Panagiotis Deloukas

List of Publications by Citations

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	Initial sequencing and analysis of the human genome. *Nature*, **2001**, 409, 860-921	50.4	17366
493	Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. *Nature*, **2007**, 447, 661-78	50.4	7801
492	The International HapMap Project. *Nature*, **2003**, 426, 789-96	50.4	5039
491	A haplotype map of the human genome. *Nature*, **2005**, 437, 1299-320	50.4	4818
490	A second generation human haplotype map of over 3.1 million SNPs. *Nature*, **2007**, 449, 851-61	50.4	3647
489	Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*, **2010**, 466, 707-13	50.4	2742
488	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
487	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics*, **2010**, 42, 937-48	36.3	2267
486	Integrating common and rare genetic variation in diverse human populations. *Nature*, **2010**, 467, 52-8	50.4	2135
485	Genome-wide association defines more than 30 distinct susceptibility loci for Crohn's disease. *Nature Genetics*, **2008**, 40, 955-62	36.3	2092
484	Genome-wide association study identifies variants at CLU and PICALM associated with Alzheimer's disease. *Nature Genetics*, **2009**, 41, 1088-93	36.3	2018
483	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. *Nature*, **2011**, 476, 214-9	50.4	1948
482	Discovery and refinement of loci associated with lipid levels. *Nature Genetics*, **2013**, 45, 1274-1283	36.3	1904
481	Replication of genome-wide association signals in UK samples reveals risk loci for type 2 diabetes. *Science*, **2007**, 316, 1336-41	33.3	1823
480	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
479	Genomewide association analysis of coronary artery disease. *New England Journal of Medicine*, **2007** , 357, 443-53	59.2	1608
478	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. *Nature* , **2011**, 478, 103-9	50.4	1564

477	Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature*, **2010**, 467, 832-8	50.4	1514
476	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. *Nature Genetics*, **2012**, 44, 981-90	36.3	1482
475	Genetics of rheumatoid arthritis contributes to biology and drug discovery. *Nature*, **2014**, 506, 376-81	50.4	1426
474	Common variants at ABCA7, MS4A6A/MS4A4E, EPHA1, CD33 and CD2AP are associated with Alzheimer's disease. *Nature Genetics*, **2011**, 43, 429-35	36.3	1421
473	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. *Nature Genetics*, **2011**, 43, 333-8	36.3	1394
472	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. *Nature Genetics*, **2009**, 41, 25-34	36.3	1368
471	Genome-wide detection and characterization of positive selection in human populations. *Nature*, **2007**, 449, 913-8	50.4	1367
470	Relative impact of nucleotide and copy number variation on gene expression phenotypes. *Science*, **2007**, 315, 848-53	33.3	1361
469	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
468	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. *Nature Genetics*, **2015**, 47, 1121-1130	36.3	1290
467	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
466	Large-scale association analysis identifies new risk loci for coronary artery disease. *Nature Genetics*, **2013**, 45, 25-33	36.3	1172
465	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. *Nature Genetics*, **2013**, 45, 1150-9	36.3	1153
464	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. *Nature Genetics*, **2007**, 39, 1329-37	36.3	1130
463	Convergent adaptation of human lactase persistence in Africa and Europe. *Nature Genetics*, **2007**, 39, 31-40	36.3	1073
462	Common variants near MC4R are associated with fat mass, weight and risk of obesity. *Nature Genetics*, **2008**, 40, 768-75	36.3	1048
461	Genome-wide association study identifies eight loci associated with blood pressure. *Nature Genetics*, **2009**, 41, 666-76	36.3	970
460	Population genomics of human gene expression. *Nature Genetics*, **2007**, 39, 1217-24	36.3	936

459	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. *Nature Genetics*, **2013**, 45, 1353-60	36.3	934
458	Sequence variants in the autophagy gene IRGM and multiple other replicating loci contribute to Crohn's disease susceptibility. *Nature Genetics*, **2007**, 39, 830-2	36.3	933
457	A Gene Map of the Human Genome. *Science*, **1996**, 274, 540-546	33.3	924
456	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
455	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
454	Genome-wide association of early-onset myocardial infarction with single nucleotide polymorphisms and copy number variants. *Nature Genetics*, **2009**, 41, 334-41	36.3	884
453	Genome-wide association study identifies 74 loci associated with educational attainment. *Nature*, **2016**, 533, 539-42	50.4	850
452	The fine-scale structure of recombination rate variation in the human genome. *Science*, **2004**, 304, 581-4	33.3	796
451	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
450	A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. *Nature Genetics*, **2010**, 42, 985-90	36.3	773
449	Imputation of sequence variants for identification of genetic risks for Parkinson's disease: a meta-analysis of genome-wide association studies. *Lancet, The*, **2011**, 377, 641-9	40	733
448	Human metabolic individuality in biomedical and pharmaceutical research. *Nature*, **2011**, 477, 54-60	50.4	728
447	Multiple common variants for celiac disease influencing immune gene expression. *Nature Genetics*, **2010**, 42, 295-302	36.3	727
446	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
445	Loss-of-function mutations in APOC3, triglycerides, and coronary disease. *New England Journal of Medicine*, **2014**, 371, 22-31	59.2	721
444	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
443	HLA-A*3101 and carbamazepine-induced hypersensitivity reactions in Europeans. *New England Journal of Medicine*, **2011**, 364, 1134-43	59.2	689
442	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. *Nature Genetics*, **2012**, 44, 1341-8	36.3	681

441	Genome-wide association analysis identifies 20 loci that influence adult height. *Nature Genetics*, **2008**, 40, 575-83	36.3	654
440	Interaction between ERAP1 and HLA-B27 in ankylosing spondylitis implicates peptide handling in the mechanism for HLA-B27 in disease susceptibility. *Nature Genetics*, **2011**, 43, 761-7	36.3	646
439	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. *Nature*, **2010**, 464, 713-20	50.4	639
438	Genetically distinct subsets within ANCA-associated vasculitis. *New England Journal of Medicine*, **2012**, 367, 214-23	59.2	627
437	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
436	A high-resolution HLA and SNP haplotype map for disease association studies in the extended human MHC. *Nature Genetics*, **2006**, 38, 1166-72	36.3	618
435	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
434	Common regulatory variation impacts gene expression in a cell type-dependent manner. *Science*, **2009**, 325, 1246-50	33.3	607
433	Common variants associated with plasma triglycerides and risk for coronary artery disease. *Nature Genetics*, **2013**, 45, 1345-52	36.3	597
432	Variants in MTNR1B influence fasting glucose levels. *Nature Genetics*, **2009**, 41, 77-81	36.3	584
431	Mapping cis- and trans-regulatory effects across multiple tissues in twins. *Nature Genetics*, **2012**, 44, 1084-9	36.3	572
430	DNA methylation and body-mass index: a genome-wide analysis. *Lancet, The*, **2014**, 383, 1990-8	40	569
429	Twenty bone-mineral-density loci identified by large-scale meta-analysis of genome-wide association studies. *Nature Genetics*, **2009**, 41, 1199-206	36.3	566
428	GWAS of 126,559 individuals identifies genetic variants associated with educational attainment. *Science*, **2013**, 340, 1467-71	33.3	563
427	Identification of multiple risk variants for ankylosing spondylitis through high-density genotyping of immune-related loci. *Nature Genetics*, **2013**, 45, 730-8	36.3	551
426	Human aging-associated DNA hypermethylation occurs preferentially at bivalent chromatin domains. *Genome Research*, **2010**, 20, 434-9	9.7	547
425	Signatures of mutation and selection in the cancer genome. *Nature*, **2010**, 463, 893-8	50.4	538
424	Bone mineral density, osteoporosis, and osteoporotic fractures: a genome-wide association study. *Lancet, The*, **2008**, 371, 1505-12	40	538

423	Dense genotyping identifies and localizes multiple common and rare variant association signals in celiac disease. *Nature Genetics*, **2011**, 43, 1193-201	36.3	535
422	A genome-wide association study in Europeans and South Asians identifies five new loci for coronary artery disease. *Nature Genetics*, **2011**, 43, 339-44	36.3	528
421	Newly identified genetic risk variants for celiac disease related to the immune response. *Nature Genetics*, **2008**, 40, 395-402	36.3	524
420	A genome-wide association study for celiac disease identifies risk variants in the region harboring IL2 and IL21. *Nature Genetics*, **2007**, 39, 827-9	36.3	518
419	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. *Nature*, **2017**, 541, 81-86	50.4	511
418	Epigenome-wide scans identify differentially methylated regions for age and age-related phenotypes in a healthy ageing population. *PLoS Genetics*, **2012**, 8, e1002629	6	501
417	Highly parallel SNP genotyping. *Cold Spring Harbor Symposia on Quantitative Biology*, **2003**, 68, 69-78	3.9	496
416	Biological interpretation of genome-wide association studies using predicted gene functions. *Nature Communications*, **2015**, 6, 5890	17.4	489
415	Genome-wide association study of ankylosing spondylitis identifies non-MHC susceptibility loci. *Nature Genetics*, **2010**, 42, 123-7	36.3	484
414	A genome-wide association study confirms VKORC1, CYP2C9, and CYP4F2 as principal genetic determinants of warfarin dose. *PLoS Genetics*, **2009**, 5, e1000433	6	484
413	A physical map of 30,000 human genes. *Science*, **1998**, 282, 744-6	33.3	472
412	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
411	The largest prospective warfarin-treated cohort supports genetic forecasting. *Blood*, **2009**, 113, 784-92	2.2	443
410	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
409	High-density genetic mapping identifies new susceptibility loci for rheumatoid arthritis. *Nature Genetics*, **2012**, 44, 1336-40	36.3	436
408	A genome-wide meta-analysis identifies 22 loci associated with eight hematological parameters in the HaemGen consortium. *Nature Genetics*, **2009**, 41, 1182-90	36.3	433
407	Genome-wide associations of gene expression variation in humans. *PLoS Genetics*, **2005**, 1, e78	6	431
406	Genome-wide association study identifies five loci associated with lung function. *Nature Genetics*, **2010**, 42, 36-44	36.3	430

405	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. *Diabetes*, **2017**, 66, 2888-2902	39	414
404	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
403	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
402	Genome-wide association study of ulcerative colitis identifies three new susceptibility loci, including the HNF4A region. *Nature Genetics*, **2009**, 41, 1330-4	36.3	411
401	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. *Nature Genetics*, **2011**, 43, 984-9	36.3	406
400	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. *Nature*, **2014**, 514, 92-97	50.4	401
399	Common VKORC1 and GGCX polymorphisms associated with warfarin dose. *Pharmacogenomics Journal*, **2005**, 5, 262-70	3.5	396
398	The metabochip, a custom genotyping array for genetic studies of metabolic, cardiovascular, and anthropometric traits. *PLoS Genetics*, **2012**, 8, e1002793	6	395
397	Genome-wide association scan meta-analysis identifies three Loci influencing adiposity and fat distribution. *PLoS Genetics*, **2009**, 5, e1000508	6	393
396	New susceptibility locus for coronary artery disease on chromosome 3q22.3. *Nature Genetics*, **2009**, 41, 280-2	36.3	389
395	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
394	Association analyses based on false discovery rate implicate new loci for coronary artery disease. *Nature Genetics*, **2017**, 49, 1385-1391	36.3	361
393	Patterns of cis regulatory variation in diverse human populations. *PLoS Genetics*, **2012**, 8, e1002639	6	361
392	Genome-wide association study identifies genes for biomarkers of cardiovascular disease: serum urate and dyslipidemia. *American Journal of Human Genetics*, **2008**, 82, 139-49	11	361
391	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. *Cell*, **2018**, 173, 1705-1715.e16	56.2	360
390	Genetic determinants of ulcerative colitis include the ECM1 locus and five loci implicated in Crohn's disease. *Nature Genetics*, **2008**, 40, 710-2	36.3	353
389	Bayesian refinement of association signals for 14 loci in 3 common diseases. *Nature Genetics*, **2012**, 44, 1294-301	36.3	347
388	A first-generation linkage disequilibrium map of human chromosome 22. *Nature*, **2002**, 418, 544-8	50.4	342

387	The architecture of gene regulatory variation across multiple human tissues: the MuTHER study. *PLoS Genetics*, **2011**, 7, e1002003	6	336
386	Integrating ethics and science in the International HapMap Project. *Nature Reviews Genetics*, **2004**, 5, 467-75	30.1	334
385	New gene functions in megakaryopoiesis and platelet formation. *Nature*, **2011**, 480, 201-8	50.4	330
384	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
383	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. *Science*, **2016**, 351, 1166-71	33.3	325
382	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
381	Common variants near ATM are associated with glycemic response to metformin in type 2 diabetes. *Nature Genetics*, **2011**, 43, 117-20	36.3	319
380	Genetic variants influencing circulating lipid levels and risk of coronary artery disease. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2010**, 30, 2264-76	9.4	318
379	Genome-wide association study identifies a variant in HDAC9 associated with large vessel ischemic stroke. *Nature Genetics*, **2012**, 44, 328-33	36.3	314
378	Common variants at 10 genomic loci influence hemoglobin A(C) levels via glycemic and nonglycemic pathways. *Diabetes*, **2010**, 59, 3229-39	0.9	314
377	Repeated replication and a prospective meta-analysis of the association between chromosome 9p21.3 and coronary artery disease. *Circulation*, **2008**, 117, 1675-84	16.7	312
376	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
375	Inactivating mutations in NPC1L1 and protection from coronary heart disease. *New England Journal of Medicine*, **2014**, 371, 2072-82	59.2	307
374	Association of warfarin dose with genes involved in its action and metabolism. *Human Genetics*, **2007**, 121, 23-34	6.3	305
373	Genome-wide and fine-resolution association analysis of malaria in West Africa. *Nature Genetics*, **2009**, 41, 657-65	36.3	297
372	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. *Nature Communications*, **2016**, 7, 10023	17.4	295
371	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. *Nature Genetics*, **2015**, 47, 1415-25	36.3	292
370	A genome-wide association meta-analysis identifies new childhood obesity loci. *Nature Genetics*, **2012**, 44, 526-31	36.3	292

369	LDL-cholesterol concentrations: a genome-wide association study. *Lancet, The*, **2008**, 371, 483-91	40	292
368	Variants near DMRT1, TERT and ATF7IP are associated with testicular germ cell cancer. *Nature Genetics*, **2010**, 42, 604-7	36.3	289
367	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
366	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. *Nature Genetics*, **2009**, 41, 1191-8	36.3	285
365	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
364	Unbiased screen for interactors of leucine-rich repeat kinase 2 supports a common pathway for sporadic and familial Parkinson disease. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 2626-31	11.5	282
363	A genome-wide association study of testicular germ cell tumor. *Nature Genetics*, **2009**, 41, 807-10	36.3	282
362	Compound inheritance of a low-frequency regulatory SNP and a rare null mutation in exon-junction complex subunit RBM8A causes TAR syndrome. *Nature Genetics*, **2012**, 44, 435-9, S1-2	36.3	279
361	Quality control and conduct of genome-wide association meta-analyses. *Nature Protocols*, **2014**, 9, 1192-1212	28.8	278
360	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
359	Genetic evidence implicates the immune system and cholesterol metabolism in the aetiology of Alzheimer's disease. *PLoS ONE*, **2010**, 5, e13950	3.7	276
358	Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. *Lancet, The*, **2012**, 380, 815-23	40	275
357	Global analysis of DNA methylation variation in adipose tissue from twins reveals links to disease-associated variants in distal regulatory elements. *American Journal of Human Genetics*, **2013**, 93, 876-90	11	269
356	Genevar: a database and Java application for the analysis and visualization of SNP-gene associations in eQTL studies. *Bioinformatics*, **2010**, 26, 2474-6	7.2	264
355	Genetic variation in LIN28B is associated with the timing of puberty. *Nature Genetics*, **2009**, 41, 729-33	36.3	258
354	Seventy-five genetic loci influencing the human red blood cell. *Nature*, **2012**, 492, 369-75	50.4	257
353	Dense genotyping of immune-related disease regions identifies 14 new susceptibility loci for juvenile idiopathic arthritis. *Nature Genetics*, **2013**, 45, 664-9	36.3	256
352	Identification of an imprinted master trans regulator at the KLF14 locus related to multiple metabolic phenotypes. *Nature Genetics*, **2011**, 43, 561-4	36.3	253

351	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
350	Mutations in the LGI1/Epitempin gene on 10q24 cause autosomal dominant lateral temporal epilepsy. *Human Molecular Genetics*, **2002**, 11, 1119-28	5.6	250
349	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
348	Meta-analysis of genome-wide association studies identifies three new risk loci for atopic dermatitis. *Nature Genetics*, **2011**, 44, 187-92	36.3	244
347	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
346	Comparison of human genetic and sequence-based physical maps. *Nature*, **2001**, 409, 951-3	50.4	237
345	Genetic variation near the hepatocyte nuclear factor-4 alpha gene predicts susceptibility to type 2 diabetes. *Diabetes*, **2004**, 53, 1141-9	0.9	229
344	Common polygenic variation enhances risk prediction for Alzheimer's disease. *Brain*, **2015**, 138, 3673-84	11.2	227
343	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
342	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	37.4	225
341	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
340	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
339	Cigarette smoking reduces DNA methylation levels at multiple genomic loci but the effect is partially reversible upon cessation. *Epigenetics*, **2014**, 9, 1382-96	5.7	222
338	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
337	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
336	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
335	Collaborative meta-analysis: associations of 150 candidate genes with osteoporosis and osteoporotic fracture. *Annals of Internal Medicine*, **2009**, 151, 528-37	8	215
334	Excessive burden of lysosomal storage disorder gene variants in Parkinson's disease. *Brain*, **2017**, 140, 3191-3203	11.2	209

333	A two-stage meta-analysis identifies several new loci for Parkinson's disease. *PLoS Genetics*, **2011**, 7, e1002142	6	209
332	A high-resolution linkage-disequilibrium map of the human major histocompatibility complex and first generation of tag single-nucleotide polymorphisms. *American Journal of Human Genetics*, **2005**, 76, 634-46	11	209
331	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. *Nature Genetics*, **2016**, 48, 1462-1472	36.3	198
330	Meta-analysis of genome-wide scans for human adult stature identifies novel Loci and associations with measures of skeletal frame size. *PLoS Genetics*, **2009**, 5, e1000445	6	198
329	A genotype calling algorithm for the Illumina BeadArray platform. *Bioinformatics*, **2007**, 23, 2741-6	7.2	194
328	Integrated genetic and epigenetic analysis identifies haplotype-specific methylation in the FTO type 2 diabetes and obesity susceptibility locus. *PLoS ONE*, **2010**, 5, e14040	3.7	193
327	Mosaic PPM1D mutations are associated with predisposition to breast and ovarian cancer. *Nature*, **2013**, 493, 406-10	50.4	191
326	Genetic variants associated with warfarin dose in African-American individuals: a genome-wide association study. *Lancet, The*, **2013**, 382, 790-6	40	191
325	Genome-wide association study identifies variants at 9p21 and 22q13 associated with development of cutaneous nevi. *Nature Genetics*, **2009**, 41, 915-9	36.3	186
324	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
323	Gene expression changes with age in skin, adipose tissue, blood and brain. *Genome Biology*, **2013**, 14, R75	18.3	185
322	The influence of recombination on human genetic diversity. *PLoS Genetics*, **2006**, 2, e148	6	185
321	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. *Nature Genetics*, **2017**, 49, 1113-1119	36.3	184
320	Integration of genetic, clinical, and INR data to refine warfarin dosing. *Clinical Pharmacology and Therapeutics*, **2010**, 87, 572-8	6.1	184
319	Variants in ADCY5 and near CCNL1 are associated with fetal growth and birth weight. *Nature Genetics*, **2010**, 42, 430-5	36.3	184
318	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
317	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180
316	Dissection of the genetics of Parkinson's disease identifies an additional association 5' of SNCA and multiple associated haplotypes at 17q21. *Human Molecular Genetics*, **2011**, 20, 345-53	5.6	178

315	Low copy number of the salivary amylase gene predisposes to obesity. *Nature Genetics*, **2014**, 46, 492-7	36.3	177
314	The DNA sequence and comparative analysis of human chromosome 20. *Nature*, **2001**, 414, 865-71	50.4	177
313	A novel Alzheimer disease locus located near the gene encoding tau protein. *Molecular Psychiatry*, **2016**, 21, 108-17	15.1	175
312	Large-scale gene-centric analysis identifies novel variants for coronary artery disease. *PLoS Genetics* , **2011**, 7, e1002260	6	175
311	The impact of SNP density on fine-scale patterns of linkage disequilibrium. *Human Molecular Genetics*, **2004**, 13, 577-88	5.6	171
310	Linkage disequilibrium mapping via cladistic analysis of single-nucleotide polymorphism haplotypes. *American Journal of Human Genetics*, **2004**, 75, 35-43	11	168
309	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. *Molecular Psychiatry*, **2015**, 20, 647-656	15.1	167
308	Metabolomic markers reveal novel pathways of ageing and early development in human populations. *International Journal of Epidemiology*, **2013**, 42, 1111-9	7.8	166
307	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
306	Genome-wide meta-analysis of observational studies shows common genetic variants associated with macronutrient intake. *American Journal of Clinical Nutrition*, **2013**, 97, 1395-402	7	161
305	ImmunoChip study implicates antigen presentation to T cells in narcolepsy. *PLoS Genetics*, **2013**, 9, e1003270	6	161
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