

Colin Palmer

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

365
papers

61,986
citations

108
h-index

247
g-index

399
ext. papers

75,118
ext. citations

12.7
avg, IF

6.24
L-index

#	Paper	IF	Citations
365	A common variant in the FTO gene is associated with body mass index and predisposes to childhood and adult obesity. <i>Science</i> , 2007 , 316, 889-94	33.3	3294
364	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015 , 518, 197-206	50.4	2687
363	The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2020 , 581, 434-443	50.4	2278
362	Common loss-of-function variants of the epidermal barrier protein filaggrin are a major predisposing factor for atopic dermatitis. <i>Nature Genetics</i> , 2006 , 38, 441-6	36.3	2158
361	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. <i>Nature</i> , 2011 , 476, 214-9	50.4	1948
360	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013 , 45, 1274-1283	36.3	1904
359	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010 , 42, 105-16	36.3	1673
358	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. <i>Nature Genetics</i> , 2008 , 40, 638-45	36.3	1496
357	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012 , 44, 981-90	36.3	1482
356	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. <i>Nature Genetics</i> , 2010 , 42, 579-89	36.3	1449
355	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014 , 46, 1173-86	36.3	1339
354	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , 2015 , 47, 1121-1130	36.3	1290
353	Large-scale association analysis identifies new risk loci for coronary artery disease. <i>Nature Genetics</i> , 2013 , 45, 25-33	36.3	1172
352	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. <i>Nature Genetics</i> , 2013 , 45, 1150-9	36.3	1153
351	Common variants near MC4R are associated with fat mass, weight and risk of obesity. <i>Nature Genetics</i> , 2008 , 40, 768-75	36.3	1048
350	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015 , 518, 187-196	50.4	920
349	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014 , 46, 234-44	36.3	784

348	A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. <i>Nature Genetics</i> , 2010 , 42, 985-90	36.3	773
347	International Union of Pharmacology. LXI. Peroxisome proliferator-activated receptors. <i>Pharmacological Reviews</i> , 2006 , 58, 726-41	22.5	749
346	Loss-of-function mutations in APOC3, triglycerides, and coronary disease. <i>New England Journal of Medicine</i> , 2014 , 371, 22-31	59.2	721
345	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016 , 536, 41-47	50.4	704
344	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. <i>Nature Genetics</i> , 2012 , 44, 1341-8	36.3	681
343	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. <i>Nature Genetics</i> , 2018 , 50, 1505-1513	36.3	675
342	Genome-wide association analysis identifies 20 loci that influence adult height. <i>Nature Genetics</i> , 2008 , 40, 575-83	36.3	654
341	Interaction between ERAP1 and HLA-B27 in ankylosing spondylitis implicates peptide handling in the mechanism for HLA-B27 in disease susceptibility. <i>Nature Genetics</i> , 2011 , 43, 761-7	36.3	646
340	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , 2012 , 44, 991-1005	36.3	621
339	Two variants on chromosome 17 confer prostate cancer risk, and the one in TCF2 protects against type 2 diabetes. <i>Nature Genetics</i> , 2007 , 39, 977-83	36.3	616
338	Common variants associated with plasma triglycerides and risk for coronary artery disease. <i>Nature Genetics</i> , 2013 , 45, 1345-52	36.3	597
337	Variants in MTNR1B influence fasting glucose levels. <i>Nature Genetics</i> , 2009 , 41, 77-81	36.3	584
336	SLC2A9 is a newly identified urate transporter influencing serum urate concentration, urate excretion and gout. <i>Nature Genetics</i> , 2008 , 40, 437-42	36.3	563
335	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. <i>Nature Genetics</i> , 2010 , 42, 142-8	36.3	527
334	An obesity-associated FTO gene variant and increased energy intake in children. <i>New England Journal of Medicine</i> , 2008 , 359, 2558-66	59.2	527
333	Comprehensive analysis of the gene encoding filaggrin uncovers prevalent and rare mutations in ichthyosis vulgaris and atopic eczema. <i>Nature Genetics</i> , 2007 , 39, 650-4	36.3	510
332	Loss-of-function variations within the filaggrin gene predispose for atopic dermatitis with allergic sensitizations. <i>Journal of Allergy and Clinical Immunology</i> , 2006 , 118, 214-9	11.5	489
331	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013 , 45, 501-12	36.3	437

330	Peroxisome Proliferator Activated Receptor- α Expression in Human Liver. <i>Molecular Pharmacology</i> , 1998 , 53, 14-22	4.3	417
329	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017 , 66, 2888-2902	39.0	414
328	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017 , 542, 186-190	50.4	412
327	Genome-wide association study of ulcerative colitis identifies three new susceptibility loci, including the HNF4A region. <i>Nature Genetics</i> , 2009 , 41, 1330-4	36.3	411
326	Genome-wide association scan meta-analysis identifies three Loci influencing adiposity and fat distribution. <i>PLoS Genetics</i> , 2009 , 5, e1000508	6	393
325	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018 , 50, 1412-1425	36.3	386
324	Association analyses based on false discovery rate implicate new loci for coronary artery disease. <i>Nature Genetics</i> , 2017 , 49, 1385-1391	36.3	361
323	Genetic risk factors for ischaemic stroke and its subtypes (the METASTROKE collaboration): a meta-analysis of genome-wide association studies. <i>Lancet Neurology</i> , 2012 , 11, 951-62	24.1	359
322	Loss-of-function variants in the filaggrin gene are a significant risk factor for peanut allergy. <i>Journal of Allergy and Clinical Immunology</i> , 2011 , 127, 661-7	11.5	342
321	A common variant of HMGA2 is associated with adult and childhood height in the general population. <i>Nature Genetics</i> , 2007 , 39, 1245-50	36.3	330
320	Novel loci for adiponectin levels and their influence on type 2 diabetes and metabolic traits: a multi-ethnic meta-analysis of 45,891 individuals. <i>PLoS Genetics</i> , 2012 , 8, e1002607	6	326
319	Coding Variation in ANGPTL4, LPL, and SVEP1 and the Risk of Coronary Disease. <i>New England Journal of Medicine</i> , 2016 , 374, 1134-44	59.2	325
318	Common variants near ATM are associated with glycemic response to metformin in type 2 diabetes. <i>Nature Genetics</i> , 2011 , 43, 117-20	36.3	319
317	Genome-wide association study identifies a variant in HDAC9 associated with large vessel ischemic stroke. <i>Nature Genetics</i> , 2012 , 44, 328-33	36.3	314
316	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017 , 49, 1758-1766	36.3	310
315	Inactivating mutations in NPC1L1 and protection from coronary heart disease. <i>New England Journal of Medicine</i> , 2014 , 371, 2072-82	59.2	307
314	Common variants in WFS1 confer risk of type 2 diabetes. <i>Nature Genetics</i> , 2007 , 39, 951-3	36.3	296
313	Genome-wide association identifies nine common variants associated with fasting proinsulin levels and provides new insights into the pathophysiology of type 2 diabetes. <i>Diabetes</i> , 2011 , 60, 2624-34	0.9	285

312	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. <i>PLoS Genetics</i> , 2013 , 9, e1003500	6	277
311	The burden of disease associated with filaggrin mutations: a population-based, longitudinal birth cohort study. <i>Journal of Allergy and Clinical Immunology</i> , 2008 , 121, 872-7.e9	11.5	276
310	Biomarkers for type 2 diabetes and impaired fasting glucose using a nontargeted metabolomics approach. <i>Diabetes</i> , 2013 , 62, 4270-6	0.9	268
309	Common variation in the FTO gene alters diabetes-related metabolic traits to the extent expected given its effect on BMI. <i>Diabetes</i> , 2008 , 57, 1419-26	0.9	260
308	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016 , 48, 1171-1184	36.3	251
307	Variation in TCF7L2 influences therapeutic response to sulfonylureas: a GoDARTs study. <i>Diabetes</i> , 2007 , 56, 2178-82	0.9	251
306	Assessing the combined impact of 18 common genetic variants of modest effect sizes on type 2 diabetes risk. <i>Diabetes</i> , 2008 , 57, 3129-35	0.9	245
305	Null mutations in the filaggrin gene (FLG) determine major susceptibility to early-onset atopic dermatitis that persists into adulthood. <i>Journal of Investigative Dermatology</i> , 2007 , 127, 564-7	4.3	241
304	Cohort Profile: Generation Scotland: Scottish Family Health Study (GS:SFHS). The study, its participants and their potential for genetic research on health and illness. <i>International Journal of Epidemiology</i> , 2013 , 42, 689-700	7.8	237
303	Novel sequence determinants in peroxisome proliferator signaling. <i>Journal of Biological Chemistry</i> , 1995 , 270, 16114-21	5.4	224
302	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. <i>PLoS Medicine</i> , 2017 , 14, e1002383	11.6	223
301	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018 , 50, 559-571	36.3	221
300	The peroxisome proliferator-activated receptor delta promotes lipid accumulation in human macrophages. <i>Journal of Biological Chemistry</i> , 2001 , 276, 44258-65	5.4	217
299	Mouse p53 inhibits SV40 origin-dependent DNA replication. <i>Nature</i> , 1987 , 329, 458-60	50.4	212
298	Unique mutations in the filaggrin gene in Japanese patients with ichthyosis vulgaris and atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2007 , 119, 434-40	11.5	191
297	Gene-environment interaction in the onset of eczema in infancy: filaggrin loss-of-function mutations enhanced by neonatal cat exposure. <i>PLoS Medicine</i> , 2008 , 5, e131	11.6	187
296	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018 , 50, 26-41	36.3	186
295	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016 , 48, 1151-1161	36.3	181

294	Dissection of the genetics of Parkinson's disease identifies an additional association 5' of SNCA and multiple associated haplotypes at 17q21. <i>Human Molecular Genetics</i> , 2011 , 20, 345-53	5.6	178
293	The PPARdelta agonist GW0742X reduces atherosclerosis in LDLR(-/-) mice. <i>Atherosclerosis</i> , 2005 , 181, 29-37	3.1	178
292	New susceptibility loci associated with kidney disease in type 1 diabetes. <i>PLoS Genetics</i> , 2012 , 8, e1002921	2.1	176
291	Filaggrin null mutations are associated with increased asthma severity in children and young adults. <i>Journal of Allergy and Clinical Immunology</i> , 2007 , 120, 64-8	11.5	175
290	Chromosome 17q21 gene variants are associated with asthma and exacerbations but not atopy in early childhood. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2009 , 179, 179-85	10.2	173
289	Generation Scotland: the Scottish Family Health Study; a new resource for researching genes and heritability. <i>BMC Medical Genetics</i> , 2006 , 7, 74	2.1	164
288	Stratifying type 2 diabetes cases by BMI identifies genetic risk variants in LAMA1 and enrichment for risk variants in lean compared to obese cases. <i>PLoS Genetics</i> , 2012 , 8, e1002741	6	162
287	Role of the peroxisome proliferator-activated receptor in cytochrome P450 4A gene regulation. <i>FASEB Journal</i> , 1996 , 10, 1241-8	0.9	162
286	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. <i>Nature Communications</i> , 2014 , 5, 5068	17.4	160
285	Activation of peroxisome proliferator-activated receptor delta stimulates the proliferation of human breast and prostate cancer cell lines. <i>Cancer Research</i> , 2004 , 64, 3162-70	10.1	155
284	Common nonsynonymous substitutions in SLCO1B1 predispose to statin intolerance in routinely treated individuals with type 2 diabetes: a go-DARTS study. <i>Clinical Pharmacology and Therapeutics</i> , 2011 , 89, 210-6	6.1	153
283	Genetically determined height and coronary artery disease. <i>New England Journal of Medicine</i> , 2015 , 372, 1608-18	59.2	152
282	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. <i>Nature Genetics</i> , 2019 , 51, 51-62	36.3	152
281	Genetic evidence that raised sex hormone binding globulin (SHBG) levels reduce the risk of type 2 diabetes. <i>Human Molecular Genetics</i> , 2010 , 19, 535-44	5.6	150
280	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2017 , 69, 823-836	15.1	146
279	Abdominal aortic aneurysm is associated with a variant in low-density lipoprotein receptor-related protein 1. <i>American Journal of Human Genetics</i> , 2011 , 89, 619-27	11	145
278	Using genome-wide complex trait analysis to quantify 'missing heritability' in Parkinson's disease. <i>Human Molecular Genetics</i> , 2012 , 21, 4996-5009	5.6	145
277	The role of adiposity in cardiometabolic traits: a Mendelian randomization analysis. <i>PLoS Medicine</i> , 2013 , 10, e1001474	11.6	144

276	Genome-wide association and functional follow-up reveals new loci for kidney function. <i>PLoS Genetics</i> , 2012 , 8, e1002584	6	143
275	Association of Organic Cation Transporter 1 With Intolerance to Metformin in Type 2 Diabetes: A GoDARTS Study. <i>Diabetes</i> , 2015 , 64, 1786-93	0.9	141
274	Association between common variation at the FTO locus and changes in body mass index from infancy to late childhood: the complex nature of genetic association through growth and development. <i>PLoS Genetics</i> , 2011 , 7, e1001307	6	141
273	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. <i>Nature Communications</i> , 2020 , 11, 163	17.4	140
272	Common variants at the MHC locus and at chromosome 16q24.1 predispose to Barrett's esophagus. <i>Nature Genetics</i> , 2012 , 44, 1131-6	36.3	139
271	A genome-wide association search for type 2 diabetes genes in African Americans. <i>PLoS ONE</i> , 2012 , 7, e29202	3.7	138
270	A polymorphism controlling ORMDL3 expression is associated with asthma that is poorly controlled by current medications. <i>Journal of Allergy and Clinical Immunology</i> , 2008 , 121, 860-3	11.5	136
269	Reduced-function SLC22A1 polymorphisms encoding organic cation transporter 1 and glycemic response to metformin: a GoDARTS study. <i>Diabetes</i> , 2009 , 58, 1434-9	0.9	132
268	Phenotype standardization for statin-induced myotoxicity. <i>Clinical Pharmacology and Therapeutics</i> , 2014 , 96, 470-6	6.1	130
267	Genome-wide association study implicates HLA-C*01:02 as a risk factor at the major histocompatibility complex locus in schizophrenia. <i>Biological Psychiatry</i> , 2012 , 72, 620-8	7.9	130
266	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019 , 570, 71-76	50.4	129
265	Neutrophil extracellular traps are associated with disease severity and microbiota diversity in patients with chronic obstructive pulmonary disease. <i>Journal of Allergy and Clinical Immunology</i> , 2018 , 141, 117-127	11.5	126
264	Energy intakes of children after preloads: adjustment, not compensation. <i>American Journal of Clinical Nutrition</i> , 2005 , 82, 302-308	7	126
263	Loss-of-function CYP2C9 variants improve therapeutic response to sulfonylureas in type 2 diabetes: a Go-DARTS study. <i>Clinical Pharmacology and Therapeutics</i> , 2010 , 87, 52-6	6.1	124
262	Arginine-16 beta2 adrenoceptor genotype predisposes to exacerbations in young asthmatics taking regular salmeterol. <i>Thorax</i> , 2006 , 61, 940-4	7.3	121
261	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015 , 523, 459-463	50.4	119
260	Specific filaggrin mutations cause ichthyosis vulgaris and are significantly associated with atopic dermatitis in Japan. <i>Journal of Investigative Dermatology</i> , 2008 , 128, 1436-41	4.3	113
259	Association of the Pro12Ala and C1431T variants of PPARG and their haplotypes with susceptibility to Type 2 diabetes. <i>Diabetologia</i> , 2004 , 47, 555-558	10.3	111

258	Tmem79/Matt is the matted mouse gene and is a predisposing gene for atopic dermatitis in human subjects. <i>Journal of Allergy and Clinical Immunology</i> , 2013 , 132, 1121-9	11.5	108
257	Variation in the glucose transporter gene SLC2A2 is associated with glycemic response to metformin. <i>Nature Genetics</i> , 2016 , 48, 1055-1059	36.3	108
256	Exome sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. <i>Diabetologia</i> , 2013 , 56, 298-310	10.3	102
255	Haplotype analysis of the PPARgamma Pro12Ala and C1431T variants reveals opposing associations with body weight. <i>BMC Genetics</i> , 2002 , 3, 21	2.6	102
254	Adiposity-related heterogeneity in patterns of type 2 diabetes susceptibility observed in genome-wide association data. <i>Diabetes</i> , 2009 , 58, 505-10	0.9	98
253	Mendelian randomization studies do not support a causal role for reduced circulating adiponectin levels in insulin resistance and type 2 diabetes. <i>Diabetes</i> , 2013 , 62, 3589-98	0.9	95
252	A gene variant near ATM is significantly associated with metformin treatment response in type 2 diabetes: a replication and meta-analysis of five cohorts. <i>Diabetologia</i> , 2012 , 55, 1971-7	10.3	92
251	Biomarkers of rapid chronic kidney disease progression in type 2 diabetes. <i>Kidney International</i> , 2015 , 88, 888-96	9.9	91
250	A PPAR response element regulates transcription of the gene for human adipose differentiation-related protein. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2005 , 1728, 95-104		88
249	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. <i>Hypertension</i> , 2017 ,	8.5	85
248	Peroxisome proliferator-activated receptor agonists, hyperlipidaemia, and atherosclerosis 2002 , 95, 47-62		83
247	Adrenergic beta(2)-receptor genotype predisposes to exacerbations in steroid-treated asthmatic patients taking frequent albuterol or salmeterol. <i>Journal of Allergy and Clinical Immunology</i> , 2009 , 124, 1188-94.e3	11.5	82
246	Increased cardiovascular morbidity and mortality in type 2 diabetes is associated with the glutathione S transferase theta-null genotype: a Go-DARTS study. <i>Circulation</i> , 2005 , 111, 2927-34	16.7	80
245	Cardiovascular risk in type 2 diabetes is associated with variation at the PPARG locus: a Go-DARTS study. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2004 , 24, 2403-7	9.4	77
244	Identification and functional characterization of G6PC2 coding variants influencing glycemic traits define an effector transcript at the G6PC2-ABCB11 locus. <i>PLoS Genetics</i> , 2015 , 11, e1004876	6	76
243	Common variants in the HLA-DRB1-HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis. <i>Nature Genetics</i> , 2013 , 45, 208-13	36.3	76
242	Heritability of variation in glycaemic response to metformin: a genome-wide complex trait analysis. <i>Lancet Diabetes and Endocrinology</i> , 2014 , 2, 481-7	18.1	76
241	A carboxyl-terminal extension of the zinc finger domain contributes to the specificity and polarity of peroxisome proliferator-activated receptor DNA binding. <i>Journal of Biological Chemistry</i> , 1998 , 273, 27988-97	5.4	76

240	A reference map of potential determinants for the human serum metabolome. <i>Nature</i> , 2020 , 588, 135-140.4	10.4	75
239	Candidate gene association study for diabetic retinopathy in persons with type 2 diabetes: the Candidate gene Association Resource (CARE) 2011 , 52, 7593-602		73
238	Risk analysis of early childhood eczema. <i>Journal of Allergy and Clinical Immunology</i> , 2009 , 123, 1355-60.e51.5	51.5	73
237	Analysis of the individual and aggregate genetic contributions of previously identified serine peptidase inhibitor Kazal type 5 (SPINK5), kallikrein-related peptidase 7 (KLK7), and filaggrin (FLG) polymorphisms to eczema risk. <i>Journal of Allergy and Clinical Immunology</i> , 2008 , 122, 560-8.e4	11.5	73
236	Expression of rabbit cytochromes P4504A which catalyze the omega-hydroxylation of arachidonic acid, fatty acids, and prostaglandins. <i>Archives of Biochemistry and Biophysics</i> , 1993 , 307, 57-65	4.1	73
235	A Genome-Wide Association Study of Diabetic Kidney Disease in Subjects With Type 2 Diabetes. <i>Diabetes</i> , 2018 , 67, 1414-1427	0.9	71
234	Meta-analysis of genome-wide association studies identifies novel loci that influence cupping and the glaucomatous process. <i>Nature Communications</i> , 2014 , 5, 4883	17.4	71
233	Diclofenac antagonizes peroxisome proliferator-activated receptor-gamma signaling. <i>Molecular Pharmacology</i> , 2002 , 61, 7-12	4.3	71
232	Long-term adherence to statin treatment in diabetes. <i>Diabetic Medicine</i> , 2008 , 25, 850-5	3.5	69
231	Activation of PPARbeta/delta causes a psoriasis-like skin disease in vivo. <i>PLoS ONE</i> , 2010 , 5, e9701	3.7	67
230	Childhood asthma exacerbations and the Arg16 G-receptor polymorphism: A meta-analysis stratified by treatment. <i>Journal of Allergy and Clinical Immunology</i> , 2016 , 138, 107-113.e5	11.5	66
229	Genome-Wide Association Study of Diabetic Kidney Disease Highlights Biology Involved in Glomerular Basement Membrane Collagen. <i>Journal of the American Society of Nephrology: JASN</i> , 2019 , 30, 2000-2016	12.7	66
228	Paradoxical lower serum triglyceride levels and higher type 2 diabetes mellitus susceptibility in obese individuals with the PNPLA3 148M variant. <i>PLoS ONE</i> , 2012 , 7, e39362	3.7	66
227	TCF7L2 in the Go-DARTS study: evidence for a gene dose effect on both diabetes susceptibility and control of glucose levels. <i>Diabetologia</i> , 2007 , 50, 1186-91	10.3	65
226	Tailored second-line therapy in asthmatic children with the Arg(16) genotype. <i>Clinical Science</i> , 2013 , 124, 521-8	6.5	64
225	The CTRB1/2 locus affects diabetes susceptibility and treatment via the incretin pathway. <i>Diabetes</i> , 2013 , 62, 3275-81	0.9	63
224	Filaggrin null alleles are not associated with hand eczema or contact allergy. <i>British Journal of Dermatology</i> , 2007 , 157, 1199-204	4	63
223	Glutathione S-transferase M1 and P1 genotype, passive smoking, and peak expiratory flow in asthma. <i>Pediatrics</i> , 2006 , 118, 710-6	7.4	61

222	Underlying genetic models of inheritance in established type 2 diabetes associations. <i>American Journal of Epidemiology</i> , 2009 , 170, 537-45	3.8	60
221	Mendelian randomization studies do not support a role for raised circulating triglyceride levels influencing type 2 diabetes, glucose levels, or insulin resistance. <i>Diabetes</i> , 2011 , 60, 1008-18	0.9	60
220	A paucimorphic variant in the HMG-CoA reductase gene is associated with lipid-lowering response to statin treatment in diabetes: a GoDARTS study. <i>Pharmacogenetics and Genomics</i> , 2008 , 18, 1021-6	1.9	60
219	Childhood obesity in relation to poor asthma control and exacerbation: a meta-analysis. <i>European Respiratory Journal</i> , 2016 , 48, 1063-1073	13.6	59
218	A genome-wide association study suggests an association of Chr8p21.3 (GFRA2) with diabetic neuropathic pain. <i>European Journal of Pain</i> , 2015 , 19, 392-9	3.7	58
217	Early life antibiotic use and the risk of asthma and asthma exacerbations in children. <i>Pediatric Allergy and Immunology</i> , 2017 , 28, 430-437	4.2	57
216	Maintenance and induction in co-cultured rat hepatocytes of components of the cytochrome P450-mediated mono-oxygenase. <i>Biochemical Pharmacology</i> , 1993 , 45, 1583-91	6	57
215	Energy balance and food intake: the role of PPARgamma gene polymorphisms. <i>Physiology and Behavior</i> , 2006 , 88, 227-33	3.5	56
214	Transcript expression-aware annotation improves rare variant interpretation. <i>Nature</i> , 2020 , 581, 452-458	0.4	55
213	A Genome-wide Association Study Provides Evidence of Sex-specific Involvement of Chr1p35.1 (ZSCAN20-TLR12P) and Chr8p23.1 (HMGB1P46) With Diabetic Neuropathic Pain. <i>EBioMedicine</i> , 2015 , 2, 1386-93	8.8	55
212	The correlation between reading and mathematics ability at age twelve has a substantial genetic component. <i>Nature Communications</i> , 2014 , 5, 4204	17.4	54
211	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. <i>Human Molecular Genetics</i> , 2012 , 21, 5329-43	5.6	54
210	Characterization of a cDNA encoding a human kidney, cytochrome P-450 4A fatty acid omega-hydroxylase and the cognate enzyme expressed in Escherichia coli. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1993 , 1172, 161-6		54
209	FCER2 T2206C variant associated with chronic symptoms and exacerbations in steroid-treated asthmatic children. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2011 , 66, 1546-52	9.3	51
208	Clinical validity of plasma and urinary desmosine as biomarkers for chronic obstructive pulmonary disease. <i>Thorax</i> , 2012 , 67, 502-8	7.3	50
207	Apolipoprotein E genotypes are associated with lipid-lowering responses to statin treatment in diabetes: a Go-DARTS study. <i>Pharmacogenetics and Genomics</i> , 2008 , 18, 279-87	1.9	49
206	Protein biomarkers for the prediction of cardiovascular disease in type 2 diabetes. <i>Diabetologia</i> , 2015 , 58, 1363-71	10.3	47
205	Heterozygous null alleles in filaggrin contribute to clinical dry skin in young adults and the elderly. <i>Journal of Investigative Dermatology</i> , 2009 , 129, 1042-5	4.3	47

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200	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. <i>Molecular Psychiatry</i> , 2020 , 25, 2392-2409	15.1	45
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198	Quantification of cytochrome P450 reductase gene expression in human tissues. <i>Archives of Biochemistry and Biophysics</i> , 1992 , 294, 168-72	4.1	44
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188	Filaggrin null mutations are associated with increased asthma exacerbations in children and young adults. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2008 , 63, 1211-7	9.3	39
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179	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. <i>Nature Communications</i> , 2018 , 9, 711	17.4	35
178	Both high and low HbA1c predict incident heart failure in type 2 diabetes mellitus. <i>Circulation: Heart Failure</i> , 2015 , 8, 236-42	7.6	35
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111	ST13 polymorphisms and their effect on exacerbations in steroid-treated asthmatic children and young adults. <i>Clinical and Experimental Allergy</i> , 2015 , 45, 1051-9	4.1	16
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51	Fluorescence-based ligand-binding assays for peroxisome proliferator-activated receptors. <i>Methods in Enzymology</i> , 2002 , 357, 188-97	1.7	3
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38	Genetic discovery and translational decision support from exome sequencing of 20,791 type 2 diabetes cases and 24,440 controls from five ancestries		2
37	Genome-wide association study of diabetic kidney disease highlights biology involved in renal basement membrane collagen		2
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