Nicole Soranzo

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.

243 papers	51,227 citations	105 h-index	226 g-index
274 ext. papers	60,642 ext. citations	18.1 avg, IF	5.97 L-index

#	Paper	IF	Citations
243	Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*, **2010**, 466, 707-13	50.4	2742
242	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics*, **2010**, 42, 937-48	36.3	2267
241	Integrating common and rare genetic variation in diverse human populations. *Nature*, **2010**, 467, 52-8	50.4	2135
240	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
239	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. *Nature* , **2011**, 478, 103-9	50.4	1564
238	Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature*, **2010**, 467, 832-8	50.4	1514
237	A reference panel of 64,976 haplotypes for genotype imputation. *Nature Genetics*, **2016**, 48, 1279-83	36.3	1447
236	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. *Nature Genetics*, **2011**, 43, 333-8	36.3	1394
235	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
234	Common genetic determinants of vitamin D insufficiency: a genome-wide association study. *Lancet, The*, **2010**, 376, 180-8	40	1183
233	Common variants near MC4R are associated with fat mass, weight and risk of obesity. *Nature Genetics*, **2008**, 40, 768-75	36.3	1048
232	Genome-wide association study identifies eight loci associated with blood pressure. *Nature Genetics*, **2009**, 41, 666-76	36.3	970
231	The UK10K project identifies rare variants in health and disease. *Nature*, **2015**, 526, 82-90	50.4	776
230	Human metabolic individuality in biomedical and pharmaceutical research. *Nature*, **2011**, 477, 54-60	50.4	728
229	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
228	An atlas of genetic influences on human blood metabolites. *Nature Genetics*, **2014**, 46, 543-550	36.3	695
227	Genome-wide association analysis identifies 20 loci that influence adult height. *Nature Genetics*, **2008**, 40, 575-83	36.3	654

226	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. *Cell*, **2016**, 167, 1415-1429.e19	56.2	637
225	Variants in MTNR1B influence fasting glucose levels. *Nature Genetics*, **2009**, 41, 77-81	36.3	584
224	Sequence variants at CHRNB3-CHRNA6 and CYP2A6 affect smoking behavior. *Nature Genetics*, **2010**, 42, 448-53	36.3	582
223	Mapping cis- and trans-regulatory effects across multiple tissues in twins. *Nature Genetics*, **2012**, 44, 1084-9	36.3	572
222	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
221	Bone mineral density, osteoporosis, and osteoporotic fractures: a genome-wide association study. *Lancet, The*, **2008**, 371, 1505-12	40	538
220	Genomic atlas of the human plasma proteome. *Nature*, **2018**, 558, 73-79	50.4	529
219	Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. *Nature Genetics*, **2015**, 47, 1114-20	36.3	522
218	A genome-wide perspective of genetic variation in human metabolism. *Nature Genetics*, **2010**, 42, 137-41	36.3	515
217	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. *Nature Genetics*, **2013**, 45, 145-54	36.3	505
216	A genome-wide association study confirms VKORC1, CYP2C9, and CYP4F2 as principal genetic determinants of warfarin dose. *PLoS Genetics*, **2009**, 5, e1000433	6	484
215	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
214	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
213	Genome-wide association study identifies five loci associated with lung function. *Nature Genetics*, **2010**, 42, 36-44	36.3	430
212	Meta-analysis of genome-wide association studies in >80 000 subjects identifies multiple loci for C-reactive protein levels. *Circulation*, **2011**, 123, 731-8	16.7	395
211	The metabochip, a custom genotyping array for genetic studies of metabolic, cardiovascular, and anthropometric traits. *PLoS Genetics*, **2012**, 8, e1002793	6	395
210	Genome-wide association scan meta-analysis identifies three Loci influencing adiposity and fat distribution. *PLoS Genetics*, **2009**, 5, e1000508	6	393
209	A general approach for haplotype phasing across the full spectrum of relatedness. *PLoS Genetics*, **2014**, 10, e1004234	6	377

208	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
207	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. *Cell*, **2016**, 167, 1398-1414.e24	30.4	339
206	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. *Nature Genetics*, **2011**, 43, 1005-11	36.3	338
205	The architecture of gene regulatory variation across multiple human tissues: the MuTHER study. *PLoS Genetics*, **2011**, 7, e1002003	6	336
204	New gene functions in megakaryopoiesis and platelet formation. *Nature*, **2011**, 480, 201-8	50.4	330
203	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
202	Common variants at 10 genomic loci influence hemoglobin A(C) levels via glycemic and nonglycemic pathways. *Diabetes*, **2010**, 59, 3229-39	0.9	314
201	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. *Nature*, **2015**, 526, 112-7	50.4	308
200	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. *Nature Communications*, **2016**, 7, 10023	17.4	295
199	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. *Nature Genetics*, **2009**, 41, 1191-8	36.3	285
198	Genetic predictors of the maximum doses patients receive during clinical use of the anti-epileptic drugs carbamazepine and phenytoin. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 5507-12	11.5	278
197	Significant Locus and Metabolic Genetic Correlations Revealed in Genome-Wide Association Study of Anorexia Nervosa. *American Journal of Psychiatry*, **2017**, 174, 850-858	11.9	276
196	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
195	Biomarkers for type 2 diabetes and impaired fasting glucose using a nontargeted metabolomics approach. *Diabetes*, **2013**, 62, 4270-6	0.9	268
194	BLUEPRINT to decode the epigenetic signature written in blood. *Nature Biotechnology*, **2012**, 30, 224-6	44.5	261
193	Novel associations of multiple genetic loci with plasma levels of factor VII, factor VIII, and von Willebrand factor: The CHARGE (Cohorts for Heart and Aging Research in Genome Epidemiology) Consortium. *Circulation*, **2010**, 121, 1382-92	16.7	260
192	Seventy-five genetic loci influencing the human red blood cell. *Nature*, **2012**, 492, 369-75	50.4	257
191	Genome-wide association study of blood pressure extremes identifies variant near UMOD associated with hypertension. *PLoS Genetics*, **2010**, 6, e1001177	6	255

190	Common variants near TERC are associated with mean telomere length. *Nature Genetics*, **2010**, 42, 197-9	36.3	255
189	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
188	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
187	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. *Nature Genetics*, **2011**, 43, 753-60	36.3	237
186	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases: A Mendelian Randomization Study. *JAMA Oncology*, **2017**, 3, 636-651	13.4	236
185	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. *Cell*, **2016**, 167, 1145-1149	56.2	232
184	A genome-wide association study of anorexia nervosa. *Molecular Psychiatry*, **2014**, 19, 1085-94	15.1	224
183	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
182	Meta-analysis of genome-wide association data identifies two loci influencing age at menarche. *Nature Genetics*, **2009**, 41, 648-50	36.3	223
181	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
180	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics*, **2013**, 45, 621-31	36.3	219
179	Genetic architecture: the shape of the genetic contribution to human traits and disease. *Nature Reviews Genetics*, **2018**, 19, 110-124	30.1	219
178	Genome-wide association and genetic functional studies identify autism susceptibility candidate 2 gene (AUTS2) in the regulation of alcohol consumption. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 7119-24	11.5	218
177	A catalog of genetic loci associated with kidney function from analyses of a million individuals. *Nature Genetics*, **2019**, 51, 957-972	36.3	217
176	Collaborative meta-analysis: associations of 150 candidate genes with osteoporosis and osteoporotic fracture. *Annals of Internal Medicine*, **2009**, 151, 528-37	8	215
175	Genome-wide association identifies OBFC1 as a locus involved in human leukocyte telomere biology. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 9293-8	11.5	209
174	Genetic loci influencing kidney function and chronic kidney disease. *Nature Genetics*, **2010**, 42, 373-5	36.3	205
173	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

172	Human serum metabolic profiles are age dependent. *Aging Cell*, **2012**, 11, 960-7	9.9	193
171	Transcriptional diversity during lineage commitment of human blood progenitors. *Science*, **2014**, 345, 1251033	33.3	187
170	Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. *Nature Communications*, **2015**, 6, 8111	17.4	186
169	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
168	Identification of rare sequence variation underlying heritable pulmonary arterial hypertension. *Nature Communications*, **2018**, 9, 1416	17.4	182
167	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
166	A brief history of human disease genetics. *Nature*, **2020**, 577, 179-189	50.4	181
165	Positive selection on a high-sensitivity allele of the human bitter-taste receptor TAS2R16. *Current Biology*, **2005**, 15, 1257-65	6.3	180
164	The impact of rare and low-frequency genetic variants in common disease. *Genome Biology*, **2017**, 18, 77	18.3	174
163	A low mutation rate for chloroplast microsatellites. *Genetics*, **1999**, 153, 943-7	4	171
162	An integration of genome-wide association study and gene expression profiling to prioritize the discovery of novel susceptibility Loci for osteoporosis-related traits. *PLoS Genetics*, **2010**, 6, e1000977	6	163
161	Association of JAG1 with bone mineral density and osteoporotic fractures: a genome-wide association study and follow-up replication studies. *American Journal of Human Genetics*, **2010**, 86, 229-39	11	156
160	Large-scale production of megakaryocytes from human pluripotent stem cells by chemically defined forward programming. *Nature Communications*, **2016**, 7, 11208	17.4	155
159	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. *American Journal of Human Genetics*, **2018**, 103, 691-706	11	151
158	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. *Nature Communications*, **2015**, 6, 5897	17.4	147
157	A meta-analysis of thyroid-related traits reveals novel loci and gender-specific differences in the regulation of thyroid function. *PLoS Genetics*, **2013**, 9, e1003266	6	146
156	A genome-wide association search for type 2 diabetes genes in African Americans. *PLoS ONE*, **2012**, 7, e29202	3.7	138
155	A single-nucleotide polymorphism tagging set for human drug metabolism and transport. *Nature Genetics*, **2005**, 37, 84-9	36.3	134

154	Ancient and recent positive selection transformed opioid cis-regulation in humans. *PLoS Biology*, **2005**, 3, e387	9.7	133
153	Genome sequencing elucidates Sardinian genetic architecture and augments association analyses for lipid and blood inflammatory markers. *Nature Genetics*, **2015**, 47, 1272-1281	36.3	129
152	A genome-wide association study reveals variants in ARL15 that influence adiponectin levels. *PLoS Genetics*, **2009**, 5, e1000768	6	129
151	Clear detection of ADIPOQ locus as the major gene for plasma adiponectin: results of genome-wide association analyses including 4659 European individuals. *Atherosclerosis*, **2010**, 208, 412-20	3.1	128
150	Large scale association analysis of novel genetic loci for coronary artery disease. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2009**, 29, 774-80	9.4	125
149	Identification of novel genetic Loci associated with thyroid peroxidase antibodies and clinical thyroid disease. *PLoS Genetics*, **2014**, 10, e1004123	6	122
148	Identification of novel risk loci for restless legs syndrome in genome-wide association studies in individuals of European ancestry: a meta-analysis. *Lancet Neurology, The*, **2017**, 16, 898-907	24.1	121
147	Loci at chromosomes 13, 19 and 20 influence age at natural menopause. *Nature Genetics*, **2009**, 41, 645-7	36.3	120
146	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	50.4	119
145	Loci influencing blood pressure identified using a cardiovascular gene-centric array. *Human Molecular Genetics*, **2013**, 22, 1663-78	5.6	119
144	A genome-wide association meta-analysis of circulating sex hormone-binding globulin reveals multiple Loci implicated in sex steroid hormone regulation. *PLoS Genetics*, **2012**, 8, e1002805	6	116
143	Positive selection on a human-specific transcription factor binding site regulating IL4 expression. *Current Biology*, **2003**, 13, 2118-23	6.3	113
142	ABCB1/MDR1 gene determines susceptibility and phenotype in ulcerative colitis: discrimination of critical variants using a gene-wide haplotype tagging approach. *Human Molecular Genetics*, **2006**, 15, 797-805	5.6	111
141	A novel variant on chromosome 7q22.3 associated with mean platelet volume, counts, and function. *Blood*, **2009**, 113, 3831-7	2.2	109
140	Multiethnic meta-analysis of genome-wide association studies in >100 000 subjects identifies 23 fibrinogen-associated Loci but no strong evidence of a causal association between circulating fibrinogen and cardiovascular disease. *Circulation*, **2013**, 128, 1310-24	16.7	107
139	Common variants in the region around Osterix are associated with bone mineral density and growth in childhood. *Human Molecular Genetics*, **2009**, 18, 1510-7	5.6	107
138	Ischemic stroke is associated with the ABO locus: the EuroCLOT study. *Annals of Neurology*, **2013**, 73, 16-31	9.4	105
137	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2011**, 88, 6-18	11	103

136	IRF4 variants have age-specific effects on nevus count and predispose to melanoma. *American Journal of Human Genetics*, **2010**, 87, 6-16	11	100
135	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. *Diabetes*, **2016**, 65, 803-17	0.9	96
134	The Polygenic and Monogenic Basis of Blood Traits and Diseases. *Cell*, **2020**, 182, 1214-1231.e11	56.2	96
133	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. *Nature Communications*, **2016**, 7, 13555	17.4	95
132	A genome-wide association study identifies three loci associated with mean platelet volume. *American Journal of Human Genetics*, **2009**, 84, 66-71	11	94
131	Identifying candidate causal variants responsible for altered activity of the ABCB1 multidrug resistance gene. *Genome Research*, **2004**, 14, 1333-44	9.7	94
130	Male-pattern baldness susceptibility locus at 20p11. *Nature Genetics*, **2008**, 40, 1282-4	36.3	93
129	Multiple loci are associated with white blood cell phenotypes. *PLoS Genetics*, **2011**, 7, e1002113	6	92
128	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. *Nature Communications*, **2017**, 8, 80	17.4	88
127	Synthetic associations are unlikely to account for many common disease genome-wide association signals. *PLoS Biology*, **2011**, 9, e1000580	9.7	88
126	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. *Cell*, **2020**, 182, 1198-1213.e14	56.2	88
125	Cardiometabolic effects of genetic upregulation of the interleukin 1 receptor antagonist: a Mendelian randomisation analysis. *Lancet Diabetes and Endocrinology,the*, **2015**, 3, 243-53	18.1	81
124	JAK2V617F leads to intrinsic changes in platelet formation and reactivity in a knock-in mouse model of essential thrombocythemia. *Blood*, **2013**, 122, 3787-97	2.2	79
123	Genetic determinants of heel bone properties: genome-wide association meta-analysis and replication in the GEFOS/GENOMOS consortium. *Human Molecular Genetics*, **2014**, 23, 3054-68	5.6	78
122	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2012**, 90, 1116-1117	11	78
121	SMIM1 underlies the Vel blood group and influences red blood cell traits. *Nature Genetics*, **2013**, 45, 542-545	36.3	77
120	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. *Cell*, **2019**, 179, 984-1002.e36	56.2	76
119	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. *Nature Communications*, **2018**, 9, 4455	17.4	75

118	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. *American Journal of Human Genetics*, **2017**, 100, 865-884	11	74
117	GARFIELD classifies disease-relevant genomic features through integration of functional annotations with association signals. *Nature Genetics*, **2019**, 51, 343-353	36.3	71
116	Height-reducing variants and selection for short stature in Sardinia. *Nature Genetics*, **2015**, 47, 1352-1356	36.3	71
115	The presence of methylation quantitative trait loci indicates a direct genetic influence on the level of DNA methylation in adipose tissue. *PLoS ONE*, **2013**, 8, e55923	3.7	71
114	Quantitative trait loci for CD4:CD8 lymphocyte ratio are associated with risk of type 1 diabetes and HIV-1 immune control. *American Journal of Human Genetics*, **2010**, 86, 88-92	11	71
113	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. *Genome Biology*, **2017**, 18, 18	18.3	70
112	A genome-wide association study identifies a novel locus on chromosome 18q12.2 influencing white cell telomere length. *Journal of Medical Genetics*, **2009**, 46, 451-4	5.8	69
111	Is the thrifty genotype hypothesis supported by evidence based on confirmed type 2 diabetes- and obesity-susceptibility variants?. *Diabetologia*, **2009**, 52, 1846-51	10.3	69
110	Eight common genetic variants associated with serum DHEAS levels suggest a key role in ageing mechanisms. *PLoS Genetics*, **2011**, 7, e1002025	6	69
109	Influence of ABCB1, ABCC1, ABCC2, and ABCG2 haplotypes on the cellular exposure of nelfinavir in vivo. *Pharmacogenetics and Genomics*, **2005**, 15, 599-608	1.9	69
108	Genome-wide association study for circulating levels of PAI-1 provides novel insights into its regulation. *Blood*, **2012**, 120, 4873-81	2.2	65
107	Positive selection on MMP3 regulation has shaped heart disease risk. *Current Biology*, **2004**, 14, 1531-9	6.3	64
106	Metabolomic identification of a novel pathway of blood pressure regulation involving hexadecanedioate. *Hypertension*, **2015**, 66, 422-9	8.5	63
105	Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. *Genome Biology*, **2017**, 18, 50	18.3	57
104	Whole-genome sequence-based analysis of thyroid function. *Nature Communications*, **2015**, 6, 5681	17.4	56
103	A multicenter study of BRD2 as a risk factor for juvenile myoclonic epilepsy. *Epilepsia*, **2007**, 48, 706-12	6.4	56
102	Genome-wide association study identifies inversion in the locus to modify risk for alcoholic and non-alcoholic chronic pancreatitis. *Gut*, **2018**, 67, 1855-1863	19.2	54
101	A genome-wide association study suggests that a locus within the ataxin 2 binding protein 1 gene is associated with hand osteoarthritis: the Treat-OA consortium. *Journal of Medical Genetics*, **2009**, 46, 614-6	5.8	54

100	A multiple-phenotype imputation method for genetic studies. *Nature Genetics*, **2016**, 48, 466-72	36.3	52
99	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
98	Identification of PLCL1 gene for hip bone size variation in females in a genome-wide association study. *PLoS ONE*, **2008**, 3, e3160	3.7	51
97	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. *Nature Genetics*, **2016**, 48, 1303-1312	36.3	51
96	Long term conservation of human metabolic phenotypes and link to heritability. *Metabolomics*, **2014**, 10, 1005-1017	4.7	50
95	Common genetic variation near the phospholamban gene is associated with cardiac repolarisation: meta-analysis of three genome-wide association studies. *PLoS ONE*, **2009**, 4, e6138	3.7	50
94	Meta-analysis of gene-level associations for rare variants based on single-variant statistics. *American Journal of Human Genetics*, **2013**, 93, 236-48	11	49
93	Human genomics: The end of the start for population sequencing. *Nature*, **2015**, 526, 52-3	50.4	48
92	Genetic Influences on Metabolite Levels: A Comparison across Metabolomic Platforms. *PLoS ONE*, **2016**, 11, e0153672	3.7	48
91	Genetic predictors of fibrin D-dimer levels in healthy adults. *Circulation*, **2011**, 123, 1864-72	16.7	47
90	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. *Nature Communications*, **2014**, 5, 4871	17.4	46
89	Association of the 9p21.3 locus with risk of first-ever myocardial infarction in Pakistanis: case-control study in South Asia and updated meta-analysis of Europeans. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2010**, 30, 1467-73	9.4	45
88	Genome-wide association analysis of eating disorder-related symptoms, behaviors, and personality traits. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2012**, 159B, 803-11	3.5	43
87	A comprehensive evaluation of potential lung function associated genes in the SpiroMeta general population sample. *PLoS ONE*, **2011**, 6, e19382	3.7	41
86	Functional interpretation of non-coding sequence variation: concepts and challenges. *BioEssays*, **2014**, 36, 191-9	4.1	38
85	A GWAS sequence variant for platelet volume marks an alternative DNM3 promoter in megakaryocytes near a MEIS1 binding site. *Blood*, **2012**, 120, 4859-68	2.2	38
84	Genes contributing to pain sensitivity in the normal population: an exome sequencing study. *PLoS Genetics*, **2012**, 8, e1003095	6	38
83	Population genetic and phylogenetic evidence for positive selection on regulatory mutations at the factor VII locus in humans. *Genetics*, **2004**, 167, 867-77	4	38

82	Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. *Nature Communications*, **2017**, 8, 15927	17.4	37
81	Significant impact of miRNA-target gene networks on genetics of human complex traits. *Scientific Reports*, **2016**, 6, 22223	4.9	36
80	The use of genome-wide eQTL associations in lymphoblastoid cell lines to identify novel genetic pathways involved in complex traits. *PLoS ONE*, **2011**, 6, e22070	3.7	35
79	Automated typing of red blood cell and platelet antigens: a whole-genome sequencing study. *Lancet Haematology,the*, **2018**, 5, e241-e251	14.6	35
78	Maps of open chromatin guide the functional follow-up of genome-wide association signals: application to hematological traits. *PLoS Genetics*, **2011**, 7, e1002139	6	34
77	A locus on chromosome 1p36 is associated with thyrotropin and thyroid function as identified by genome-wide association study. *American Journal of Human Genetics*, **2010**, 87, 430-5	11	34
76	Genome-wide association study for circulating tissue plasminogen activator levels and functional follow-up implicates endothelial STXBP5 and STX2. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2014**, 34, 1093-101	9.4	33
75	Genome-wide association study identifies 48 common genetic variants associated with handedness. *Nature Human Behaviour*, **2021**, 5, 59-70	12.8	33
74	Long- and short-term outcomes in renal allografts with deceased donors: A large recipient and donor genome-wide association study. *American Journal of Transplantation*, **2018**, 18, 1370-1379	8.7	32
73	Evidence for three genetic loci involved in both anorexia nervosa risk and variation of body mass index. *Molecular Psychiatry*, **2017**, 22, 192-201	15.1	31
72	Maps of open chromatin highlight cell type-restricted patterns of regulatory sequence variation at hematological trait loci. *Genome Research*, **2013**, 23, 1130-41	9.7	31
71	Modulation of genetic associations with serum urate levels by body-mass-index in humans. *PLoS ONE*, **2015**, 10, e0119752	3.7	31
70	Whole-Exome Sequencing Identifies Loci Associated with Blood Cell Traits and Reveals a Role for Alternative GFI1B Splice Variants in Human Hematopoiesis. *American Journal of Human Genetics*, **2016**, 99, 481-8	11	31
69	and Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. *Journal of the American Society of Nephrology: JASN*, **2017**, 28, 981-994	12.7	30
68	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. *Nature Communications*, **2017**, 8, 16058	17.4	30
67	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. *Nature Communications*, **2021**, 12, 24	17.4	30
66	Silencing of RhoA nucleotide exchange factor, ARHGEF3, reveals its unexpected role in iron uptake. *Blood*, **2011**, 118, 4967-76	2.2	29
65	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

64	A map of transcriptional heterogeneity and regulatory variation in human microglia. *Nature Genetics*, **2021**, 53, 861-868	36.3	26
63	A genome-wide screen for interactions reveals a new locus on 4p15 modifying the effect of waist-to-hip ratio on total cholesterol. *PLoS Genetics*, **2011**, 7, e1002333	6	25
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