effect of multiple nutrients on plasma parathyroid hormone level in healthy individuals. *International Journal of Food Sciences and Nutrition*, **2019**, 70, 638-644	3.7	0
414	Genome-Wide and Abdominal MRI Data Provide Evidence That a Genetically Determined Favorable Adiposity Phenotype Is Characterized by Lower Ectopic Liver Fat and Lower Risk of Type 2 Diabetes, Heart Disease, and Hypertension. *Diabetes*, **2019**, 68, 207-219	0.9	46
413	Genome-wide meta-analysis identifies novel gender specific loci associated with thyroid antibodies level in Croatians. *Genomics*, **2019**, 111, 737-743	4.3	8
412	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. *Nature Genetics*, **2018**, 50, 381-389	36.3	787
411	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics*, **2018**, 50, 559-571	36.3	221
410	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. *Nature Communications*, **2018**, 9, 260	17.4	174
409	Genome-wide meta-analyses of stratified depression in Generation Scotland and UK Biobank. *Translational Psychiatry*, **2018**, 8, 9	8.6	48

408	Genomic analysis of family data reveals additional genetic effects on intelligence and personality. *Molecular Psychiatry*, **2018**, 23, 2347-2362	15.1	96
407	Genome-wide meta-analysis identifies novel loci associated with parathyroid hormone level. *Molecular Medicine*, **2018**, 24, 15	6.2	4
406	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. *Nature Genetics*, **2018**, 50, 668-681	36.3	1301
405	Phenotypic and genetic analysis of cognitive performance in Major Depressive Disorder in the Generation Scotland: Scottish Family Health Study. *Translational Psychiatry*, **2018**, 8, 63	8.6	7
404	Genome-Wide Meta-Analysis Unravels Interactions between Magnesium Homeostasis and Metabolic Phenotypes. *Journal of the American Society of Nephrology: JASN*, **2018**, 29, 335-348	12.7	19
403	Does Childhood Trauma Moderate Polygenic Risk for Depression? A Meta-analysis of 5765 Subjects From the Psychiatric Genomics Consortium. *Biological Psychiatry*, **2018**, 84, 138-147	7.9	48
402	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. *Nature Genetics*, **2018**, 50, 1112-1121	36.3	950
401	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. *Nature Communications*, **2018**, 9, 2904	17.4	39
400	Genome-Wide Association Study on Immunoglobulin G Glycosylation Patterns. *Frontiers in Immunology*, **2018**, 9, 277	8.4	36
399	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. *Genome Biology*, **2018**, 19, 87	18.3	25
398	Common variants on 6q16.2, 12q24.31 and 16p13.3 are associated with major depressive disorder. *Neuropsychopharmacology*, **2018**, 43, 2146-2153	8.7	27
397	Comparison between High-Sensitivity Cardiac Troponin T and Cardiac Troponin I in a Large General Population Cohort. *Clinical Chemistry*, **2018**, 64, 1607-1616	5.5	61
396	Exploring causality in the association between circulating 25-hydroxyvitamin D and colorectal cancer risk: a large Mendelian randomisation study. *BMC Medicine*, **2018**, 16, 142	11.4	40
395	Probabilistic partial least squares model: Identifiability, estimation and application. *Journal of Multivariate Analysis*, **2018**, 167, 331-346	1.4	3
394	DNA sequence-level analyses reveal potential phenotypic modifiers in a large family with psychiatric disorders. *Molecular Psychiatry*, **2018**, 23, 2254-2265	15.1	13
393	Multi-ethnic genome-wide association study for atrial fibrillation. *Nature Genetics*, **2018**, 50, 1225-1233	36.3	277
392	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. *PLoS ONE*, **2018**, 13, e0198166	3.7	31
391	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*, **2018**, 3, 4	4.8	16

390	Genetic and environmental determinants of stressful life events and their overlap with depression and neuroticism. *Wellcome Open Research*, **2018**, 3, 11	4.8	11
389	Genetic and environmental determinants of stressful life events and their overlap with depression and neuroticism. *Wellcome Open Research*, **2018**, 3, 11	4.8	13
388	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
387	N-Glycan Profile and Kidney Disease in Type 1 Diabetes. *Diabetes Care*, **2018**, 41, 79-87	14.6	43
386	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. *Nature Neuroscience*, **2018**, 21, 1656-1669	25.5	257
385	Genome-wide interaction study of a proxy for stress-sensitivity and its prediction of major depressive disorder. *PLoS ONE*, **2018**, 13, e0209160	3.7	6
384	Neuroticism and pain catastrophizing aggravate response to pain in healthy adults: an experimental study. *Korean Journal of Pain*, **2018**, 31, 16-26	2.1	13
383	Genome-wide meta-analysis of 158,000 individuals of European ancestry identifies three loci associated with chronic back pain. *PLoS Genetics*, **2018**, 14, e1007601	6	60
382	ExomeChip-Wide Analysis of 95 626 Individuals Identifies 10 Novel Loci Associated With QT and JT Intervals. *Circulation Genomic and Precision Medicine*, **2018**, 11, e001758	5.2	14
381	Integrating omics datasets with the OmicsPLS package. *BMC Bioinformatics*, **2018**, 19, 371	3.6	23
380	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. *American Journal of Human Genetics*, **2018**, 103, 691-706	11	151
379	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. *Nature Genetics*, **2018**, 50, 1412-1425	36.3	386
378	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. *Nature Genetics*, **2018**, 50, 834-848	36.3	135
377	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. *Circulation Genomic and Precision Medicine*, **2018**, 11, e002037	5.2	11
376	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. *Nature Communications*, **2018**, 9, 2098	17.4	254
375	Cross-ancestry genome-wide association analysis of corneal thickness strengthens link between complex and Mendelian eye diseases. *Nature Communications*, **2018**, 9, 1864	17.4	37
374	A Combined Pathway and Regional Heritability Analysis Indicates NETRIN1 Pathway Is Associated With Major Depressive Disorder. *Biological Psychiatry*, **2017**, 81, 336-346	7.9	25
373	Genome-wide Association for Major Depression Through Age at Onset Stratification: Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. *Biological Psychiatry*, **2017**, 81, 325-335	7.9	129

372	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. *International Journal of Epidemiology*, **2017**, 46, 894-904	7.8	25
371	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. *Nature Genetics*, **2017**, 49, 403-415	36.3	313
370	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
369	Exploration of haplotype research consortium imputation for genome-wide association studies in 20,032 Generation Scotland participants. *Genome Medicine*, **2017**, 9, 23	14.4	85
368	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. *Nature Genetics*, **2017**, 49, 416-425	36.3	170
367	Discovery of novel heart rate-associated loci using the Exome Chip. *Human Molecular Genetics*, **2017**, 26, 2346-2363	5.6	17
366	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. *Nature Genetics*, **2017**, 49, 834-841	36.3	257
365	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. *Nature Genetics*, **2017**, 49, 946-952	36.3	176
364	Assessing the presence of shared genetic architecture between Alzheimer's disease and major depressive disorder using genome-wide association data. *Translational Psychiatry*, **2017**, 7, e1094	8.6	25
363	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. *Nature Communications*, **2017**, 8, 14977	17.4	105
362	Common variants in CLDN14 are associated with differential excretion of magnesium over calcium in urine. *Pflugers Archiv European Journal of Physiology*, **2017**, 469, 91-103	4.6	21
361	Validation of Surrogates of Urine Osmolality in Population Studies. *American Journal of Nephrology*, **2017**, 46, 26-36	4.6	7
360	Genetic effects influencing risk for major depressive disorder in China and Europe. *Translational Psychiatry*, **2017**, 7, e1074	8.6	48
359	and Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. *Journal of the American Society of Nephrology: JASN*, **2017**, 28, 981-994	12.7	30
358	Genome-wide Regional Heritability Mapping Identifies a Locus Within the TOX2 Gene Associated With Major Depressive Disorder. *Biological Psychiatry*, **2017**, 82, 312-321	7.9	17
357	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
356	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. *Nature Communications*, **2017**, 8, 744	17.4	37
355	Regional variation in health is predominantly driven by lifestyle rather than genetics. *Nature Communications*, **2017**, 8, 801	17.4	11

354	Novel pathogenic mutations in C1QTNF5 support a dominant negative disease mechanism in late-onset retinal degeneration. *Scientific Reports*, **2017**, 7, 12147	4.9	17
353	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. *Nature Communications*, **2017**, 8, 910	17.4	78
352	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475 000 Individuals. *Circulation: Cardiovascular Genetics*, **2017**, 10,		33
351	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. *PLoS Medicine*, **2017**, 14, e1002383	11.6	223
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30	Genome-wide association study of alcohol consumption and genetic overlap with other health-related traits in UK Biobank (N=112,117)	9
29	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes	4
28	Electronic Health Record and Genome-wide Genetic Data in Generation Scotland Participants	2
27	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depressive disorder	21
26	Ninety-nine independent genetic loci influencing general cognitive function include genes associated with brain health and structure (N = 280,360)	6
25	Genome-wide interaction study of a proxy for stress-sensitivity and its prediction of major depressive disorder	1
24	Genetic analysis of over one million people identifies 535 novel loci for blood pressure	4
23	Epigenetic clocks predict prevalence and incidence of leading causes of death and disease burden	8
22	Genome-wide association studies identify 137 loci for DNA methylation biomarkers of ageing	8
21	Using symptom-based case predictions to identify host genetic factors that contribute to COVID-19 susceptibility	1
20	Genetic mechanisms of critical illness in Covid-19	51
19	Epigenetic scores for the circulating proteome as tools for disease prediction	2
18	New genetic signals for lung function highlight pathways and pleiotropy, and chronic obstructive pulmonary disease associations across multiple ancestries	5
17	Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution	1
16	Global variability of the human IgG glycome	2
15	Genetic and shared couple environmental contributions to smoking and alcohol use in the UK population	1
14	Genetic analysis identifies molecular systems and biological pathways associated with household income	1
13	A meta-analysis of genome-wide association studies of epigenetic age acceleration	2

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11	Distinguishing pedigree relationships using multi-way identical by descent sharing and sex-specific genetic maps		2
10	Tissue-Specific Alteration of Metabolic Pathways Influences Glycemic Regulation		4
9	Systematic evaluation of normalization methods for glycomics data based on performance of network inference		1
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