Panagiotis Deloukas

List of Publications by Year in Descending Order

494 papers	160,153 citations	178 h-index	399 g-index
523 ext. papers	183,922 ext. citations	17.3 avg, IF	8.26 L-index

#	Paper	IF	Citations
494	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function.. *Nature Genetics*, **2022**,	36.3	6
493	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals.. *Nature Genetics*, **2022**,	36.3	7
492	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases.. *Nature Communications*, **2022**, 13, 2408	17.4	1
491	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
490	Thyroid Function and the Risk of Alzheimer's Disease: A Mendelian Randomization Study. *Thyroid*, **2021**,	6.2	2
489	Genome-Wide association between EYA1 and Aspirin-induced peptic ulceration. *EBioMedicine*, **2021** , 74, 103728	8.8	0
488	Effect of Mastiha supplementation on NAFLD: The MAST4HEALTH Randomised, Controlled Trial. *Molecular Nutrition and Food Research*, **2021**, 65, e2001178	5.9	6
487	Thyroid Function and Mood Disorders: A Mendelian Randomization Study. *Thyroid*, **2021**, 31, 1171-1181	6.2	2
486	Nutrigenetic Interactions Might Modulate the Antioxidant and Anti-Inflammatory Status in Mastiha-Supplemented Patients With NAFLD. *Frontiers in Immunology*, **2021**, 12, 683028	8.4	4
485	Fine-mapping, trans-ancestral and genomic analyses identify causal variants, cells, genes and drug targets for type 1 diabetes. *Nature Genetics*, **2021**, 53, 962-971	36.3	28
484	Variation in Normal Range Thyroid Function Affects Serum Cholesterol Levels, Blood Pressure, and Type 2 Diabetes Risk: A Mendelian Randomization Study. *Thyroid*, **2021**, 31, 721-731	6.2	12
483	Genome-wide association study identifies 48 common genetic variants associated with handedness. *Nature Human Behaviour*, **2021**, 5, 59-70	12.8	33
482	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. *Nature Communications*, **2021**, 12, 24	17.4	30
481	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. *Human Molecular Genetics*, **2021**, 30, 393-409	5.6	6
480	Thyroid function, sex hormones and sexual function: a Mendelian randomization study. *European Journal of Epidemiology*, **2021**, 36, 335-344	12.1	6
479	A zebrafish forward genetic screen identifies an indispensable threonine residue in the kinase domain of PRKD2. *Biology Open*, **2021**, 10,	2.2	1
478	Effects of Thyroid Function on Hemostasis, Coagulation, and Fibrinolysis: A Mendelian Randomization Study. *Thyroid*, **2021**, 31, 1305-1315	6.2	2

477	Epigenome-wide association study detects a novel loci associated with central obesity in healthy subjects. *BMC Medical Genomics*, **2021**, 14, 233	3.7	0
476	COVID-19 susceptibility variants associate with blood clots, thrombophlebitis and circulatory diseases. *PLoS ONE*, **2021**, 16, e0256988	3.7	3
475	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. *Cell*, **2021**, 184, 4784-4818.e17	36.1	24
474	Thyroid Function Affects the Risk of Stroke via Atrial Fibrillation: A Mendelian Randomization Study. *Journal of Clinical Endocrinology and Metabolism*, **2020**, 105,	5.6	16
473	Genetics of educational attainment and coronary risk in Mendelian randomization studies. *European Heart Journal*, **2020**, 41, 894-895	9.5	3
472	Identification of Genetic Variants Associated With Myocardial Infarction in Saudi Arabia. *Heart Surgery Forum*, **2020**, 23, E517-E523	0.7	
471	Association of Factor V Leiden With Subsequent Atherothrombotic Events: A GENIUS-CHD Study of Individual Participant Data. *Circulation*, **2020**, 142, 546-555	16.7	5
470	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
469	Genome-wide association analysis of type 2 diabetes in the EPIC-InterAct study. *Scientific Data*, **2020**, 7, 393	8.2	7
468	The contribution of non-coding regulatory elements to cardiovascular disease. *Open Biology*, **2020**, 10, 200088	7	2
467	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. *Circulation Genomic and Precision Medicine*, **2020**, 13, e002769	5.2	1
466	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
465	Concordance for clonal hematopoiesis is limited in elderly twins. *Blood*, **2020**, 135, 269-273	2.2	18
464	Association of Birth Weight With Type 2 Diabetes and Glycemic Traits: A Mendelian Randomization Study. *JAMA Network Open*, **2019**, 2, e1910915	10.4	14
463	Genetically modulated educational attainment and coronary disease risk. *European Heart Journal*, **2019**, 40, 2413-2420	9.5	20
462	Genetic Risk Score for Coronary Disease Identifies Predispositions to Cardiovascular and Noncardiovascular Diseases. *Journal of the American College of Cardiology*, **2019**, 73, 2932-2942	15.1	26
461	Dairy Intake and Body Composition and Cardiometabolic Traits among Adults: Mendelian Randomization Analysis of 182041 Individuals from 18 Studies. *Clinical Chemistry*, **2019**, 65, 751-760	5.5	11
460	Subsequent Event Risk in Individuals With Established Coronary Heart Disease. *Circulation Genomic and Precision Medicine*, **2019**, 12, e002470	5.2	13

459	Association of Chromosome 9p21 With Subsequent Coronary Heart Disease Events. *Circulation Genomic and Precision Medicine*, **2019**, 12, e002471	5.2	14
458	Genome-wide survey of copy number variants finds MAPT duplications in progressive supranuclear palsy. *Movement Disorders*, **2019**, 34, 1049-1059	7	15
457	Epigenome-Wide Association Study (EWAS) of Blood Lipids in Healthy Population from STANISLAS Family Study (SFS). *International Journal of Molecular Sciences*, **2019**, 20,	6.3	11
456	Dissecting features of epigenetic variants underlying cardiometabolic risk using full-resolution epigenome profiling in regulatory elements. *Nature Communications*, **2019**, 10, 1209	17.4	9
455	Mendelian randomisation analyses find pulmonary factors mediate the effect of height on coronary artery disease. *Communications Biology*, **2019**, 2, 119	6.7	18
454	First genotype-phenotype study reveals HLA-DQ1 insertion heterogeneity in high-resolution manometry achalasia subtypes. *United European Gastroenterology Journal*, **2019**, 7, 45-51	5.3	4
453	Population-based identity-by-descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2019**, 180, 223-231	3.5	2
452	Genome-wide meta-analysis of macronutrient intake of 91,114 European ancestry participants from the cohorts for heart and aging research in genomic epidemiology consortium. *Molecular Psychiatry*, **2019**, 24, 1920-1932	15.1	30
451	Potential Interplay between Dietary Saturated Fats and Genetic Variants of the NLRP3 Inflammasome to Modulate Insulin Resistance and Diabetes Risk: Insights from a Meta-Analysis of 19005 Individuals. *Molecular Nutrition and Food Research*, **2019**, 63, e1900226	5.9	11
450	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates A, tau, immunity and lipid processing. *Nature Genetics*, **2019**, 51, 414-430	36.3	917
449	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
448	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. *Journal of the American College of Cardiology*, **2019**, 73, 58-66	15.1	86
447	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol Use. *Biological Psychiatry*, **2019**, 85, 946-955	7.9	35
446	Effect of CYP4F2, VKORC1, and CYP2C9 in Influencing Coumarin Dose: A Single-Patient Data Meta-Analysis in More Than 15,000 Individuals. *Clinical Pharmacology and Therapeutics*, **2019**, 105, 1477-1491	6.1	12
445	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
444	Emerging applications of genome-editing technology to examine functionality of GWAS-associated variants for complex traits. *Physiological Genomics*, **2018**, 50, 510-522	3.6	13
443	Human candidate gene polymorphisms and risk of severe malaria in children in Kilifi, Kenya: a case-control association study. *Lancet Haematology,the*, **2018**, 5, e333-e345	14.6	38
442	Joint genome-wide association study of progressive supranuclear palsy identifies novel susceptibility loci and genetic correlation to neurodegenerative diseases. *Molecular Neurodegeneration*, **2018**, 13, 41	19	41

441	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. *Cell*, **2018**, 173, 1705-1715.e16	56.2	360
440	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
439	A transnational collaborative network dedicated to the study and applications of the vascular endothelial growth factor-A in medical practice: the VEGF Consortium. *Clinical Chemistry and Laboratory Medicine*, **2018**, 56, 83-86	5.9	0
438	Investigation of common, low-frequency and rare genome-wide variation in anorexia nervosa. *Molecular Psychiatry*, **2018**, 23, 1169-1180	15.1	24
437	Genomic Risk Prediction of Coronary Artery Disease in 480,000 Adults: Implications for Primary Prevention. *Journal of the American College of Cardiology*, **2018**, 72, 1883-1893	15.1	285
436	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health. *Clinical Epigenetics*, **2018**, 10, 126	7.7	56
435	Genome-wide association study of nevirapine hypersensitivity in a sub-Saharan African HIV-infected population. *Journal of Antimicrobial Chemotherapy*, **2017**, 72, 1152-1162	5.1	33
434	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
433	Epigenetic Patterns in Blood Associated With Lipid Traits Predict Incident Coronary Heart Disease Events and Are Enriched for Results From Genome-Wide Association Studies. *Circulation: Cardiovascular Genetics*, **2017**, 10,		72
432	Meta-analysis identifies novel risk loci and yields systematic insights into the biology of male-pattern baldness. *Nature Communications*, **2017**, 8, 14694	17.4	36
431	Genetic invalidation of Lp-PLA as a therapeutic target: Large-scale study of five functional Lp-PLA-lowering alleles. *European Journal of Preventive Cardiology*, **2017**, 24, 492-504	3.9	16
430	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. *Journal of the American College of Cardiology*, **2017**, 69, 823-836	15.1	146
429	Discovery of novel heart rate-associated loci using the Exome Chip. *Human Molecular Genetics*, **2017**, 26, 2346-2363	5.6	17
428	Loss of Cardioprotective Effects at the Locus as a Result of Gene-Smoking Interactions. *Circulation*, **2017**, 135, 2336-2353	16.7	36
427	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
426	Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. *Circulation Research*, **2017**, 120, 341-353	15.7	97
425	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. *Nature Genetics*, **2017**, 49, 1113-1119	36.3	184
424	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. *Diabetes*, **2017**, 66, 2888-2902	8.9	414

423	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. *Diabetes*, **2017**, 66, 2019-2032	0.9	29
422	Higher Nevus Count Exhibits a Distinct DNA Methylation Signature in Healthy Human Skin: Implications for Melanoma. *Journal of Investigative Dermatology*, **2017**, 137, 910-920	4.3	16
421	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. *Nature*, **2017**, 541, 81-86	50.4	511
420	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
419	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. *Nature Communications*, **2017**, 8, 744	17.4	37
418	Impact of Selection Bias on Estimation of Subsequent Event Risk. *Circulation: Cardiovascular Genetics*, **2017**, 10,		19
417	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475 000 Individuals. *Circulation: Cardiovascular Genetics*, **2017**, 10,		33
416	Genome-wide association meta-analysis of fish and EPA+DHA consumption in 17 US and European cohorts. *PLoS ONE*, **2017**, 12, e0186456	3.7	15
415	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
414	Cohort-specific imputation of gene expression improves prediction of warfarin dose for African Americans. *Genome Medicine*, **2017**, 9, 98	14.4	5
413	Novel genetic loci associated with long-term deterioration in blood lipid concentrations and coronary artery disease in European adults. *International Journal of Epidemiology*, **2017**, 46, 1211-1222	7.8	12
412	Association analyses based on false discovery rate implicate new loci for coronary artery disease. *Nature Genetics*, **2017**, 49, 1385-1391	36.3	361
411	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
410	Excessive burden of lysosomal storage disorder gene variants in Parkinson's disease. *Brain*, **2017**, 140, 3191-3203	11.2	209
409	Effect of Genetic Variability in the , , and Genes on Liver mRNA Levels and Warfarin Response. *Frontiers in Pharmacology*, **2017**, 8, 323	5.6	9
408	Evaluating the glucose raising effect of established loci via a genetic risk score. *PLoS ONE*, **2017**, 12, e0186669	3.7	5
407	A novel interaction between the FLJ33534 locus and smoking in obesity: a genome-wide study of 14 131 Pakistani adults. *International Journal of Obesity*, **2016**, 40, 186-90	5.5	13
406	A novel Alzheimer disease locus located near the gene encoding tau protein. *Molecular Psychiatry*, **2016**, 21, 108-17	15.1	175

405	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. *Nature Communications*, **2016**, 7, 13357	17.4	46
404	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
403	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. *Nature Genetics*, **2016**, 48, 1162-70	36.3	152
402	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
401	Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. *Journal of the American Heart Association*, **2016**, 5,	6	34
400	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. *Scientific Reports*, **2016**, 6, 35278	4.9	18
399	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. *Science Translational Medicine*, **2016**, 8, 341ra76	17.5	77
398	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. *Nature Genetics*, **2016**, 48, 1462-1472	36.3	198
397	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
396	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. *American Journal of Human Genetics*, **2016**, 99, 40-55	11	61
395	Integrative DNA methylome analysis of pan-cancer biomarkers in cancer discordant monozygotic twin-pairs. *Clinical Epigenetics*, **2016**, 8, 7	7.7	21
394	Polymorphism in a lincRNA Associates with a Doubled Risk of Pneumococcal Bacteremia in Kenyan Children. *American Journal of Human Genetics*, **2016**, 98, 1092-1100	11	30
393	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. *Science*, **2016**, 351, 1166-71	33.3	325
392	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180
391	A multi-factorial analysis of response to warfarin in a UK prospective cohort. *Genome Medicine*, **2016**, 8, 2	14.4	32
390	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. *Nature Communications*, **2016**, 7, 10023	17.4	295
389	Exome-wide analysis of rare coding variation identifies novel associations with COPD and airflow limitation in MOCS3, IFIT3 and SERPINA12. *Thorax*, **2016**, 71, 501-9	7.3	18
388	Loss of VPS13C Function in Autosomal-Recessive Parkinsonism Causes Mitochondrial Dysfunction and Increases PINK1/Parkin-Dependent Mitophagy. *American Journal of Human Genetics*, **2016**, 98, 500-513	11	225

387	Polygenic risk of ischemic stroke is associated with cognitive ability. *Neurology*, **2016**, 86, 611-8	6.5	13
386	Lifestyle may modify the glucose-raising effect of genetic loci. A study in the Greek population. *Nutrition, Metabolism and Cardiovascular Diseases*, **2016**, 26, 201-6	4.5	2
385	The genetic associations of acute anterior uveitis and their overlap with the genetics of ankylosing spondylitis. *Genes and Immunity*, **2016**, 17, 46-51	4.4	27
384	Admixture into and within sub-Saharan Africa. *ELife*, **2016**, 5,	8.9	77
383	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
382	Higher chylomicron remnants and LDL particle numbers associate with CD36 SNPs and DNA methylation sites that reduce CD36. *Journal of Lipid Research*, **2016**, 57, 2176-2184	6.3	20
381	Common and Rare Genetic Variation in CCR2, CCR5, or CX3CR1 and Risk of Atherosclerotic Coronary Heart Disease and Glucometabolic Traits. *Circulation: Cardiovascular Genetics*, **2016**, 9, 250-8		14
380	Coding Variation in ANGPTL4, LPL, and SVEP1 and the Risk of Coronary Disease. *New England Journal of Medicine*, **2016**, 374, 1134-44	59.2	325
379	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. *American Journal of Human Genetics*, **2016**, 98, 857-868	11	14
378	Genome-wide association study identifies 74 loci associated with educational attainment. *Nature*, **2016**, 533, 539-42	50.4	850
377	Association Between Low-Density Lipoprotein Cholesterol-Lowering Genetic Variants and Risk of Type 2 Diabetes: A Meta-analysis. *JAMA - Journal of the American Medical Association*, **2016**, 316, 1383-1391	27.4	225
376	Analysis with the exome array identifies multiple new independent variants in lipid loci. *Human Molecular Genetics*, **2016**, 25, 4094-4106	5.6	14
375	Replication of Associations of Genetic Loci Outside the HLA Region With Susceptibility to Anti-Cyclic Citrullinated Peptide-Negative Rheumatoid Arthritis. *Arthritis and Rheumatology*, **2016**, 68, 1603-13	9.5	24
374	DNA methylation of lipid-related genes affects blood lipid levels. *Circulation: Cardiovascular Genetics*, **2015**, 8, 334-42		122
373	Biological interpretation of genome-wide association studies using predicted gene functions. *Nature Communications*, **2015**, 6, 5890	17.4	489
372	A common variant mapping to CACNA1A is associated with susceptibility to exfoliation syndrome. *Nature Genetics*, **2015**, 47, 387-92	36.3	70
371	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	50.4	119
370	Gene-Environment Interactions of Circadian-Related Genes for Cardiometabolic Traits. *Diabetes Care*, **2015**, 38, 1456-66	14.6	36

369	NeuroX, a fast and efficient genotyping platform for investigation of neurodegenerative diseases. *Neurobiology of Aging*, **2015**, 36, 1605.e7-12	5.6	70
368	Predicting genome-wide DNA methylation using methylation marks, genomic position, and DNA regulatory elements. *Genome Biology*, **2015**, 16, 14	18.3	108
367	Meta-analysis of 65,734 individuals identifies TSPAN15 and SLC44A2 as two susceptibility loci for venous thromboembolism. *American Journal of Human Genetics*, **2015**, 96, 532-42	11	163
366	Quantitative interaction proteomics of neurodegenerative disease proteins. *Cell Reports*, **2015**, 11, 1134-46	1666	62
365	Epigenome-wide association study (EWAS) of BMI, BMI change and waist circumference in African American adults identifies multiple replicated loci. *Human Molecular Genetics*, **2015**, 24, 4464-79	5.6	219
364	Genetically determined height and coronary artery disease. *New England Journal of Medicine*, **2015**, 372, 1608-18	59.2	152
363	Novel insights into the genetics of smoking behaviour, lung function, and chronic obstructive pulmonary disease (UK BiLEVE): a genetic association study in UK Biobank. *Lancet Respiratory Medicine,the*, **2015**, 3, 769-81	35.1	245
362	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. *Nature Genetics*, **2015**, 47, 1282-1293	36.3	223
361	Circulating brain-derived neurotrophic factor concentrations and the risk of cardiovascular disease in the community. *Journal of the American Heart Association*, **2015**, 4, e001544	6	70
360	Common polygenic variation enhances risk prediction for Alzheimer's disease. *Brain*, **2015**, 138, 3673-84	11.2	227
359	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. *Nature Genetics*, **2015**, 47, 1121-1130	36.3	1290
358	Consumption of meat is associated with higher fasting glucose and insulin concentrations regardless of glucose and insulin genetic risk scores: a meta-analysis of 50,345 Caucasians. *American Journal of Clinical Nutrition*, **2015**, 102, 1266-78	7	51
357	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. *Nature Genetics*, **2015**, 47, 1415-25	36.3	292
356	Habitual sleep duration is associated with BMI and macronutrient intake and may be modified by CLOCK genetic variants. *American Journal of Clinical Nutrition*, **2015**, 101, 135-43	7	75
355	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. *Molecular Psychiatry*, **2015**, 20, 647-656	15.1	167
354	Population whole-genome bisulfite sequencing across two tissues highlights the environment as the principal source of human methylome variation. *Genome Biology*, **2015**, 16, 290	18.3	70
353	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
352	Associations between Potentially Modifiable Risk Factors and Alzheimer Disease: A Mendelian Randomization Study. *PLoS Medicine*, **2015**, 12, e1001841; discussion e1001841	11.6	115

351	Fine mapping of type 1 diabetes susceptibility loci and evidence for colocalization of causal variants with lymphoid gene enhancers. *Nature Genetics*, **2015**, 47, 381-6	36.3	414
350	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25,000 subjects. *Molecular Psychiatry*, **2015**, 20, 735-43	15.1	39
349	Characterization of functional methylomes by next-generation capture sequencing identifies novel disease-associated variants. *Nature Communications*, **2015**, 6, 7211	17.4	66
348	Shared genetic basis for migraine and ischemic stroke: A genome-wide analysis of common variants. *Neurology*, **2015**, 84, 2132-45	6.5	71
347	Investigation of association between hip osteoarthritis susceptibility loci and radiographic proximal femur shape. *Arthritis and Rheumatology*, **2015**, 67, 2076-84	9.5	21
346	Gene dietary pattern interactions in obesity: analysis of up to 68 317 adults of European ancestry. *Human Molecular Genetics*, **2015**, 24, 4728-38	5.6	68
345	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. *Nature Communications*, **2015**, 6, 8658	17.4	79
344	Rare coding variants and X-linked loci associated with age at menarche. *Nature Communications*, **2015**, 6, 7756	17.4	23
343	Glucose-6-phosphate dehydrogenase deficiency and the risk of malaria and other diseases in children in Kenya: a case-control and a cohort study. *Lancet Haematology,the*, **2015**, 2, e437-44	14.6	49
342	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
341	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
340	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. *Nature Communications*, **2015**, 6, 5897	17.4	147
339	Low copy number of the salivary amylase gene predisposes to obesity. *Nature Genetics*, **2014**, 46, 492-7	36.3	177
338	DNA methylation and body-mass index: a genome-wide analysis. *Lancet, The*, **2014**, 383, 1990-8	40	569
337	Multi-ethnic fine-mapping of 14 central adiposity loci. *Human Molecular Genetics*, **2014**, 23, 4738-44	5.6	38
336	Variability in working memory performance explained by epistasis vs polygenic scores in the ZNF804A pathway. *JAMA Psychiatry*, **2014**, 71, 778-785	14.5	24
335	Genetics of rheumatoid arthritis contributes to biology and drug discovery. *Nature*, **2014**, 506, 376-81	50.4	1426
334	Genetic comorbidities in Parkinson's disease. *Human Molecular Genetics*, **2014**, 23, 831-41	5.6	49

333	Genome-wide estimates of inbreeding in unrelated individuals and their association with cognitive ability. *European Journal of Human Genetics*, **2014**, 22, 386-90	5.3	16
332	A gene pathway analysis highlights the role of cellular adhesion molecules in multiple sclerosis susceptibility. *Genes and Immunity*, **2014**, 15, 126-32	4.4	23
331	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. *Nature Communications*, **2014**, 5, 4926	17.4	121
330	Allelic expression mapping across cellular lineages to establish impact of non-coding SNPs. *Molecular Systems Biology*, **2014**, 10, 754	12.2	16
329	Inactivating mutations in NPC1L1 and protection from coronary heart disease. *New England Journal of Medicine*, **2014**, 371, 2072-82	59.2	307
328	Novel genetic approach to investigate the role of plasma secretory phospholipase A2 (sPLA2)-V isoenzyme in coronary heart disease: modified Mendelian randomization analysis using PLA2G5 expression levels. *Circulation: Cardiovascular Genetics*, **2014**, 7, 144-50		21
327	Effects of long-term averaging of quantitative blood pressure traits on the detection of genetic associations. *American Journal of Human Genetics*, **2014**, 95, 49-65	11	52
326	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. *Nature Genetics*, **2014**, 46, 989-93	36.3	1261
325	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. *Nature*, **2014**, 514, 92-97	50.4	401
324	Obesity accelerates epigenetic aging of human liver. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 15538-43	11.5	456
323	Whole-exome sequencing in an extended family with myocardial infarction unmasks familial hypercholesterolemia. *BMC Cardiovascular Disorders*, **2014**, 14, 108	2.3	18
322	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
321	The correlation between reading and mathematics ability at age twelve has a substantial genetic component. *Nature Communications*, **2014**, 5, 4204	17.4	54
320	Quality control and conduct of genome-wide association meta-analyses. *Nature Protocols*, **2014**, 9, 1192-212	28.8	278
319	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
318	A genome-wide association analysis of a broad psychosis phenotype identifies three loci for further investigation. *Biological Psychiatry*, **2014**, 75, 386-97	7.9	36
317	Expression of phosphofructokinase in skeletal muscle is influenced by genetic variation and associated with insulin sensitivity. *Diabetes*, **2014**, 63, 1154-65	0.9	25
316	Loss-of-function mutations in APOC3, triglycerides, and coronary disease. *New England Journal of Medicine*, **2014**, 371, 22-31	59.2	721

315	The sex-specific associations of the aromatase gene with Alzheimer's disease and its interaction with IL10 in the Epistasis Project. *European Journal of Human Genetics*, **2014**, 22, 216-20	5.3	32
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4	Genomic risk prediction of coronary artery disease in nearly 500,000 adults: implications for early screening and primary prevention		17
3	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health		2
2	Tissue-Specific Alteration of Metabolic Pathways Influences Glycemic Regulation		4
1	Discovery and systematic characterization of risk variants and genes for coronary artery disease in over a million participants		5