Colin Palmer

List of Publications by Year
in descending order

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368 papers	84,312 citations	944 115 h-index	470 271 g-index
399 all docs	399 docs citations	399 times ranked	79686 citing authors

#	Article	IF	Citations
1	The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2020, 581, 434-443.	13.7	6,140
2	A Common Variant in the FTO Gene Is Associated with Body Mass Index and Predisposes to Childhood and Adult Obesity. Science, 2007, 316, 889-894.	6.0	3,884
3	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
4	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	9.4	2,641
5	Common loss-of-function variants of the epidermal barrier protein filaggrin are a major predisposing factor for atopic dermatitis. Nature Genetics, 2006, 38, 441-446.	9.4	2,584
6	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	13.7	2,400
7	A comprehensive 1000 Genomesâ€“based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	9.4	2,054
8	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	9.4	1,982
9	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
10	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	9.4	1,748
11	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. Nature Genetics, 2008, 40, 638-645.	9.4	1,683
12	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	9.4	1,631
13	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	9.4	1,439
14	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. Nature Genetics, 2013, 45, 1150-1159.	9.4	1,395
15	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. Nature Genetics, 2018, 50, 1505-1513.	9.4	1,331
16	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
17	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	9.4	1,179
18	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959

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19	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
20	Loss-of-Function Mutations inAPOC3,Triglycerides, and Coronary Disease. New England Journal of Medicine, 2014, 371, 22-31.	13.9	936
21	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	9.4	924
22	A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. Nature Genetics, 2010, 42, 985-990.	9.4	918
23	International Union of Pharmacology. LXI. Peroxisome Proliferator-Activated Receptors. Pharmacological Reviews, 2006, 58, 726-741.	7.1	869
24	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. Nature Genetics, 2012, 44, 1341-1348.	9.4	848
25	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, 761-767.	9.4	778
26	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	9.4	754
27	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	9.4	746
28	Genome-wide association analysis identifies 20 loci that influence adult height. Nature Genetics, 2008, 40, 575-583.	9.4	742
29	SLC2A9 is a newly identified urate transporter influencing serum urate concentration, urate excretion and gout. Nature Genetics, 2008, 40, 437-442.	9.4	678
30	Two variants on chromosome 17 confer prostate cancer risk, and the one in TCF2 protects against type 2 diabetes. Nature Genetics, 2007, 39, 977-983.	9.4	670
31	Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81.	9.4	662
32	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
33	An Obesity-AssociatedFTOGene Variant and Increased Energy Intake in Children. New England Journal of Medicine, 2008, 359, 2558-2566.	13.9	608
34	Comprehensive analysis of the gene encoding filaggrin uncovers prevalent and rare mutations in ichthyosis vulgaris and atopic eczema. Nature Genetics, 2007, 39, 650-654.	9.4	598
35	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	9.4	591
36	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578

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37	Association analyses based on false discovery rate implicate new loci for coronary artery disease. Nature Genetics, 2017, 49, 1385-1391.	9.4	571
38	Loss-of-function variations within the filaggrin gene predispose for atopic dermatitis with allergic sensitizations. Journal of Allergy and Clinical Immunology, 2006, 118, 214-219.	1.5	567
39	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
40	Genome-wide association study of ulcerative colitis identifies three new susceptibility loci, including the HNF4A region. Nature Genetics, 2009, 41, 1330-1334.	9.4	483
41	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
42	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	5.8	466
43	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	1.5	453
44	Peroxisome Proliferator Activated Receptor-Î± Expression in Human Liver. Molecular Pharmacology, 1998, 53, 14-22.	1.0	447
45	Genetic risk factors for ischaemic stroke and its subtypes (the METASTROKE Collaboration): a meta-analysis of genome-wide association studies. Lancet Neurology, The, 2012, 11, 951-962.	4.9	445
46	Coding Variation inANGPTL4,LPL,andSVEP1and the Risk of Coronary Disease. New England Journal of Medicine, 2016, 374, 1134-1144.	13.9	427
47	Loss-of-function variants in the filaggrin gene are a significant risk factor for peanut allergy. Journal of Allergy and Clinical Immunology, 2011, 127, 661-667.	1.5	424
48	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.	1.5	419
49	Common variants near ATM are associated with glycemic response to metformin in type 2 diabetes. Nature Genetics, 2011, 43, 117-120.	9.4	390
50	Inactivating Mutations in NPC1L1 and Protection from Coronary Heart Disease. New England Journal of Medicine, 2014, 371, 2072-2082.	13.9	386
51	Genome-wide association study identifies a variant in HDAC9 associated with large vessel ischemic stroke. Nature Genetics, 2012, 44, 328-333.	9.4	375
52	A common variant of HMGA2 is associated with adult and childhood height in the general population. Nature Genetics, 2007, 39, 1245-1250.	9.4	373
53	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	1.5	371
54	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	9.4	362

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55	Biomarkers for Type 2 Diabetes and Impaired Fasting Glucose Using a Nontargeted Metabolomics Approach. Diabetes, 2013, 62, 4270-4276.	0.3	356
56	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	9.4	356
57	Cohort Profile: Generation Scotland: Scottish Family Health Study (GS:SFHS). The study, its participants and their potential for genetic research on health and illness. International Journal of Epidemiology, 2013, 42, 689-700.	0.9	353
58	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
59	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.	3.9	341
60	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
61	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, 2624-2634.	0.3	335
62	Common variants in WFS1 confer risk of type 2 diabetes. Nature Genetics, 2007, 39, 951-953.	9.4	333
63	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	9.4	328
64	The burden of disease associated with filaggrin mutations: A population-based, longitudinal birth cohort study. Journal of Allergy and Clinical Immunology, 2008, 121, 872-877.e9.	1.5	318
65	Null Mutations in the Filaggrin Gene (FLG) Determine Major Susceptibility to Early-Onset Atopic Dermatitis that Persists into Adulthood. Journal of Investigative Dermatology, 2007, 127, 564-567.	0.3	298
66	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
67	Variation in TCF7L2 Influences Therapeutic Response to Sulfonylureas. Diabetes, 2007, 56, 2178-2182.	0.3	284
68	Assessing the Combined Impact of 18 Common Genetic Variants of Modest Effect Sizes on Type 2 Diabetes Risk. Diabetes, 2008, 57, 3129-3135.	0.3	279
69	Common Variation in the FTO Gene Alters Diabetes-Related Metabolic Traits to the Extent Expected Given Its Effect on BMI. Diabetes, 2008, 57, 1419-1426.	0.3	277
70	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
71	Novel Sequence Determinants in Peroxisome Proliferator Signaling. Journal of Biological Chemistry, 1995, 270, 16114-16121.	1.6	252
72	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250

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73	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	13.7	248
74	Mouse p53 inhibits SV40 origin-dependent DNA replication. Nature, 1987, 329, 458-460.	13.7	243
75	The Peroxisome Proliferator-activated Receptor Î´ Promotes Lipid Accumulation in Human Macrophages. Journal of Biological Chemistry, 2001, 276, 44258-44265.	1.6	243
76	Unique mutations in the filaggrin gene in Japanese patients with ichthyosis vulgaris andÂatopic dermatitis. Journal of Allergy and Clinical Immunology, 2007, 119, 434-440.	1.5	233
77	A reference map of potential determinants for the human serum metabolome. Nature, 2020, 588, 135-140.	13.7	230
78	Generation Scotland: the Scottish Family Health Study; a new resource for researching genes and heritability. BMC Medical Genetics, 2006, 7, 74.	2.1	227
79	Genetically Determined Height and Coronary Artery Disease. New England Journal of Medicine, 2015, 372, 1608-1618.	13.9	220
80	New Susceptibility Loci Associated with Kidney Disease in Type 1 Diabetes. PLoS Genetics, 2012, 8, e1002921.	1.5	216
81	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. Nature Communications, 2014, 5, 5068.	5.8	216
82	Gene-Environment Interaction in the Onset of Eczema in Infancy: Filaggrin Loss-of-Function Mutations Enhanced by Neonatal Cat Exposure. PLoS Medicine, 2008, 5, e131.	3.9	215
83	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	1.2	214
84	Neutrophil extracellular traps are associated with disease severity and microbiota diversity in patients with chronic obstructive pulmonary disease. Journal of Allergy and Clinical Immunology, 2018, 141, 117-127.	1.5	207
85	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, 345-353.	1.4	202
86	Filaggrin null mutations are associated with increased asthma severity in children and young adults. Journal of Allergy and Clinical Immunology, 2007, 120, 64-68.	1.5	199
87	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
88	Chromosome 17q21 Gene Variants Are Associated with Asthma and Exacerbations but Not Atopy in Early Childhood. American Journal of Respiratory and Critical Care Medicine, 2009, 179, 179-185.	2.5	196
89	The PPARÎ´ agonist GW0742X reduces atherosclerosis in LDLRâ^'/â^' mice. Atherosclerosis, 2005, 181, 29-37.	0.4	194
90	Stratifying Type 2 Diabetes Cases by BMI Identifies Genetic Risk Variants in LAMA1 and Enrichment for Risk Variants in Lean Compared to Obese Cases. PLoS Genetics, 2012, 8, e1002741.	1.5	190

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91	Association of Organic Cation Transporter 1 With Intolerance to Metformin in Type 2 Diabetes: A GoDARTS Study. Diabetes, 2015, 64, 1786-1793.	0.3	188
92	Abdominal Aortic Aneurysm Is Associated with a Variant in Low-Density Lipoprotein Receptor-Related Protein 1. American Journal of Human Genetics, 2011, 89, 619-627.	2.6	185
93	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. PLoS Medicine, 2013, 10, e1001474.	3.9	178
94	Common Nonsynonymous Substitutions in SLCO1B1 Predispose to Statin Intolerance in Routinely Treated Individuals With Type 2 Diabetes: A Go-DARTS Study. Clinical Pharmacology and Therapeutics, 2011, 89, 210-216.	2.3	177
95	Genetic evidence that raised sex hormone binding globulin (SHBG) levels reduce the risk of type 2 diabetes. Human Molecular Genetics, 2010, 19, 535-544.	1.4	176
96	Using genome-wide complex trait analysis to quantify 'missing heritability' in Parkinson's disease. Human Molecular Genetics, 2012, 21, 4996-5009.	1.4	176
97	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
98	Role of the peroxisome proliferatorâ€activated receptor in cytochrome P450 4A gene regulation. FASEB Journal, 1996, 10, 1241-1248.	0.2	169
99	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	1.5	166
100	Phenotype Standardization for Statin-Induced Myotoxicity. Clinical Pharmacology and Therapeutics, 2014, 96, 470-476.	2.3	166
101	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. PLoS Genetics, 2011, 7, e1001307.	1.5	165
102	Variation in the glucose transporter gene SLC2A2 is associated with glycemic response to metformin. Nature Genetics, 2016, 48, 1055-1059.	9.4	165
103	Activation of Peroxisome Proliferator-Activated Receptor Î´ Stimulates the Proliferation of Human Breast and Prostate Cancer Cell Lines. Cancer Research, 2004, 64, 3162-3170.	0.4	163
104	Common variants at the MHC locus and at chromosome 16q24.1 predispose to Barrett's esophagus. Nature Genetics, 2012, 44, 1131-1136.	9.4	162
105	Genome-Wide Association Study Implicates HLA-C*01:02 as a Risk Factor at the Major Histocompatibility Complex Locus in Schizophrenia. Biological Psychiatry, 2012, 72, 620-628.	0.7	156
106	Reduced-Function SLC22A1 Polymorphisms Encoding Organic Cation Transporter 1 and Glycemic Response to Metformin: A GoDARTS Study. Diabetes, 2009, 58, 1434-1439.	0.3	153
107	Energy intakes of children after preloads: adjustment, not compensation. American Journal of Clinical Nutrition, 2005, 82, 302-308.	2.2	145
108	A polymorphism controlling ORMDL3 expression is associated with asthma that is poorly controlled by current medications. Journal of Allergy and Clinical Immunology, 2008, 121, 860-863.	1.5	145

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109	Arginine-16 Â2 adrenoceptor genotype predisposes to exacerbations in young asthmatics taking regular salmeterol. Thorax, 2006, 61, 940-944.	2.7	142
110	Transcript expression-aware annotation improves rare variant interpretation. Nature, 2020, 581, 452-458.	13.7	142
111	Loss-of-Function CYP2C9 Variants Improve Therapeutic Response to Sulfonylureas in Type 2 Diabetes: A Go-DARTS Study. Clinical Pharmacology and Therapeutics, 2010, 87, 52-56.	2.3	141
112	A Genome-Wide Association Study of Diabetic Kidney Disease in Subjects With Type 2 Diabetes. Diabetes, 2018, 67, 1414-1427.	0.3	136
113	Tmem79/Matt is the matted mouse gene and is a predisposing gene for atopic dermatitis in human subjects. Journal of Allergy and Clinical Immunology, 2013, 132, 1121-1129.	1.5	135
114	Genome-Wide Association Study of Diabetic Kidney Disease Highlights Biology Involved in Glomerular Basement Membrane Collagen. Journal of the American Society of Nephrology: JASN, 2019, 30, 2000-2016.	3.0	135
115	Specific Filaggrin Mutations Cause Ichthyosis Vulgaris and Are Significantly Associated with Atopic Dermatitis in Japan. Journal of Investigative Dermatology, 2008, 128, 1436-1441.	0.3	128
116	Biomarkers of rapid chronic kidney disease progression in type 2 diabetes. Kidney International, 2015, 88, 888-896.	2.6	124
117	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	1.3	123
118	Association of the Pro12Ala and C1431T variants of PPARG and their haplotypes with susceptibility to Type 2 diabetes. Diabetologia, 2004, 47, 555-558.	2.9	122
119	Exome sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. Diabetologia, 2013, 56, 298-310.	2.9	119
120	Mendelian Randomization Studies Do Not Support a Causal Role for Reduced Circulating Adiponectin Levels in Insulin Resistance and Type 2 Diabetes. Diabetes, 2013, 62, 3589-3598.	0.3	116
121	Haplotype analysis of the PPARgamma Pro12Ala and C1431T variants reveals opposing associations with body weight. BMC Genetics, 2002, 3, 21.	2.7	113
122	Novel subgroups of type 2 diabetes and their association with microvascular outcomes in an Asian Indian population: a data-driven cluster analysis: the INSPIRED study. BMJ Open Diabetes Research and Care, 2020, 8, e001506.	1.2	112
123	Adiposity-Related Heterogeneity in Patterns of Type 2 Diabetes Susceptibility Observed in Genome-Wide Association Data. Diabetes, 2009, 58, 505-510.	0.3	109
124	A gene variant near ATM is significantly associated with metformin treatment response in type 2 diabetes: a replication and meta-analysis of five cohorts. Diabetologia, 2012, 55, 1971-1977.	2.9	107
125	A PPAR response element regulates transcription of the gene for human adipose differentiation-related protein. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2005, 1728, 95-104.	2.4	101
126	Heritability of variation in glycaemic response to metformin: a genome-wide complex trait analysis. Lancet Diabetes and Endocrinology,the, 2014, 2, 481-487.	5.5	101

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127	Increased Cardiovascular Morbidity and Mortality in Type 2 Diabetes Is Associated With the Glutathione S Transferase Thetaâ€“Null Genotype. Circulation, 2005, 111, 2927-2934.	1.6	96
128	Adrenergic Î²2-receptor genotype predisposes to exacerbations in steroid-treated asthmatic patients taking frequent albuterol or salmeterol. Journal of Allergy and Clinical Immunology, 2009, 124, 1188-1194.e3.	1.5	96
129	The CTRB1/2 Locus Affects Diabetes Susceptibility and Treatment via the Incretin Pathway. Diabetes, 2013, 62, 3275-3281.	0.3	96
130	Peroxisome proliferator-activated receptor agonists, hyperlipidaemia, and atherosclerosis. , 2002, 95, 47-62.		95
131	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. PLoS Genetics, 2015, 11, e1004876.	1.5	95
132	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	9.4	91
133	A Carboxyl-terminal Extension of the Zinc Finger Domain Contributes to the Specificity and Polarity of Peroxisome Proliferator-activated Receptor DNA Binding. Journal of Biological Chemistry, 1998, 273, 27988-27997.	1.6	89
134	Zhou et al. reply. Nature Genetics, 2012, 44, 361-362.	9.4	89
135	Meta-analysis of genome-wide association studies identifies novel loci that influence cupping and the glaucomatous process. Nature Communications, 2014, 5, 4883.	5.8	89
136	Childhood obesity in relation to poor asthma control and exacerbation: a meta-analysis. European Respiratory Journal, 2016, 48, 1063-1073.	3.1	89
137	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	5.8	87
138	Cardiovascular Risk in Type 2 Diabetes Is Associated With Variation at the PPARG Locus. Arteriosclerosis, Thrombosis, and Vascular Biology, 2004, 24, 2403-2407.	1.1	86
139	Common variants in the HLA-DRB1â€“HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis. Nature Genetics, 2013, 45, 208-213.	9.4	86
140	A review of machine learning methods for retinal blood vessel segmentation and artery/vein classification. Medical Image Analysis, 2021, 68, 101905.	7.0	86
141	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
142	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. Journal of Allergy and Clinical Immunology, 2008, 122, 560-568.e4.	1.5	83
143	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	4.1	83
144	Diclofenac Antagonizes Peroxisome Proliferator-Activated Receptor-Î³ Signaling. Molecular Pharmacology, 2002, 61, 7-12.	1.0	82

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145	Risk analysis of early childhood eczema. Journal of Allergy and Clinical Immunology, 2009, 123, 1355-1360.e5.	1.5	82
146	Candidate Gene Association Study for Diabetic Retinopathy in Persons with Type 2 Diabetes: The Candidate Gene Association Resource (CARe). , 2011, 52, 7593.		82
147	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. PLoS Genetics, 2014, 10, e1004508.	1.5	80
148	Childhood asthma exacerbations and the Arg16 Î²2-receptor polymorphism: AÂmeta-analysis stratified by treatment. Journal of Allergy and Clinical Immunology, 2016, 138, 107-113.e5.	1.5	80
149	Expression of Rabbit Cytochromes P4504A Which Catalyze the Ï‰-Hydroxylation of Arachidonic Acid, Fatty Acids, and Prostaglandins. Archives of Biochemistry and Biophysics, 1993, 307, 57-65.	1.4	78
150	Paradoxical Lower Serum Triglyceride Levels and Higher Type 2 Diabetes Mellitus Susceptibility in Obese Individuals with the PNPLA3 148M Variant. PLoS ONE, 2012, 7, e39362.	1.1	78
151	Activation of PPARÎ²/Î´ Causes a Psoriasis-Like Skin Disease In Vivo. PLoS ONE, 2010, 5, e9701.	1.1	77
152	Mendelian Randomization Studies Do Not Support a Role for Raised Circulating Triglyceride Levels Influencing Type 2 Diabetes, Glucose Levels, or Insulin Resistance. Diabetes, 2011, 60, 1008-1018.	0.3	77
153	Early life antibiotic use and the risk of asthma and asthma exacerbations in children. Pediatric Allergy and Immunology, 2017, 28, 430-437.	1.1	77
154	N-Glycan Profile and Kidney Disease in Type 1 Diabetes. Diabetes Care, 2018, 41, 79-87.	4.3	75
155	TCF7L2 in the Go-DARTS study: evidence for a gene dose effect on both diabetes susceptibility and control of glucose levels. Diabetologia, 2007, 50, 1186-1191.	2.9	74
156	Longâ€term adherence to statin treatment in diabetes. Diabetic Medicine, 2008, 25, 850-855.	1.2	74
157	Tailored second-line therapy in asthmatic children with the Arg16 genotype. Clinical Science, 2013, 124, 521-528.	1.8	74
158	A paucimorphic variant in the HMG-CoA reductase gene is associated with lipid-lowering response to statin treatment in diabetes: a GoDARTS study. Pharmacogenetics and Genomics, 2008, 18, 1021-1026.	0.7	73
159	Filaggrin null alleles are not associated with hand eczema or contact allergy. British Journal of Dermatology, 2007, 157, 1199-1204.	1.4	72
160	The correlation between reading and mathematics ability at age twelve has a substantial genetic component. Nature Communications, 2014, 5, 4204.	5.8	72
161	A genomeâ€wide association study suggests an association of <scp>C</scp>hr8p21.3 (<scp>GFRA2</scp>) with diabetic neuropathic pain. European Journal of Pain, 2015, 19, 392-399.	1.4	71
162	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and AlcoholÂUse. Biological Psychiatry, 2019, 85, 946-955.	0.7	69

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163	Clinical validity of plasma and urinary desmosine as biomarkers for chronic obstructive pulmonary disease. Thorax, 2012, 67, 502-508.	2.7	68
164	Glutathione S-Transferase M1 and P1 Genotype, Passive Smoking, and Peak Expiratory Flow in Asthma. Pediatrics, 2006, 118, 710-716.	1.0	67
165	A Genome-wide Association Study Provides Evidence of Sex-specific Involvement of Chr1p35.1 () Tj ETQq1 1 0.784314 rgBT /Overlock 1386-1393.	2.7	67
166	A â€œCandidate-Interactomeâ€•Aggregate Analysis of Genome-Wide Association Data in Multiple Sclerosis. PLoS ONE, 2013, 8, e63300.	1.1	66
167	Characterization of a cDNA encoding a human kidney, cytochrome 4A fatty acid Ï‰-hydroxylase and the cognate enzyme expressed in Escherichia coli. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1993, 1172, 161-166.	2.4	65
168	Energy balance and food intake: The role of PPARÎ³ gene polymorphisms. Physiology and Behavior, 2006, 88, 227-233.	1.0	65
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