Caroline Hayward

List of Publications by Citations

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	Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*, **2010**, 466, 707-13	50.4	2742
532	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
531	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics*, **2010**, 42, 937-48	36.3	2267
530	Discovery and refinement of loci associated with lipid levels. *Nature Genetics*, **2013**, 45, 1274-1283	36.3	1904
529	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. *Nature Genetics*, **2010**, 42, 105-16	36.3	1673
528	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. *Nature* , **2011**, 478, 103-9	50.4	1564
527	Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature*, **2010**, 467, 832-8	50.4	1514
526	Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86	36.3	1339
525	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
524	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
523	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
522	Genome-wide association study identifies 74 loci associated with educational attainment. *Nature*, **2016**, 533, 539-42	50.4	850
521	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
520	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. *Nature Genetics*, **2014**, 46, 234-44	36.3	784
519	A large genome-wide association study of age-related macular degeneration highlights contributions of rare and common variants. *Nature Genetics*, **2016**, 48, 134-43	36.3	769
518	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, 949-60	36.3	724
517	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. *Nature Genetics*, **2009**, 41, 47-55	36.3	708

516	Complement C3 variant and the risk of age-related macular degeneration. *New England Journal of Medicine*, **2007**, 357, 553-61	59.2	675
515	Runs of homozygosity in European populations. *American Journal of Human Genetics*, **2008**, 83, 359-72	11	624
514	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. *Nature Genetics*, **2012**, 44, 991-1005	36.3	621
513	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. *Nature Genetics*, **2012**, 44, 659-69	36.3	615
512	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. *Nature Genetics*, **2016**, 48, 624-33	36.3	602
511	New loci associated with kidney function and chronic kidney disease. *Nature Genetics*, **2010**, 42, 376-84	36.3	599
510	Common variants associated with plasma triglycerides and risk for coronary artery disease. *Nature Genetics*, **2013**, 45, 1345-52	36.3	597
509	GWAS of 126,559 individuals identifies genetic variants associated with educational attainment. *Science*, **2013**, 340, 1467-71	33.3	563
508	SLC2A9 is a newly identified urate transporter influencing serum urate concentration, urate excretion and gout. *Nature Genetics*, **2008**, 40, 437-42	36.3	563
507	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. *Nature Genetics*, **2010**, 42, 436-40	36.3	521
506	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. *Nature Genetics*, **2013**, 45, 145-54	36.3	505
505	Genetic mechanisms of critical illness in COVID-19. *Nature*, **2021**, 591, 92-98	50.4	451
504	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics*, **2013**, 45, 501-12	36.3	437
503	Genome-wide association study identifies five loci associated with lung function. *Nature Genetics*, **2010**, 42, 36-44	36.3	430
502	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
501	Meta-analysis of genome-wide association studies in >80 000 subjects identifies multiple loci for C-reactive protein levels. *Circulation*, **2011**, 123, 731-8	16.7	395
500	Mutations in SOX2 cause anophthalmia. *Nature Genetics*, **2003**, 33, 461-3	36.3	391
499	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

498	A general approach for haplotype phasing across the full spectrum of relatedness. *PLoS Genetics*, **2014**, 10, e1004234	6	377
497	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. *Nature Genetics*, **2010**, 42, 1077-85	36.3	372
496	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. *Nature Genetics*, **2011**, 43, 1005-11	36.3	338
495	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	6	326
494	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. *Science*, **2016**, 351, 1166-71	33.3	325
493	Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. *Nature Genetics*, **2013**, 45, 314-8	36.3	314
492	Common variants at 10 genomic loci influence hemoglobin A[C) levels via glycemic and nonglycemic pathways. *Diabetes*, **2010**, 59, 3229-39	0.9	314
491	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
490	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. *Nature Genetics*, **2011**, 43, 1082-90	36.3	313
489	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
488	FTO genotype is associated with phenotypic variability of body mass index. *Nature*, **2012**, 490, 267-72	50.4	304
487	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. *Nature Communications*, **2016**, 7, 10023	17.4	295
486	Genome-wide association identifies nine common variants associated with fasting proinsulin levels and provides new insights into the pathophysiology of type 2 diabetes. *Diabetes*, **2011**, 60, 2624-34	0.9	285
485	Multi-ethnic genome-wide association study for atrial fibrillation. *Nature Genetics*, **2018**, 50, 1225-1233	36.3	277
484	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. *PLoS Genetics*, **2013**, 9, e1003500	6	277
483	Novel associations of multiple genetic loci with plasma levels of factor VII, factor VIII, and von Willebrand factor: The CHARGE (Cohorts for Heart and Aging Research in Genome Epidemiology) Consortium. *Circulation*, **2010**, 121, 1382-92	16.7	260
482	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
481	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. *Nature Neuroscience*, **2018**, 21, 1656-1669	25.5	257

480	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. *Nature Communications*, **2018**, 9, 2098	17.4	254
479	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. *Nature Genetics*, **2016**, 48, 1171-1184	36.3	251
478	Genetic contributions to variation in general cognitive function: a meta-analysis of genome-wide association studies in the CHARGE consortium (N=53949). *Molecular Psychiatry*, **2015**, 20, 183-92	15.1	250
477	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. *Nature Genetics*, **2010**, 42, 1068-76	36.3	249
476	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. *Nature Genetics*, **2012**, 44, 260-8	36.3	243
475	Loci associated with N-glycosylation of human immunoglobulin G show pleiotropy with autoimmune diseases and haematological cancers. *PLoS Genetics*, **2013**, 9, e1003225	6	242
474	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. *Nature Genetics*, **2011**, 43, 753-60	36.3	237
473	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, 223-32	11	233
472	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. *Nature Genetics*, **2015**, 47, 1294-1303	36.3	226
471	Genome-wide association study of alcohol consumption and genetic overlap with other health-related traits in UK Biobank (N=112 117). *Molecular Psychiatry*, **2017**, 22, 1376-1384	15.1	225
470	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
469	Cognitive change and the APOE epsilon 4 allele. *Nature*, **2002**, 418, 932	50.4	223
468	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. *JAMA Psychiatry*, **2015**, 72, 642-50	14.5	222
467	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. *Nature Genetics*, **2013**, 45, 155-63	36.3	222
466	Genome-Wide Association Analyses in 128,266 Individuals Identifies New Morningness and Sleep Duration Loci. *PLoS Genetics*, **2016**, 12, e1006125	6	222
465	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
464	Genome-wide association study of cognitive functions and educational attainment in UK Biobank (N=112 151). *Molecular Psychiatry*, **2016**, 21, 758-67	15.1	221
463	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	6	220

462	Ultra-High-Throughput Clinical Proteomics Reveals Classifiers of COVID-19 Infection. *Cell Systems*, **2020**, 11, 11-24.e4	10.6	219
461	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics*, **2013**, 45, 621-31	36.3	219
460	A catalog of genetic loci associated with kidney function from analyses of a million individuals. *Nature Genetics*, **2019**, 51, 957-972	36.3	217
459	Identification of SATB2 as the cleft palate gene on 2q32-q33. *Human Molecular Genetics*, **2003**, 12, 2491-501	5.6	209
458	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. *Nature Genetics*, **2014**, 46, 826-36	36.3	199
457	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. *Nature Genetics*, **2016**, 48, 1462-1472	36.3	198
456	Glycans are a novel biomarker of chronological and biological ages. *Journals of Gerontology - Series A Biological Sciences and Medical Sciences*, **2014**, 69, 779-89	6.4	192
455	Variability, heritability and environmental determinants of human plasma N-glycome. *Journal of Proteome Research*, **2009**, 8, 694-701	5.6	191
454	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
453	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
452	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, 13790-4	11.5	181
451	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180
450	Genomics meets glycomics-the first GWAS study of human N-Glycome identifies HNF1 as a master regulator of plasma protein fucosylation. *PLoS Genetics*, **2010**, 6, e1001256	6	177
449	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
448	Genome-wide analysis of over 106 000 individuals identifies 9 neuroticism-associated loci. *Molecular Psychiatry*, **2016**, 21, 749-57	15.1	175
447	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
446	Application of high-dimensional feature selection: evaluation for genomic prediction in man. *Scientific Reports*, **2015**, 5, 10312	4.9	171
445	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

444	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. *American Journal of Human Genetics*, **2014**, 94, 233-45	11	170
443	CUBN is a gene locus for albuminuria. *Journal of the American Society of Nephrology: JASN*, **2011**, 22, 555-70	12.7	170
442	Meta-analysis of genome-wide association studies from the CHARGE consortium identifies common variants associated with carotid intima media thickness and plaque. *Nature Genetics*, **2011**, 43, 940-7	36.3	168
441	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
440	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. *Nature Genetics*, **2019**, 51, 51-62	36.3	152
439	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
438	Genetic determinants of circulating sphingolipid concentrations in European populations. *PLoS Genetics*, **2009**, 5, e1000672	6	150
437	Effects of genome-wide heterozygosity on a range of biomedically relevant human quantitative traits. *Human Molecular Genetics*, **2007**, 16, 233-41	5.6	150
436	Mutation in a short-chain collagen gene, CTRP5, results in extracellular deposit formation in late-onset retinal degeneration: a genetic model for age-related macular degeneration. *Human Molecular Genetics*, **2003**, 12, 2657-67	5.6	150
435	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. *Nature Communications*, **2015**, 6, 5897	17.4	147
434	Genome-wide association study identifies novel loci associated with circulating phospho- and sphingolipid concentrations. *PLoS Genetics*, **2012**, 8, e1002490	6	145
433	Genome-wide association and functional follow-up reveals new loci for kidney function. *PLoS Genetics*, **2012**, 8, e1002584	6	143
432	A genome-wide association search for type 2 diabetes genes in African Americans. *PLoS ONE*, **2012**, 7, e29202	3.7	138
431	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. *Nature Genetics*, **2018**, 50, 834-848	36.3	135
430	Molecular genetic contributions to socioeconomic status and intelligence. *Intelligence*, **2014**, 44, 26-32	3	131
429	The brain-derived neurotrophic factor Val66Met polymorphism is associated with age-related change in reasoning skills. *Molecular Psychiatry*, **2006**, 11, 505-13	15.1	130
428	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
427	New loci associated with central cornea thickness include COL5A1, AKAP13 and AVGR8. *Human Molecular Genetics*, **2010**, 19, 4304-11	5.6	125

426	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. *Nature Genetics*, **2019**, 51, 1459-1474	36.3	122
425	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. *Behavior Genetics*, **2016**, 46, 170-82	3.2	122
424	Comparative performance of four methods for high-throughput glycosylation analysis of immunoglobulin G in genetic and epidemiological research. *Molecular and Cellular Proteomics*, **2014** , 13, 1598-610	7.6	120
423	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	30.4	119
422	Investigating the possible causal association of smoking with depression and anxiety using Mendelian randomisation meta-analysis: the CARTA consortium. *BMJ Open*, **2014**, 4, e006141	3	115
421	A K(ATP) channel gene effect on sleep duration: from genome-wide association studies to function in Drosophila. *Molecular Psychiatry*, **2013**, 18, 122-32	15.1	113
420	Evidence for a familial pregnancy-induced hypertension locus in the eNOS-gene region. *American Journal of Human Genetics*, **1997**, 61, 354-62	11	113
419	Identification of susceptibility loci for colorectal cancer in a genome-wide meta-analysis. *Human Molecular Genetics*, **2014**, 23, 4729-37	5.6	107
418	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. *Circulation*, **2013**, 128, 1310-24	16.7	107
417	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
416	Genome-wide association analysis identifies six new loci associated with forced vital capacity. *Nature Genetics*, **2014**, 46, 669-77	36.3	104
415	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. *PLoS Genetics*, **2017**, 13, e1006528	6	103
414	Common polygenic risk for autism spectrum disorder (ASD) is associated with cognitive ability in the general population. *Molecular Psychiatry*, **2016**, 21, 419-25	15.1	101
413	Meta-analysis of genome-wide association studies identifies six new Loci for serum calcium concentrations. *PLoS Genetics*, **2013**, 9, e1003796	6	100
412	Evidence of association of APOE with age-related macular degeneration: a pooled analysis of 15 studies. *Human Mutation*, **2011**, 32, 1407-16	4.7	99
411	Genome-wide association uncovers shared genetic effects among personality traits and mood states. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2012**, 159B, 684-95	3.5	98
410	Genomic analysis of family data reveals additional genetic effects on intelligence and personality. *Molecular Psychiatry*, **2018**, 23, 2347-2362	15.1	96
409	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. *Diabetes*, **2016**, 65, 803-17	0.9	96

408	Common genetic variants associate with serum phosphorus concentration. *Journal of the American Society of Nephrology: JASN*, **2010**, 21, 1223-32	12.7	93
407	Cardiac Troponin T and Troponin I in the General Population. *Circulation*, **2019**, 139, 2754-2764	16.7	90
406	Genetic variants linked to education predict longevity. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 13366-13371	11.5	90
405	Systems genetics identifies a convergent gene network for cognition and neurodevelopmental disease. *Nature Neuroscience*, **2016**, 19, 223-32	25.5	88
404	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. *Nature Communications*, **2017**, 8, 80	17.4	88
403	Genetic Evidence for a Link Between Favorable Adiposity and Lower Risk of Type 2 Diabetes, Hypertension, and Heart Disease. *Diabetes*, **2016**, 65, 2448-60	0.9	86
402	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. *Molecular Psychiatry*, **2016**, 21, 189-197	15.1	85
401	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
400	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. *Hypertension*, **2017**,	8.5	85
399	Association between chromosome 9p21 variants and the ankle-brachial index identified by a meta-analysis of 21 genome-wide association studies. *Circulation: Cardiovascular Genetics*, **2012**, 5, 100-12		84
398	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. *Nature Communications*, **2019**, 10, 2154	17.4	81
397	Common variants in the JAZF1 gene associated with height identified by linkage and genome-wide association analysis. *Human Molecular Genetics*, **2009**, 18, 373-80	5.6	81
396	Harmonization of Neuroticism and Extraversion phenotypes across inventories and cohorts in the Genetics of Personality Consortium: an application of Item Response Theory. *Behavior Genetics*, **2014**, 44, 295-313	3.2	80
395	Meta-analysis of gene-environment-wide association scans accounting for education level identifies additional loci for refractive error. *Nature Communications*, **2016**, 7, 11008	17.4	79
394	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. *Nature Communications*, **2015**, 6, 8658	17.4	79
393	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. *Nature Communications*, **2017**, 8, 910	17.4	78
392	Genetic determinants of heel bone properties: genome-wide association meta-analysis and replication in the GEFOS/GENOMOS consortium. *Human Molecular Genetics*, **2014**, 23, 3054-68	5.6	78
391	Marfan Database (third edition): new mutations and new routines for the software. *Nucleic Acids Research*, **1998**, 26, 229-3	20.1	78

390	52 Genetic Loci Influencing Myocardial Mass. *Journal of the American College of Cardiology*, **2016**, 68, 1435-1448	15.1	76
389	Localising loci underlying complex trait variation using Regional Genomic Relationship Mapping. *PLoS ONE*, **2012**, 7, e46501	3.7	75
388	Mutations in HNF1A result in marked alterations of plasma glycan profile. *Diabetes*, **2013**, 62, 1329-37	0.9	74
387	The functional COMT polymorphism, Val 158 Met, is associated with logical memory and the personality trait intellect/imagination in a cohort of healthy 79 year olds. *Neuroscience Letters*, **2005**, 385, 1-6	3.3	73
386	Complement factor D in age-related macular degeneration **2011**, 52, 8828-34		72
385	Cognitive ability at age 11 and 70 years, information processing speed, and APOE variation: the Lothian Birth Cohort 1936 study. *Psychology and Aging*, **2009**, 24, 129-38	3.6	72
384	Common variants in UMOD associate with urinary uromodulin levels: a meta-analysis. *Journal of the American Society of Nephrology: JASN*, **2014**, 25, 1869-82	12.7	71
383	Genome wide association identifies common variants at the SERPINA6/SERPINA1 locus influencing plasma cortisol and corticosteroid binding globulin. *PLoS Genetics*, **2014**, 10, e1004474	6	71
382	Fibrillin-1 mutations in Marfan syndrome and other type-1 fibrillinopathies. *Human Mutation*, **1997**, 10, 415-23	4.7	71
381	KLOTHO genotype and cognitive ability in childhood and old age in the same individuals. *Neuroscience Letters*, **2005**, 378, 22-7	3.3	70
380	Variations in apolipoprotein E frequency with age in a pooled analysis of a large group of older people. *American Journal of Epidemiology*, **2011**, 173, 1357-64	3.8	67
379	Genome-wide association study of age-related macular degeneration identifies associated variants in the TNXB-FKBPL-NOTCH4 region of chromosome 6p21.3. *Human Molecular Genetics*, **2012**, 21, 4138-50	5.6	66
378	Increased genetic vulnerability to smoking at CHRNA5 in early-onset smokers. *Archives of General Psychiatry*, **2012**, 69, 854-60		65
377	IgG glycan patterns are associated with type 2 diabetes in independent European populations. *Biochimica Et Biophysica Acta - General Subjects*, **2017**, 1861, 2240-2249	4	64
376	Molecular genetic analysis of the APEX nuclease gene in amyotrophic lateral sclerosis. *Neurology*, **1999**, 52, 1899-901	6.5	64
375	Genetic influences on plasma CFH and CFHR1 concentrations and their role in susceptibility to age-related macular degeneration. *Human Molecular Genetics*, **2013**, 22, 4857-69	5.6	62
374	Evidence of inbreeding depression on human height. *PLoS Genetics*, **2012**, 8, e1002655	6	62
373	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. *American Journal of Human Genetics*, **2016**, 99, 40-55	11	61

372	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
371	Polymorphisms in B3GAT1, SLC9A9 and MGAT5 are associated with variation within the human plasma N-glycome of 3533 European adults. *Human Molecular Genetics*, **2011**, 20, 5000-11	5.6	61
370	Estimating human inbreeding coefficients: comparison of genealogical and marker heterozygosity approaches. *Annals of Human Genetics*, **2006**, 70, 666-76	2.2	61
369	Apolipoprotein e gene variability and cognitive functions at age 79: a follow-up of the Scottish mental survey of 1932. *Psychology and Aging*, **2004**, 19, 367-71	3.6	61
368	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. *Nature Metabolism*, **2020**, 2, 1135-1148	14.6	61
367	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
366	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
365	Hearing function and thresholds: a genome-wide association study in European isolated populations identifies new loci and pathways. *Journal of Medical Genetics*, **2011**, 48, 369-74	5.8	59
364	Discovery and fine mapping of serum protein loci through transethnic meta-analysis. *American Journal of Human Genetics*, **2012**, 91, 744-53	11	58
363	3000 years of solitude: extreme differentiation in the island isolates of Dalmatia, Croatia. *European Journal of Human Genetics*, **2006**, 14, 478-87	5.3	58
362	Large scale international replication and meta-analysis study confirms association of the 15q14 locus with myopia. The CREAM consortium. *Human Genetics*, **2012**, 131, 1467-80	6.3	57
361	Genome-wide linkage analysis of serum creatinine in three isolated European populations. *Kidney International*, **2009**, 76, 297-306	9.9	57
360	A genetic association analysis of cognitive ability and cognitive ageing using 325 markers for 109 genes associated with oxidative stress or cognition. *BMC Genetics*, **2007**, 8, 43	2.6	57
359	Identification of myopia-associated WNT7B polymorphisms provides insights into the mechanism underlying the development of myopia. *Nature Communications*, **2015**, 6, 6689	17.4	56
358	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. *Human Molecular Genetics*, **2016**, 25, 358-70	5.6	54
357	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. *Human Molecular Genetics*, **2012**, 21, 5329-43	5.6	54
356	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. *American Journal of Human Genetics*, **2019**, 104, 112-138	11	54
355	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

354	Molecular mechanisms underlying variations in lung function: a systems genetics analysis. *Lancet Respiratory Medicine,the*, **2015**, 3, 782-95	35.1	52
353	Meta-analysis of genome-wide association studies in five cohorts reveals common variants in RBFOX1, a regulator of tissue-specific splicing, associated with refractive error. *Human Molecular Genetics*, **2013**, 22, 2754-64	5.6	52
352	Prospective prenatal diagnosis of cystic fibrosis. *Lancet, The*, **1985**, 1, 1175-8	40	52
351	Novel association to the proprotein convertase PCSK7 gene locus revealed by analysing soluble transferrin receptor (sTfR) levels. *Human Molecular Genetics*, **2011**, 20, 1042-7	5.6	51
350	The Eysenck personality factors: Psychometric structure, reliability, heritability and phenotypic and genetic correlations with psychological distress in an isolated Croatian population. *Personality and Individual Differences*, **2007**, 42, 123-133	3.3	51
349	Genetic mechanisms of critical illness in Covid-19		51
348	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
347	Pedigree- and SNP-Associated Genetics and Recent Environment are the Major Contributors to Anthropometric and Cardiometabolic Trait Variation. *PLoS Genetics*, **2016**, 12, e1005804	6	50
346	Meta-analysis of gene-level associations for rare variants based on single-variant statistics. *American Journal of Human Genetics*, **2013**, 93, 236-48	11	49
345	Genetic effects influencing risk for major depressive disorder in China and Europe. *Translational Psychiatry*, **2017**, 7, e1074	8.6	48
344	Genome-wide studies of verbal declarative memory in nondemented older people: the Cohorts for Heart and Aging Research in Genomic Epidemiology consortium. *Biological Psychiatry*, **2015**, 77, 749-63	7.9	48
343	Genome-wide meta-analyses of stratified depression in Generation Scotland and UK Biobank. *Translational Psychiatry*, **2018**, 8, 9	8.6	48
342	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
341	Multivariate discovery and replication of five novel loci associated with Immunoglobulin G N-glycosylation. *Nature Communications*, **2017**, 8, 447	17.4	48
340	Association of adiposity genetic variants with menarche timing in 92,105 women of European descent. *American Journal of Epidemiology*, **2013**, 178, 451-60	3.8	48
339	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
338	Genome-wide association study of biochemical traits in Korcula Island, Croatia. *Croatian Medical Journal*, **2009**, 50, 23-33	1.6	47
337	Genetic predictors of fibrin D-dimer levels in healthy adults. *Circulation*, **2011**, 123, 1864-72	16.7	47

336	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. *American Journal of Human Genetics*, **2016**, 99, 8-21	11	47
335	Differential effects of the APOE e4 allele on different domains of cognitive ability across the life-course. *European Journal of Human Genetics*, **2016**, 24, 919-23	5.3	47
334	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. *Nature Communications*, **2016**, 7, 13357	17.4	46
333	Modeling of environmental effects in genome-wide association studies identifies SLC2A2 and HP as novel loci influencing serum cholesterol levels. *PLoS Genetics*, **2010**, 6, e1000798	6	46
332	Disease mechanisms in late-onset retinal macular degeneration associated with mutation in C1QTNF5. *Human Molecular Genetics*, **2006**, 15, 1680-9	5.6	46
331	Homozygosity for Asn86Ser mutation in the CuZn-superoxide dismutase gene produces a severe clinical phenotype in a juvenile onset case of familial amyotrophic lateral sclerosis. *Journal of Medical Genetics*, **1998**, 35, 174	5.8	46
330	Tissue localization and chromosomal assignment of a serum protein that tracks the cystic fibrosis gene. *Nature*, **1985**, 315, 513-5	50.4	46
329	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
328	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. *Blood*, **2015**, 126, e19-29	2.2	45
327	Novel approach identifies SNPs in SLC2A10 and KCNK9 with evidence for parent-of-origin effect on body mass index. *PLoS Genetics*, **2014**, 10, e1004508	6	45
326	Uncovering networks from genome-wide association studies via circular genomic permutation. *G3: Genes, Genomes, Genetics*, **2012**, 2, 1067-75	3.2	45
325	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
324	Recurrence of SOX2 anophthalmia syndrome with gonosomal mosaicism in a phenotypically normal mother. *American Journal of Medical Genetics, Part A*, **2006**, 140, 636-9	2.5	44
323	The trans-ancestral genomic architecture of glycemic traits. *Nature Genetics*, **2021**, 53, 840-860	36.3	44
322	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
321	An epigenome-wide association study of sex-specific chronological ageing. *Genome Medicine*, **2019**, 12, 1	14.4	43
320	A large-scale genome-wide association study meta-analysis of cannabis use disorder. *Lancet Psychiatry,the*, **2020**, 7, 1032-1045	23.3	43
319	N-Glycan Profile and Kidney Disease in Type 1 Diabetes. *Diabetes Care*, **2018**, 41, 79-87	14.6	43

318	The Role of Recent Admixture in Forming the Contemporary West Eurasian Genomic Landscape. *Current Biology*, **2015**, 25, 2518-26	6.3	42
317	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. *American Journal of Human Genetics*, **2016**, 99, 22-39	11	42
316	Genome-wide analysis identifies molecular systems and 149 genetic loci associated with income. *Nature Communications*, **2019**, 10, 5741	17.4	42
315	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. *Nature Communications*, **2019**, 10, 376	17.4	41
314	Pedigree and genotyping quality analyses of over 10,000 DNA samples from the Generation Scotland: Scottish Family Health Study. *BMC Medical Genetics*, **2013**, 14, 38	2.1	41
313	Gel electrophoresis of amniotic fluid acetylcholinesterase as an aid to the prenatal diagnosis of fetal defects. *Clinica Chimica Acta*, **1980**, 108, 135-41	6.2	41
312	Genetic and Environmental Risk for Chronic Pain and the Contribution of Risk Variants for Major Depressive Disorder: A Family-Based Mixed-Model Analysis. *PLoS Medicine*, **2016**, 13, e1002090	11.6	41
311	A comprehensive evaluation of potential lung function associated genes in the SpiroMeta general population sample. *PLoS ONE*, **2011**, 6, e19382	3.7	41
310	An exclusion map for pre-eclampsia: assuming autosomal recessive inheritance. *American Journal of Human Genetics*, **1992**, 50, 749-57	11	41
309	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
308	Associations of autozygosity with a broad range of human phenotypes. *Nature Communications*, **2019**, 10, 4957	17.4	40
307	Stratification by smoking status reveals an association of CHRNA5-A3-B4 genotype with body mass index in never smokers. *PLoS Genetics*, **2014**, 10, e1004799	6	40
306	Concordant association of insulin degrading enzyme gene (IDE) variants with IDE mRNA, Abeta, and Alzheimer's disease. *PLoS ONE*, **2010**, 5, e8764	3.7	40
305	Variation in the dysbindin gene and normal cognitive function in three independent population samples. *Genes, Brain and Behavior*, **2009**, 8, 218-27	3.6	40
304	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
303	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. *American Journal of Epidemiology*, **2019**, 188, 1033-1054	3.8	39
302	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
301	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

300	Heavier smoking may lead to a relative increase in waist circumference: evidence for a causal relationship from a Mendelian randomisation meta-analysis. The CARTA consortium. *BMJ Open*, **2015**, 5, e008808	3	39
299	A meta-analysis of genome-wide data from five European isolates reveals an association of COL22A1, SYT1, and GABRR2 with serum creatinine level. *BMC Medical Genetics*, **2010**, 11, 41	2.1	39
298	Glycosylation of immunoglobulin G is regulated by a large network of genes pleiotropic with inflammatory diseases. *Science Advances*, **2020**, 6, eaax0301	14.3	38
297	Variation in the uric acid transporter gene SLC2A9 and its association with AAO of Parkinson's disease. *Journal of Molecular Neuroscience*, **2011**, 43, 246-50	3.3	38
296	Association of existing and new candidate genes for anxiety, depression and personality traits in older people. *Behavior Genetics*, **2010**, 40, 518-32	3.2	38
295	Rare Functional Variant in TM2D3 is Associated with Late-Onset Alzheimer's Disease. *PLoS Genetics*, **2016**, 12, e1006327	6	38
294	A meta-analysis of genome-wide association studies of epigenetic age acceleration. *PLoS Genetics*, **2019**, 15, e1008104	6	38
293	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. *Nature Communications*, **2017**, 8, 744	17.4	37
292	Do regional brain volumes and major depressive disorder share genetic architecture? A study of Generation Scotland (n=19 762), UK Biobank (n=24 048) and the English Longitudinal Study of Ageing (n=5766). *Translational Psychiatry*, **2017**, 7, e1205	8.6	37
291	Causal and synthetic associations of variants in the SERPINA gene cluster with alpha1-antitrypsin serum levels. *PLoS Genetics*, **2013**, 9, e1003585	6	37
290	A common biological basis of obesity and nicotine addiction. *Translational Psychiatry*, **2013**, 3, e308	8.6	37
289	Bayesian methods for instrumental variable analysis with genetic instruments ('Mendelian randomization'): example with urate transporter SLC2A9 as an instrumental variable for effect of urate levels on metabolic syndrome. *International Journal of Epidemiology*, **2010**, 39, 907-18	7.8	37
288	Linkage and genome-wide association analysis of obesity-related phenotypes: association of weight with the MGAT1 gene. *Obesity*, **2010**, 18, 803-8	8	37
287	Mutation screening of all 65 exons of the fibrillin-1 gene in 60 patients with Marfan syndrome: report of 12 novel mutations. *Human Mutation*, **1997**, 10, 280-9	4.7	37
286	Serum C-reactive protein in assessment of pulmonary exacerbations and antimicrobial therapy in cystic fibrosis. *Journal of Pediatrics*, **1988**, 113, 76-9	3.6	37
285	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
284	Genome-Wide Association Study on Immunoglobulin G Glycosylation Patterns. *Frontiers in Immunology*, **2018**, 9, 277	8.4	36
283	Genome-wide meta-analysis of myopia and hyperopia provides evidence for replication of 11 loci. *PLoS ONE*, **2014**, 9, e107110	3.7	36

282	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. *Human Molecular Genetics*, **2014**, 23, 2490-7	5.6	35
281	A novel mutation in the fibrillin gene (FBN1) in familial arachnodactyly. *Molecular and Cellular Probes*, **1994**, 8, 325-7	3.3	35
280	Mapping genomic loci implicates genes and synaptic biology in schizophrenia.. *Nature*, **2022**,	50.4	35
279	Genome-wide association studies identify genetic loci for low von Willebrand factor levels. *European Journal of Human Genetics*, **2016**, 24, 1035-40	5.3	34
278	Extent of linkage disequilibrium in a Sardinian sub-isolate: sampling and methodological considerations. *Human Molecular Genetics*, **2004**, 13, 25-33	5.6	34
277	Two novel mutations and a neutral polymorphism in EGF-like domains of the fibrillin gene (FBN1): SSCP screening of exons 15-21 in Marfan syndrome patients. *Human Molecular Genetics*, **1994**, 3, 373-5	5.6	34
276	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475 000 Individuals. *Circulation: Cardiovascular Genetics*, **2017**, 10,		33
275	Recent genomic heritage in Scotland. *BMC Genomics*, **2015**, 16, 437	4.5	33
274	The association between galactosylation of immunoglobulin G and body mass index. *Progress in Neuro-Psychopharmacology and Biological Psychiatry*, **2014**, 48, 20-5	5.5	33
273	Genome-wide association study for circulating tissue plasminogen activator levels and functional follow-up implicates endothelial STXBP5 and STX2. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2014**, 34, 1093-101	9.4	33
272	Genome-wide association study identifies 48 common genetic variants associated with handedness. *Nature Human Behaviour*, **2021**, 5, 59-70	12.8	33
271	Genome of The Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. *Nature Communications*, **2015**, 6, 6065	17.4	32
270	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. *Nature Human Behaviour*, **2019**, 3, 950-961	12.8	32
269	Genetic influences on oxidative stress and their association with normal cognitive ageing. *Neuroscience Letters*, **2005**, 386, 116-20	3.3	32
268	Lack of association between polymorphisms in angiotensin-converting-enzyme and methylenetetrahydrofolate reductase genes and normal cognitive ageing in humans. *Neuroscience Letters*, **2003**, 347, 175-8	3.3	32
267	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
266	A time-resolved proteomic and prognostic map of COVID-19. *Cell Systems*, **2021**, 12, 780-794.e7	10.6	32
265	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

264	Epigenetic silencing of HNF1A associates with changes in the composition of the human plasma N-glycome. *Epigenetics*, **2012**, 7, 164-72	5.7	31
263	Prenatal diagnosis of cystic fibrosis by assay of amniotic fluid microvillar enzymes. *Human Genetics*, **1984**, 65, 248-51	6.3	31
262	Modulation of genetic associations with serum urate levels by body-mass-index in humans. *PLoS ONE*, **2015**, 10, e0119752	3.7	31
261	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
260	The Uromodulin Gene Locus Shows Evidence of Pathogen Adaptation through Human Evolution. *Journal of the American Society of Nephrology: JASN*, **2016**, 27, 2983-2996	12.7	30
259	Common genetic variants explain the majority of the correlation between height and intelligence: the generation Scotland study. *Behavior Genetics*, **2014**, 44, 91-6	3.2	30
258	Marfan Database (second edition): software and database for the analysis of mutations in the human FBN1 gene. *Nucleic Acids Research*, **1997**, 25, 147-50	20.1	30
257	Quantifying the extent to which index event biases influence large genetic association studies. *Human Molecular Genetics*, **2017**, 26, 1018-1030	5.6	30
256	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. *Nature Communications*, **2021**, 12, 24	17.4	30
255	Assessing the genetic overlap between BMI and cognitive function. *Molecular Psychiatry*, **2016**, 21, 1477-82	15.1	29
254	Association of medication with the human plasma N-glycome. *Journal of Proteome Research*, **2012**, 11, 1821-31	5.6	29
253	The TCF7L2 diabetes risk variant is associated with HbA[C) levels: a genome-wide association meta-analysis. *Annals of Human Genetics*, **2010**, 74, 471-8	2.2	29
252	Variation in the uric acid transporter gene (SLC2A9) and memory performance. *Human Molecular Genetics*, **2010**, 19, 2321-30	5.6	29
251	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
250	Genome-wide association study identifies genetic risk underlying primary rhegmatogenous retinal detachment. *Human Molecular Genetics*, **2013**, 22, 3174-85	5.6	28
249	The influence of the 4 allele of the apolipoprotein E gene on childhood IQ, nonverbal reasoning in old age, and lifetime cognitive change. *Intelligence*, **2003**, 31, 85-92	3	28
248	Genetic insights into biological mechanisms governing human ovarian ageing. *Nature*, **2021**, 596, 393-397	50.4	28
247	Common variants on 6q16.2, 12q24.31 and 16p13.3 are associated with major depressive disorder. *Neuropsychopharmacology*, **2018**, 43, 2146-2153	8.7	27

246	Common variants in Mendelian kidney disease genes and their association with renal function. *Journal of the American Society of Nephrology: JASN*, **2013**, 24, 2105-17	12.7	27
245	The power of regional heritability analysis for rare and common variant detection: simulations and application to eye biometrical traits. *Frontiers in Genetics*, **2013**, 4, 232	4.5	27
244	Genome-wide association study of anthropometric traits in Korcula Island, Croatia. *Croatian Medical Journal*, **2009**, 50, 7-16	1.6	27
243	Apolipoprotein E is not related to memory abilities at 70 years of age. *Behavior Genetics*, **2009**, 39, 6-14	3.2	27
242	Meta-analysis of 49 549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant in ANGPTL4 determining fasting TG levels. *Journal of Medical Genetics*, **2016**, 53, 441-9	5.8	27
241	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
240	Shared Genetics and Couple-Associated Environment Are Major Contributors to the Risk of Both Clinical and Self-Declared Depression. *EBioMedicine*, **2016**, 14, 161-167	8.8	26
239	Network inference from glycoproteomics data reveals new reactions in the IgG glycosylation pathway. *Nature Communications*, **2017**, 8, 1483	17.4	26
238	Genome-wide analysis of epistasis in body mass index using multiple human populations. *European Journal of Human Genetics*, **2012**, 20, 857-62	5.3	26
237	Comparative assessment of methods for estimating individual genome-wide homozygosity-by-descent from human genomic data. *BMC Genomics*, **2010**, 11, 139	4.5	26
236	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
235	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
234	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. *International Journal of Epidemiology*, **2017**, 46, 894-904	7.8	25
233	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
232	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. *Genome Biology*, **2018**, 19, 87	18.3	25
231	Complement factor h autoantibodies and age-related macular degeneration **2010**, 51, 5858-63		25
230	50bp deletion in the promoter for superoxide dismutase 1 (SOD1) reduces SOD1 expression in vitro and may correlate with increased age of onset of sporadic amyotrophic lateral sclerosis. *Amyotrophic Lateral Sclerosis and Other Motor Neuron Disorders*, **2008**, 9, 229-37		25
229	Disentangling the genetics of lean mass. *American Journal of Clinical Nutrition*, **2019**, 109, 276-287	7	24

228	Genome-wide meta-analysis of common variant differences between men and women. *Human Molecular Genetics*, **2012**, 21, 4805-15	5.6	24
227	Amniotic fluid microvillar enzyme activities in the early detection of fetal abnormalities. *Prenatal Diagnosis*, **1984**, 4, 261-6	3.2	24
226	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
225	Genome-Wide Association Study of Suicide Death and Polygenic Prediction of Clinical Antecedents. *American Journal of Psychiatry*, **2020**, 177, 917-927	11.9	24
224	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
223	Rare coding variants and X-linked loci associated with age at menarche. *Nature Communications*, **2015**, 6, 7756	17.4	23
222	Salt-inducible kinase 3, SIK3, is a new gene associated with hearing. *Human Molecular Genetics*, **2014**, 23, 6407-18	5.6	23
221	Mediterranean diet in the southern Croatia - does it still exist?. *Croatian Medical Journal*, **2016**, 57, 415-424	2.6	23
220	Integrating omics datasets with the OmicsPLS package. *BMC Bioinformatics*, **2018**, 19, 371	3.6	23
219	Increased level of linkage disequilibrium in rural compared with urban communities: a factor to consider in association-study design. *American Journal of Human Genetics*, **2005**, 76, 763-72	11	22
218	The Greeks in the West: genetic signatures of the Hellenic colonisation in southern Italy and Sicily. *European Journal of Human Genetics*, **2016**, 24, 429-36	5.3	21
217	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
216	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. *Nature Communications*, **2019**, 10, 1383	17.4	21
215	Genetic Stratification to Identify Risk Groups for Alzheimer's Disease. *Journal of Alzheimer's Disease* , **2017**, 57, 275-283	4.3	21
214	Recurrent Coding Sequence Variation Explains Only A Small Fraction of the Genetic Architecture of Colorectal Cancer. *Scientific Reports*, **2015**, 5, 16286	4.9	21
213	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depressive disorder		21
212	Polygenic risk for alcohol dependence associates with alcohol consumption, cognitive function and social deprivation in a population-based cohort. *Addiction Biology*, **2016**, 21, 469-80	4.6	21
211	Genome-wide association study for refractive astigmatism reveals genetic co-determination with spherical equivalent refractive error: the CREAM consortium. *Human Genetics*, **2015**, 134, 131-46	6.3	20

210	Integrative pathway genomics of lung function and airflow obstruction. *Human Molecular Genetics*, **2015**, 24, 6836-48	5.6	20
209	Major depressive disorder and current psychological distress moderate the effect of polygenic risk for obesity on body mass index. *Translational Psychiatry*, **2015**, 5, e592	8.6	20
208	Investigating shared aetiology between type 2 diabetes and major depressive disorder in a population based cohort. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2017**, 174, 227-234	3.5	20
207	Genetic variation in complement regulators and susceptibility to age-related macular degeneration. *Immunobiology*, **2012**, 217, 158-61	3.4	20
206	Copy number variation across European populations. *PLoS ONE*, **2011**, 6, e23087	3.7	20
205	Quantifying the increase in average human heterozygosity due to urbanisation. *European Journal of Human Genetics*, **2008**, 16, 1097-102	5.3	20
204	Nicastrin gene polymorphisms, cognitive ability level and cognitive ageing. *Neuroscience Letters*, **2005**, 373, 110-4	3.3	20
203	Identification of a novel nonsense mutation in the fibrillin gene (FBN1) using nonisotopic techniques. *Human Mutation*, **1994**, 3, 159-62	4.7	20
202	Common schizophrenia alleles are enriched in mutation-intolerant genes and maintained by background selection		20
201	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
200	Dissection of major depressive disorder using polygenic risk scores for schizophrenia in two independent cohorts. *Translational Psychiatry*, **2016**, 6, e938	8.6	19
199	Genomic prediction of complex human traits: relatedness, trait architecture and predictive meta-models. *Human Molecular Genetics*, **2015**, 24, 4167-82	5.6	19
198	Genetic architecture of circulating lipid levels. *European Journal of Human Genetics*, **2011**, 19, 813-9	5.3	19
197	Genes predict village of origin in rural Europe. *European Journal of Human Genetics*, **2010**, 18, 1269-70	5.3	19
196	Heritabilities of ocular biometrical traits in two croatian isolates with extended pedigrees **2010**, 51, 737-43		19
195	No evidence of association between complement factor I genetic variant rs10033900 and age-related macular degeneration. *European Journal of Human Genetics*, **2012**, 20, 1-2; author reply 3	5.3	19
194	A linkage map of 10 loci flanking the Marfan syndrome locus on 15q: results of an International Consortium study. *Journal of Medical Genetics*, **1992**, 29, 75-80	5.8	19
193	Understanding biological mechanisms underlying adverse birth outcomes in developing countries: protocol for a prospective cohort (AMANHI bio-banking) study. *Journal of Global Health*, **2017**, 7, 021202	4.3	18

192	Homozygous loss-of-function variants in European cosmopolitan and isolate populations. *Human Molecular Genetics*, **2015**, 24, 5464-74	5.6	18
191	Quantitative immunoassays for diagnosis and carrier detection in cystic fibrosis. *Clinical Genetics*, **1982**, 21, 336-41	4	18
190	Genetic variants in RBFOX3 are associated with sleep latency. *European Journal of Human Genetics*, **2016**, 24, 1488-95	5.3	18
189	Discovery of novel heart rate-associated loci using the Exome Chip. *Human Molecular Genetics*, **2017** , 26, 2346-2363	5.6	17
188	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
187	Novel pathogenic mutations in C1QTNF5 support a dominant negative disease mechanism in late-onset retinal degeneration. *Scientific Reports*, **2017**, 7, 12147	4.9	17
186	A validation of the diathesis-stress model for depression in Generation Scotland. *Translational Psychiatry*, **2019**, 9, 25	8.6	17
185	The total burden of rare, non-synonymous exome genetic variants is not associated with childhood or late-life cognitive ability. *Proceedings of the Royal Society B: Biological Sciences*, **2014**, 281, 20140117	4.4	17
184	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. *Nature Communications*, **2020**, 11, 2542	17.4	16
183	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
182	Nut Consumption and Cardiovascular Risk Factors: A Cross-Sectional Study in a Mediterranean Population. *Nutrients*, **2017**, 9,	6.7	16
181	Individual multi-locus heterozygosity is associated with lower morning plasma cortisol concentrations. *European Journal of Endocrinology*, **2013**, 169, 59-64	6.5	16
180	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*, **2018**, 3, 4	4.8	16
179	Polygenic risk for coronary artery disease is associated with cognitive ability in older adults. *International Journal of Epidemiology*, **2016**, 45, 433-440	7.8	15
178	Regional heritability mapping method helps explain missing heritability of blood lipid traits in isolated populations. *Heredity*, **2016**, 116, 333-8	3.6	15
177	Genome-wide haplotype-based association analysis of major depressive disorder in Generation Scotland and UK Biobank. *Translational Psychiatry*, **2017**, 7, 1263	8.6	15
176	Characterisation of genome-wide association epistasis signals for serum uric acid in human population isolates. *PLoS ONE*, **2011**, 6, e23836	3.7	15
175	Global variability of the human IgG glycome. *Aging*, **2020**, 12, 15222-15259	5.6	15

174	Characterisation of an inflammation-related epigenetic score and its association with cognitive ability. *Clinical Epigenetics*, **2020**, 12, 113	7.7	15
173	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. *Genetic Epidemiology*, **2016**, 40, 404-15	2.6	15
172	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
171	Controlled trial of serum isoelectric focusing in the detection of the cystic fibrosis gene. *Human Genetics*, **1982**, 60, 30-1	6.3	14
170	Within-sibship GWAS improve estimates of direct genetic effects		14
169	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. *Genome Biology*, **2021**, 22, 194	18.3	14
168	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
167	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
166	Polygenic risk of ischemic stroke is associated with cognitive ability. *Neurology*, **2016**, 86, 611-8	6.5	13
165	DNA sequence-level analyses reveal potential phenotypic modifiers in a large family with psychiatric disorders. *Molecular Psychiatry*, **2018**, 23, 2254-2265	15.1	13
164	Automated workflow-based exploitation of pathway databases provides new insights into genetic associations of metabolite profiles. *BMC Genomics*, **2013**, 14, 865	4.5	13
163	The low single nucleotide polymorphism heritability of plasma and saliva cortisol levels. *Psychoneuroendocrinology*, **2017**, 85, 88-95	5	13
162	Inference of identity by descent in population isolates and optimal sequencing studies. *European Journal of Human Genetics*, **2013**, 21, 1140-5	5.3	13
161	Serum concentrations of a granulocyte-derived calcium-binding protein in cystic fibrosis patients and heterozygotes. *Clinica Chimica Acta*, **1987**, 170, 45-55	6.2	13
160	A monoclonal antibody-based immunoassay for human lactoferrin. *Journal of Immunological Methods*, **1985**, 84, 135-41	2.5	13
159	High-Performance Mixed Models Based Genome-Wide Association Analysis with omicABEL software. *F1000Research*, **2014**, 3, 200	3.6	13
158	Genetic and environmental determinants of stressful life events and their overlap with depression and neuroticism. *Wellcome Open Research*, **2018**, 3, 11	4.8	13
157	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

156	Low-frequency variation in TP53 has large effects on head circumference and intracranial volume. *Nature Communications*, **2019**, 10, 357	17.4	12
155	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
154	Polymorphisms in the gene encoding 11B-hydroxysteroid dehydrogenase type 1 (HSD11B1) and lifetime cognitive change. *Neuroscience Letters*, **2006**, 393, 74-7	3.3	12
153	Monoclonal antibodies to cystic fibrosis antigen. *Journal of Immunological Methods*, **1986**, 91, 117-22	2.5	12
152	Prenatal diagnosis of cystic fibrosis by methylumbelliferylguanidinobenzoate protease titration in amniotic fluid. *Prenatal Diagnosis*, **1983**, 3, 1-5	3.2	12
151	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
150	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
149	Regional variation in health is predominantly driven by lifestyle rather than genetics. *Nature Communications*, **2017**, 8, 801	17.4	11
148	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
147	Fructose-1,6-bisphosphatase: genetic and physical mapping to human chromosome 9q22.3 and evaluation in non-insulin-dependent diabetes mellitus. *Genomics*, **1995**, 29, 187-94	4.3	11
146	Is experimentally induced pain associated with socioeconomic status? Do poor people hurt more?. *Medical Science Monitor*, **2014**, 20, 1232-8	3.2	11
145	Genetic and environmental determinants of stressful life events and their overlap with depression and neuroticism. *Wellcome Open Research*, **2018**, 3, 11	4.8	11
144	SMAD7 variant rs4939827 is associated with colorectal cancer risk in Croatian population. *PLoS ONE* , **2013**, 8, e74042	3.7	11
143	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
142	The Association between Salt Taste Perception, Mediterranean Diet and Metabolic Syndrome: A Cross-Sectional Study. *Nutrients*, **2020**, 12,	6.7	11
141	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. *Circulation Genomic and Precision Medicine*, **2018**, 11, e002037	5.2	11
140	Identification of epigenome-wide DNA methylation differences between carriers of APOE 4 and APOE 2 alleles. *Genome Medicine*, **2021**, 13, 1	14.4	11
139	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

138	Current versus lifetime depression, APOE variation, and their interaction on cognitive performance in younger and older adults. *Psychosomatic Medicine*, **2015**, 77, 480-92	3.7	10
137	Runs of Homozygosity in European Populations. *American Journal of Human Genetics*, **2008**, 83, 658	11	10
136	Methylumbelliferyl-guanidinobenzoate reactive proteases and prenatal diagnosis of cystic fibrosis. *Lancet, The*, **1979**, 1, 1245-6	40	10
135	Distinguishing neural tube defects and congenital nephrosis by amniotic fluid assay. *Lancet, The*, **1980**, 1, 773	40	10
134	Soluble transferrin receptor levels are positively associated with insulin resistance but not with the metabolic syndrome or its individual components. *British Journal of Nutrition*, **2016**, 116, 1165-1174	3.6	10
133	Multi-trait genome-wide association study identifies new loci associated with optic disc parameters. *Communications Biology*, **2019**, 2, 435	6.7	10
132	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
131	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
130	Late-onset retinal degeneration pathology due to mutations in CTRP5 is mediated through HTRA1. *Aging Cell*, **2019**, 18, e13011	9.9	9
129	Sequencing of high-complexity DNA pools for identification of nucleotide and structural variants in regions associated with complex traits. *European Journal of Human Genetics*, **2012**, 20, 77-83	5.3	9
128	Fibrillin (FBN1) mutations in Marfan syndrome. *Human Mutation*, **1992**, 1, 79	4.7	9
127	Electronic health record and genome-wide genetic data in Generation Scotland participants. *Wellcome Open Research*, **2017**, 2, 85	4.8	9
126	Genome-wide association study of alcohol consumption and genetic overlap with other health-related traits in UK Biobank (N=112,117)		9
125	Insights into the genetic basis of retinal detachment. *Human Molecular Genetics*, **2020**, 29, 689-702	5.6	9
124	Historic, demographic, and genetic evidence for increased population frequencies of CCR5Delta32 mutation in Croatian Island isolates after lethal 15th century epidemics. *Croatian Medical Journal*, **2009**, 50, 34-42	1.6	8
123	Beckwith-Wiedemann syndrome in a child with chromosome 18q deletion. *Journal of Medical Genetics*, **1998**, 35, 162-4	5.8	8
122	Local exome sequences facilitate imputation of less common variants and increase power of genome wide association studies. *PLoS ONE*, **2013**, 8, e68604	3.7	8
121	Epigenetic clocks predict prevalence and incidence of leading causes of death and disease burden		8

120	Genome-wide association studies identify 137 loci for DNA methylation biomarkers of ageing		8
119	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
118	Genome-wide meta-analysis identifies novel gender specific loci associated with thyroid antibodies level in Croatians. *Genomics*, **2019**, 111, 737-743	4.3	8
117	Biochemical characterisation of the C1QTNF5 gene associated with late-onset retinal degeneration. A genetic model of age-related macular degeneration. *Advances in Experimental Medicine and Biology*, **2006**, 572, 41-8	3.6	8
116	Validation of Surrogates of Urine Osmolality in Population Studies. *American Journal of Nephrology*, **2017**, 46, 26-36	4.6	7
115	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
114	HLA-DR and pre-eclampsia in Edinburgh. *Lancet, The*, **1990**, 335, 1458-9	40	7
113	Amniotic fluid GGTP in prenatal diagnosis of cystic fibrosis: a word of warning. *Lancet, The*, **1983**, 1, 1099	40	7
112	CovidLife: a resource to understand mental health, well-being and behaviour during the COVID-19 pandemic in the UK. *Wellcome Open Research*,6, 176	4.8	7
111	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
110	Can genetics aggravate the health of isolated and remote populations? The case of gout, hyperuricaemia and osteoarthritis in Dalmatia. *Rural and Remote Health*, **2013**, 13, 2153	1.3	7
109	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals.. *Nature Genetics*, **2022**,	36.3	7
108	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
107	Exome sequencing to detect rare variants associated with general cognitive ability: a pilot study. *Twin Research and Human Genetics*, **2015**, 18, 117-25	2.2	6
106	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
105	Genome-wide association study identifies FUT8 and ESR2 as co-regulators of a bi-antennary N-linked glycan A2 (GlcNAc~2~Man~3~GlcNAc~2~) in human plasma proteins. *Nature Precedings*, **2009**,		6
104	Genetic comparison of a Croatian isolate and CEPH European founders. *Genetic Epidemiology*, **2010**, 34, 140-5	2.6	6
103	High prevalence of glaucoma in Veli Brgud, Croatia, is caused by a dominantly inherited T377M mutation in the MYOC gene. *British Journal of Ophthalmology*, **2008**, 92, 1567-8	5.5	6

102	Immunoreactive trypsin and the prenatal diagnosis of cystic fibrosis. *BJOG: an International Journal of Obstetrics and Gynaecology*, **1984**, 91, 449-52	3.7	6
101	A proteomic survival predictor for COVID-19 patients in intensive care **2022**, 1, e0000007		6
100	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*,3, 4	4.8	6
99	Global Biobank Meta-analysis Initiative: powering genetic discovery across human diseases		6
98	Sex- and age-specific genetic analysis of chronic back pain. *Pain*, **2021**, 162, 1176-1187	8	6
97	Ninety-nine independent genetic loci influencing general cognitive function include genes associated with brain health and structure (N = 280,360)		6
96	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
95	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects.. *Nature Genetics*, **2022**, 54, 581-592	36.3	6
94	Systematic Evaluation of Normalization Methods for Glycomics Data Based on Performance of Network Inference. *Metabolites*, **2020**, 10,	5.6	5
93	Whole-exome sequencing in an isolated population from the Dalmatian island of Vis. *European Journal of Human Genetics*, **2016**, 24, 1479-87	5.3	5
92	Dietary Factors Associated with Plasma Thyroid Peroxidase and Thyroglobulin Antibodies. *Nutrients* , **2017**, 9,	6.7	5
91	Fine mapping the region reveals a common intronic insertion associated to HDL-C. *Npj Aging and Mechanisms of Disease*, **2015**, 1, 15011	5.5	5
90	No evidence for genome-wide interactions on plasma fibrinogen by smoking, alcohol consumption and body mass index: results from meta-analyses of 80,607 subjects. *PLoS ONE*, **2014**, 9, e111156	3.7	5
89	Leprosy epidemics during history increased protective allele frequency of PARK2/PACRG genes in the population of the Mljet Island, Croatia. *European Journal of Medical Genetics*, **2011**, 54, e548-52	2.6	5
88	SNP mistyping in genotyping arrays--an important cause of spurious association in case-control studies. *Genetic Epidemiology*, **2011**, 35, 423-6	2.6	5
87	Historic exposure to plague and present-day frequency of CCR5del32 in two isolated island communities of Dalmatia, Croatia. *Croatian Medical Journal*, **2006**, 47, 579-84	1.6	5
86	New genetic signals for lung function highlight pathways and pleiotropy, and chronic obstructive pulmonary disease associations across multiple ancestries		5
85	A strategy to incorporate prior knowledge into correlation network cutoff selection. *Nature Communications*, **2020**, 11, 5153	17.4	5

84	Genome-wide association study of cardiac troponin I in the general population. *Human Molecular Genetics*, **2021**, 30, 2027-2039	5.6	5
83	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
82	The influence of X chromosome variants on trait neuroticism. *Molecular Psychiatry*, **2021**, 26, 483-491	15.1	5
81	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. *PLoS ONE*, **2020**, 15, e0230815	3.7	4
80	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
79	Genome-wide meta-analysis identifies novel loci associated with parathyroid hormone level. *Molecular Medicine*, **2018**, 24, 15	6.2	4
78	Mendelian randomization to assess causality between uromodulin, blood pressure and chronic kidney disease. *Kidney International*, **2021**, 100, 1282-1291	9.9	4
77	Genomic analysis of family data reveals additional genetic effects on intelligence and personality		4
76	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes		4
75	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4
74	Tissue-Specific Alteration of Metabolic Pathways Influences Glycemic Regulation		4
73	Evaluation of Shared Genetic Susceptibility to High and Low Myopia and Hyperopia. *JAMA Ophthalmology*, **2021**, 139, 601-609	3.9	4
72	Genetic and shared couple environmental contributions to smoking and alcohol use in the UK population. *Molecular Psychiatry*, **2021**, 26, 4344-4354	15.1	4
71	Identifying the Common Genetic Basis of Antidepressant Response. *Biological Psychiatry Global Open Science*, **2021**,		4
70	Genome-wide association meta-analysis for total thyroid hormone levels in Croatian population. *Journal of Human Genetics*, **2019**, 64, 473-480	4.3	3
69	Genetic Variants in the Gene Are Associated with Thyroglobulin Plasma Level in Healthy Individuals. *Thyroid*, **2019**, 29, 886-893	6.2	3
68	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
67	Probabilistic partial least squares model: Identifiability, estimation and application. *Journal of Multivariate Analysis*, **2018**, 167, 331-346	1.4	3

66	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
65	Haplotype-based association analysis of general cognitive ability in Generation Scotland, the English Longitudinal Study of Ageing, and UK Biobank. *Wellcome Open Research*, **2017**, 2, 61	4.8	3
64	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
63	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. *Genome Medicine*, **2021**, 13, 74	14.4	3
62	Using symptom-based case predictions to identify host genetic factors that contribute to COVID-19 susceptibility. *PLoS ONE*, **2021**, 16, e0255402	3.7	3
61	Genome-Wide Association Study of NAFLD Using Electronic Health Records. *Hepatology Communications*, **2021**,	6	3
60	Lost in transition--the Island of Susak (1951-2001). *Collegium Antropologicum*, **2004**, 28, 403-21	0.1	3
59	Does inbreeding affect N-glycosylation of human plasma proteins?. *Molecular Genetics and Genomics*, **2011**, 285, 427-32	3.1	2
58	Epigenetic scores for the circulating proteome as tools for disease prediction.. *ELife*, **2022**, 11,	8.9	2
57	Genome-wide association study to identify common variants associated with brachial circumference: a meta-analysis of 14 cohorts. *PLoS ONE*, **2012**, 7, e31369	3.7	2
56	TeenCovidLife: a resource to understand the impact of the COVID-19 pandemic on adolescents in Scotland. *Wellcome Open Research*,6, 277	4.8	2
55	Genetic comorbidity between major depression and cardio-metabolic disease, stratified by age at onset of major depression		2
54	Electronic Health Record and Genome-wide Genetic Data in Generation Scotland Participants		2
53	Using symptom-based case predictions to identify host genetic factors that contribute to COVID-19 susceptibility		2
52	Epigenetic scores for the circulating proteome as tools for disease prediction		2
51	Global variability of the human IgG glycome		2
50	A meta-analysis of genome-wide association studies of epigenetic age acceleration		2
49	Distinguishing pedigree relationships using multi-way identical by descent sharing and sex-specific genetic maps		2

48	Genome-wide meta-analyses of stratified depression in Generation Scotland and UK Biobank		2
47	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
46	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
45	Heritability analysis suggests comparable genetic component of mechanical pain threshold and tolerance. *Pain Medicine*, **2012**, 13, 1248-9	2.8	1
44	Immunoglobulin levels in maternal and neonatal sera from normal and abnormal pregnancies. *Journal of Perinatal Medicine*, **1988**, 16, 233-9	2.7	1
43	Lifestyle and Genetic Factors Modify Parent-of-Origin Effects on the Human Methylome. *EBioMedicine*, **2021**, 74, 103730	8.8	1
42	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*,3, 4	4.8	1
41	Genome-wide interaction study with major depression identifies novel variants associated with cognitive function. *Molecular Psychiatry*, **2021**,	15.1	1
40	Novel blood pressure locus and gene discovery using GWAS and expression datasets from blood and the kidney		1
39	Genome-wide interaction study of a proxy for stress-sensitivity and its prediction of major depressive disorder		1
38	Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution		1
37	Genetic and shared couple environmental contributions to smoking and alcohol use in the UK population		1
36	Genetic analysis identifies molecular systems and biological pathways associated with household income		1
35	Associations of Relative corticosterone deficiency with genetic variation in CYP17A1 and metabolic syndrome features		1
34	Systematic evaluation of normalization methods for glycomics data based on performance of network inference		1
33	Do Regional Brain Volumes and Major Depressive Disorder Share Genetic Architecture?: a study of Generation Scotland (n=19,762), UK Biobank (n=24,048) and the English Longitudinal Study of Ageing (n=5,766)		1
32	Genome-wide haplotype-based association analysis of major depressive disorder in Generation Scotland and UK Biobank		1
31	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

30	Contribution of common risk variants to multiple sclerosis in Orkney and Shetland. *European Journal of Human Genetics*, **2021**, 29, 1701-1709	5.3	1
29	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
28	Genome-wide methylation data improves dissection of the effect of smoking on body mass index. *PLoS Genetics*, **2021**, 17, e1009750	6	1
27	The effect of food groups and nutrients on thyroid hormone levels in healthy individuals. *Nutrition*, **2021**, 91-92, 111394	4.8	1
26	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. *Communications Biology*, **2022**, 5,	6.7	1
25	A multi-omics study of circulating phospholipid markers of blood pressure.. *Scientific Reports*, **2022**, 12, 574	4.9	0
24	A catalogue of omics biological ageing clocks reveals substantial commonality and associations with disease risk.. *Aging*, **2022**, 14, 623-659	5.6	0
23	Association of low-frequency and rare coding variants with information processing speed. *Translational Psychiatry*, **2021**, 11, 613	8.6	0
22	Association of Genetic Variant at Chromosome 12q23.1 With Neuropathic Pain Susceptibility. *JAMA Network Open*, **2021**, 4, e2136560	10.4	0
21	Variants associated with HHIP expression have sex-differential effects on lung function. *Wellcome Open Research*, **2020**, 5, 111	4.8	0
20	Genome-wide association study of susceptibility to hospitalised respiratory infections. *Wellcome Open Research*,6, 290	4.8	0
19	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
18	Variants associated with expression have sex-differential effects on lung function. *Wellcome Open Research*, **2020**, 5, 111	4.8	0
17	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
16	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
15	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus.. *Nature Communications*, **2022**, 13, 1222	17.4	0
14	Genetic regulation of post-translational modification of two distinct proteins.. *Nature Communications*, **2022**, 13, 1586	17.4	0
13	TeenCovidLife: a resource to understand the impact of the COVID-19 pandemic on adolescents in Scotland. *Wellcome Open Research*,6, 277	4.8	0

12	Genome-wide association study of copy number variation with lung function identifies a novel signal of association near BANP for forced vital capacity. *BMC Genetics*, **2016**, 17, 116	2.6
11	The PediGFR consortium: studying the genetics of complex kidney traits in children. *Nephrology Dialysis Transplantation*, **2016**, 31, 173-5	4.3
10	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
9	RuralCovidLife: Study protocol and description of the data. *Wellcome Open Research*,6, 317	4.8
8	Face covering adherence is positively associated with better mental health and wellbeing: a longitudinal analysis of the CovidLife surveys. *Wellcome Open Research*,6, 62	4.8
7	General Framework for Meta-Analysis of Haplotype Association Tests. *Genetic Epidemiology*, **2016**, 40, 244-52	2.6
6	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
5	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815	
4	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815	
3	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815	
2	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose **2020**, 15, e0230815	
1	RuralCovidLife: A new resource for the impact of the pandemic on rural Scotland.. *Wellcome Open Research*,6, 317	4.8