Nicole Soranzo

List of Publications by Year in Descending Order

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	Higher body mass index raises immature platelet count: potential contribution to obesity-related thrombosis.. *Platelets*, **2022**, 1-10	3.6	1
242	Machine learning optimized polygenic scores for blood cell traits identify sex-specific trajectories and genetic correlations with disease.. *Cell Genomics*, **2022**, 2, None		1
241	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function.. *Nature Genetics*, **2022**,	36.3	6
240	Genetic associations at regulatory phenotypes improve fine-mapping of causal variants for 12 immune-mediated diseases.. *Nature Genetics*, **2022**, 54, 251-262	36.3	1
239	Integrative analysis of the plasma proteome and polygenic risk of cardiometabolic diseases. *Nature Metabolism*, **2021**, 3, 1476-1483	14.6	6
238	Genetic perturbation of PU.1 binding and chromatin looping at neutrophil enhancers associates with autoimmune disease. *Nature Communications*, **2021**, 12, 2298	17.4	7
237	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. *American Journal of Human Genetics*, **2021**, 108, 874-893	11	5
236	A map of transcriptional heterogeneity and regulatory variation in human microglia. *Nature Genetics*, **2021**, 53, 861-868	36.3	26
235	FUT6 deficiency compromises basophil function by selectively abrogating their sialyl-Lewis x expression. *Communications Biology*, **2021**, 4, 832	6.7	2
234	Genome-wide association study identifies 48 common genetic variants associated with handedness. *Nature Human Behaviour*, **2021**, 5, 59-70	12.8	33
233	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. *Nature Communications*, **2021**, 12, 24	17.4	30
232	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. *Communications Biology*, **2021**, 4, 156	6.7	11
231	Effects of adiposity on the human plasma proteome: observational and Mendelian randomisation estimates. *International Journal of Obesity*, **2021**, 45, 2221-2229	5.5	2
230	Mitochondrial DNA variants modulate N-formylmethionine, proteostasis and risk of late-onset human diseases. *Nature Medicine*, **2021**, 27, 1564-1575	50.5	4
229	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. *American Journal of Human Genetics*, **2021**, 108, 1836-1851	11	1
228	Paired rRNA-depleted and polyA-selected RNA sequencing data and supporting multi-omics data from human T cells. *Scientific Data*, **2020**, 7, 376	8.2	4
227	The influence of rare variants in circulating metabolic biomarkers. *PLoS Genetics*, **2020**, 16, e1008605	6	3

226	No Evidence of Persistence or Inheritance of Mitochondrial DNA Copy Number in Holocaust Survivors and Their Descendants. *Frontiers in Genetics*, **2020**, 11, 87	4.5	2
225	Personalized and graph genomes reveal missing signal in epigenomic data. *Genome Biology*, **2020**, 21, 124	18.3	13
224	A brief history of human disease genetics. *Nature*, **2020**, 577, 179-189	50.4	181
223	A bird@-eye view of Italian genomic variation through whole-genome sequencing. *European Journal of Human Genetics*, **2020**, 28, 435-444	5.3	16
222	The Polygenic and Monogenic Basis of Blood Traits and Diseases. *Cell*, **2020**, 182, 1214-1231.e11	56.2	96
221	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
220	Large genome-wide association study identifies three novel risk variants for restless legs syndrome. *Communications Biology*, **2020**, 3, 703	6.7	11
219	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
218	GARFIELD classifies disease-relevant genomic features through integration of functional annotations with association signals. *Nature Genetics*, **2019**, 51, 343-353	36.3	71
217	A catalog of genetic loci associated with kidney function from analyses of a million individuals. *Nature Genetics*, **2019**, 51, 957-972	36.3	217
216	Associations Between Attention-Deficit/Hyperactivity Disorder and Various Eating Disorders: A Swedish Nationwide Population Study Using Multiple Genetically Informative Approaches. *Biological Psychiatry*, **2019**, 86, 577-586	7.9	24
215	The impact of donor and recipient common clinical and genetic variation on estimated glomerular filtration rate in a European renal transplant population. *American Journal of Transplantation*, **2019**, 19, 2262-2273	8.7	4
214	Resolving variant-to-function relationships in hematopoiesis. *Nature Genetics*, **2019**, 51, 581-583	36.3	2
213	Disentangling the genetics of lean mass. *American Journal of Clinical Nutrition*, **2019**, 109, 276-287	7	24
212	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. *Cell*, **2019**, 179, 984-1002.e36	56.2	76
211	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
210	Identification of rare sequence variation underlying heritable pulmonary arterial hypertension. *Nature Communications*, **2018**, 9, 1416	17.4	182
209	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

208	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
207	Genomic atlas of the human plasma proteome. *Nature*, **2018**, 558, 73-79	50.4	529
206	Genetic architecture: the shape of the genetic contribution to human traits and disease. *Nature Reviews Genetics*, **2018**, 19, 110-124	30.1	219
205	Investigation of common, low-frequency and rare genome-wide variation in anorexia nervosa. *Molecular Psychiatry*, **2018**, 23, 1169-1180	15.1	24
204	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. *Nature Communications*, **2018**, 9, 4455	17.4	75
203	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
202	Automated typing of red blood cell and platelet antigens: a whole-genome sequencing study. *Lancet Haematology,the*, **2018**, 5, e241-e251	14.6	35
201	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
200	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. *Genome Biology*, **2017**, 18, 18	18.3	70
199	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
198	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
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	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. *American Journal of Human Genetics*, **2017**, 100, 865-884	11	74
195	The impact of rare and low-frequency genetic variants in common disease. *Genome Biology*, **2017**, 18, 77	18.3	174
194	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
193	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
192	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
191	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. *Nature Communications*, **2017**, 8, 80	17.4	88

190	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. *Nature Communications*, **2017**, 8, 16058	17.4	30
189	Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. *Nature Communications*, **2017**, 8, 15927	17.4	37
188	A reference panel of 64,976 haplotypes for genotype imputation. *Nature Genetics*, **2016**, 48, 1279-83	36.3	1447
187	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
186	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. *Cell*, **2016**, 167, 1415-1429.e19	56.2	637
185	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. *Cell*, **2016**, 167, 1145-1149	56.2	232
184	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. *Cell*, **2016**, 167, 1398-1414.e24	56.2	339
183	Large-scale production of megakaryocytes from human pluripotent stem cells by chemically defined forward programming. *Nature Communications*, **2016**, 7, 11208	17.4	155
182	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. *Diabetes*, **2016**, 65, 803-17	0.9	96
181	From GWAS to function: lessons from blood cells. *ISBT Science Series*, **2016**, 11, 211-219	1.1	9
180	A multiple-phenotype imputation method for genetic studies. *Nature Genetics*, **2016**, 48, 466-72	36.3	52
179	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. *Nature Communications*, **2016**, 7, 10023	17.4	295
178	Genetic Influences on Metabolite Levels: A Comparison across Metabolomic Platforms. *PLoS ONE*, **2016**, 11, e0153672	3.7	48
177	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. *Nature Communications*, **2016**, 7, 13555	17.4	95
176	Significant impact of miRNA-target gene networks on genetics of human complex traits. *Scientific Reports*, **2016**, 6, 22223	4.9	36
175	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. *Nature Genetics*, **2016**, 48, 1303-1312	36.3	51
174	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
173	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	50.4	119

172	Nonadditive Effects of Genes in Human Metabolomics. *Genetics*, **2015**, 200, 707-18	4	14
171	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
170	Human genomics: The end of the start for population sequencing. *Nature*, **2015**, 526, 52-3	50.4	48
169	An interactive genome browser of association results from the UK10K cohorts project. *Bioinformatics*, **2015**, 31, 4029-31	7.2	9
168	Multicohort analysis of the maternal age effect on recombination. *Nature Communications*, **2015**, 6, 7846	17.4	21
167	Metabolomic identification of a novel pathway of blood pressure regulation involving hexadecanedioate. *Hypertension*, **2015**, 66, 422-9	8.5	63
166	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
165	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. *Nature*, **2015**, 526, 112-7	50.4	308
164	The UK10K project identifies rare variants in health and disease. *Nature*, **2015**, 526, 82-90	50.4	776
163	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
162	Height-reducing variants and selection for short stature in Sardinia. *Nature Genetics*, **2015**, 47, 1352-1356	36.3	71
161	Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. *Nature Communications*, **2015**, 6, 8111	17.4	186
160	Whole-genome sequence-based analysis of thyroid function. *Nature Communications*, **2015**, 6, 5681	17.4	56
159	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. *Nature Communications*, **2015**, 6, 5897	17.4	147
158	Modulation of genetic associations with serum urate levels by body-mass-index in humans. *PLoS ONE*, **2015**, 10, e0119752	3.7	31
157	Long term conservation of human metabolic phenotypes and link to heritability. *Metabolomics*, **2014**, 10, 1005-1017	4.7	50
156	Functional interpretation of non-coding sequence variation: concepts and challenges. *BioEssays*, **2014**, 36, 191-9	4.1	38
155	An atlas of genetic influences on human blood metabolites. *Nature Genetics*, **2014**, 46, 543-550	36.3	695

154	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. *Nature Communications*, **2014**, 5, 4871	17.4	46
153	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
152	Transcriptional diversity during lineage commitment of human blood progenitors. *Science*, **2014**, 345, 1251033	33.3	187
151	A genome-wide association study of anorexia nervosa. *Molecular Psychiatry*, **2014**, 19, 1085-94	15.1	224
150	Common genetic variants do not associate with CAD in familial hypercholesterolemia. *European Journal of Human Genetics*, **2014**, 22, 809-13	5.3	2
149	Identification of novel genetic Loci associated with thyroid peroxidase antibodies and clinical thyroid disease. *PLoS Genetics*, **2014**, 10, e1004123	6	122
148	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
147	A loss of function screen of identified genome-wide association study Loci reveals new genes controlling hematopoiesis. *PLoS Genetics*, **2014**, 10, e1004450	6	18
146	A general approach for haplotype phasing across the full spectrum of relatedness. *PLoS Genetics*, **2014**, 10, e1004234	6	377
145	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
144	Novel genetic associations with serum level metabolites identified by phenotype set enrichment analyses. *Human Molecular Genetics*, **2014**, 23, 5847-57	5.6	23
143	Interrogating causal pathways linking genetic variants, small molecule metabolites, and circulating lipids. *Genome Medicine*, **2014**, 6, 25	14.4	14
142	Biomarkers for type 2 diabetes and impaired fasting glucose using a nontargeted metabolomics approach. *Diabetes*, **2013**, 62, 4270-6	0.9	268
141	Small effective population size and genetic homogeneity in the Val Borbera isolate. *European Journal of Human Genetics*, **2013**, 21, 89-94	5.3	20
140	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
139	Loci influencing blood pressure identified using a cardiovascular gene-centric array. *Human Molecular Genetics*, **2013**, 22, 1663-78	5.6	119
138	Ischemic stroke is associated with the ABO locus: the EuroCLOT study. *Annals of Neurology*, **2013**, 73, 16-31	9.4	105
137	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. *Nature Genetics*, **2013**, 45, 145-54	36.3	505

136	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
135	Platelet Genomics **2013**, 67-89		2
134	SMIM1 underlies the Vel blood group and influences red blood cell traits. *Nature Genetics*, **2013**, 45, 542-545	36.3	77
133	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
132	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics*, **2013**, 45, 621-31	36.3	219
131	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
130	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
129	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
128	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
127	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
126	Genome wide association analysis of a founder population identified TAF3 as a gene for MCHC in humans. *PLoS ONE*, **2013**, 8, e69206	3.7	9
125	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
124	Human serum metabolic profiles are age dependent. *Aging Cell*, **2012**, 11, 960-7	9.9	193
123	Genome-wide association study for circulating levels of PAI-1 provides novel insights into its regulation. *Blood*, **2012**, 120, 4873-81	2.2	65
122	Seventy-five genetic loci influencing the human red blood cell. *Nature*, **2012**, 492, 369-75	50.4	257
121	Genome-wide meta-analysis of common variant differences between men and women. *Human Molecular Genetics*, **2012**, 21, 4805-15	5.6	24
120	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
119	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

118	Copy number variation of the APC gene is associated with regulation of bone mineral density. *Bone*, **2012**, 51, 939-43	4.7	10
117	Mapping cis- and trans-regulatory effects across multiple tissues in twins. *Nature Genetics*, **2012**, 44, 1084-9	36.3	572
116	A genome-wide association search for type 2 diabetes genes in African Americans. *PLoS ONE*, **2012**, 7, e29202	3.7	138
115	BLUEPRINT to decode the epigenetic signature written in blood. *Nature Biotechnology*, **2012**, 30, 224-6	44.5	261
114	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
113	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
112	The metabochip, a custom genotyping array for genetic studies of metabolic, cardiovascular, and anthropometric traits. *PLoS Genetics*, **2012**, 8, e1002793	6	395
111	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
110	Genes contributing to pain sensitivity in the normal population: an exome sequencing study. *PLoS Genetics*, **2012**, 8, e1003095	6	38
109	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. *Nature Genetics*, **2011**, 43, 753-60	36.3	237
108	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. *Nature* , **2011**, 478, 103-9	50.4	1564
107	New gene functions in megakaryopoiesis and platelet formation. *Nature*, **2011**, 480, 201-8	50.4	330
106	Human metabolic individuality in biomedical and pharmaceutical research. *Nature*, **2011**, 477, 54-60	50.4	728
105	Interpreting Association Signals **2011**, 261-276		
104	Silencing of RhoA nucleotide exchange factor, ARHGEF3, reveals its unexpected role in iron uptake. *Blood*, **2011**, 118, 4967-76	2.2	29
103	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. *Nature Genetics*, **2011**, 43, 333-8	36.3	1394
102	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
101	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

100	Genetic determinants of variability in glycated hemoglobin (HbA(1c)) in humans: review of recent progress and prospects for use in diabetes care. *Current Diabetes Reports*, **2011**, 11, 562-9	5.6	23
99	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
98	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
97	Genetic predictors of fibrin D-dimer levels in healthy adults. *Circulation*, **2011**, 123, 1864-72	16.7	47
96	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. *Nature Genetics*, **2011**, 43, 1005-11	36.3	338
95	Multiple loci are associated with white blood cell phenotypes. *PLoS Genetics*, **2011**, 7, e1002113	6	92
94	Synthetic associations are unlikely to account for many common disease genome-wide association signals. *PLoS Biology*, **2011**, 9, e1000580	9.7	88
93	The architecture of gene regulatory variation across multiple human tissues: the MuTHER study. *PLoS Genetics*, **2011**, 7, e1002003	6	336
92	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
91	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
90	Eight common genetic variants associated with serum DHEAS levels suggest a key role in ageing mechanisms. *PLoS Genetics*, **2011**, 7, e1002025	6	69
89	A comprehensive evaluation of potential lung function associated genes in the SpiroMeta general population sample. *PLoS ONE*, **2011**, 6, e19382	3.7	41
88	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
87	Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*, **2010**, 466, 707-13	50.4	2742
86	Integrating common and rare genetic variation in diverse human populations. *Nature*, **2010**, 467, 52-8	50.4	2135
85	Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature*, **2010**, 467, 832-8	50.4	1514
84	Genome-wide association study identifies five loci associated with lung function. *Nature Genetics*, **2010**, 42, 36-44	36.3	430
83	A genome-wide perspective of genetic variation in human metabolism. *Nature Genetics*, **2010**, 42, 137-41	36.3	515

82	Genetic loci influencing kidney function and chronic kidney disease. *Nature Genetics*, **2010**, 42, 373-5	36.3	205
81	Sequence variants at CHRNB3-CHRNA6 and CYP2A6 affect smoking behavior. *Nature Genetics*, **2010**, 42, 448-53	36.3	582
80	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
79	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics*, **2010**, 42, 937-48	36.3	2267
78	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
77	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
76	Common variants at 10 genomic loci influence hemoglobin A[C) levels via glycemic and nonglycemic pathways. *Diabetes*, **2010**, 59, 3229-39	0.9	314
75	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
74	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
73	Genome-wide association study identifies two novel regions at 11p15.5-p13 and 1p31 with major impact on acute-phase serum amyloid A. *PLoS Genetics*, **2010**, 6, e1001213	6	20
72	Genome-wide association study of blood pressure extremes identifies variant near UMOD associated with hypertension. *PLoS Genetics*, **2010**, 6, e1001177	6	255
71	Genetic determinants of major blood lipids in Pakistanis compared with Europeans. *Circulation: Cardiovascular Genetics*, **2010**, 3, 348-57		20
70	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
69	Common variants near TERC are associated with mean telomere length. *Nature Genetics*, **2010**, 42, 197-9	36.3	255
68	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
67	Common genetic determinants of vitamin D insufficiency: a genome-wide association study. *Lancet, The*, **2010**, 376, 180-8	40	1183
66	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
65	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

64	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
63	IRF4 variants have age-specific effects on nevus count and predispose to melanoma. *American Journal of Human Genetics*, **2010**, 87, 6-16	11	100
62	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
61	Genome-wide association scan meta-analysis identifies three Loci influencing adiposity and fat distribution. *PLoS Genetics*, **2009**, 5, e1000508	6	393
60	Large scale association analysis of novel genetic loci for coronary artery disease. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2009**, 29, 774-80	9.4	125
59	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
58	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
57	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
56	A genome-wide association study reveals variants in ARL15 that influence adiponectin levels. *PLoS Genetics*, **2009**, 5, e1000768	6	129
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14	Variation in PU.1 binding and chromatin looping at neutrophil enhancers influences autoimmune disease susceptibility		1
13	A reference panel of 64,976 haplotypes for genotype imputation		15
12	Network-based metabolite ratios for an improved functional characterization of genome-wide association study results		2
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