

## List of Publications by Citations

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294  
papers

60,305  
citations

106  
h-index

245  
g-index

329  
ext. papers

79,878  
ext. citations

18.8  
avg. IF

5.7  
L-index

#	Paper	IF	Citations
294	Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans. <i>Science</i> , <b>2015</b> , 348, 648-60	33.3	3242
293	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , <b>2015</b> , 518, 197-206	50.4	2687
292	The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , <b>2020</b> , 581, 434-443	50.4	2278
291	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , <b>2010</b> , 42, 937-48	36.3	2267
290	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , <b>2013</b> , 45, 1274-1283	36.3	1904
289	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , <b>2010</b> , 467, 832-8	50.4	1514
288	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , <b>2012</b> , 44, 981-90	36.3	1482
287	Genetics of rheumatoid arthritis contributes to biology and drug discovery. <i>Nature</i> , <b>2014</b> , 506, 376-81	50.4	1426
286	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , <b>2014</b> , 46, 1173-86	36.3	1339
285	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , <b>2018</b> , 50, 668-681	36.3	1301
284	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , <b>2015</b> , 47, 1121-1130	36.3	1290
283	Systematic identification of trans eQTLs as putative drivers of known disease associations. <i>Nature Genetics</i> , <b>2013</b> , 45, 1238-1243	36.3	1244
282	Large-scale association analysis identifies new risk loci for coronary artery disease. <i>Nature Genetics</i> , <b>2013</b> , 45, 25-33	36.3	1172
281	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. <i>Nature Genetics</i> , <b>2018</b> , 50, 1112-1121	36.3	950
280	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , <b>2015</b> , 518, 187-196	50.4	920
279	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , <b>2016</b> , 533, 539-42	50.4	850
278	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , <b>2014</b> , 46, 234-44	36.3	784

277	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , <b>2010</b> , 42, 949-60	36.3	724
276	The genetic architecture of type 2 diabetes. <i>Nature</i> , <b>2016</b> , 536, 41-47	50.4	704
275	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. <i>Nature Genetics</i> , <b>2012</b> , 44, 1341-8	36.3	681
274	Genome-wide association study identifies 30 loci associated with bipolar disorder. <i>Nature Genetics</i> , <b>2019</b> , 51, 793-803	36.3	662
273	Identification of seven loci affecting mean telomere length and their association with disease. <i>Nature Genetics</i> , <b>2013</b> , 45, 422-7, 427e1-2	36.3	624
272	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , <b>2012</b> , 44, 991-1005	36.3	621
271	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. <i>Nature Genetics</i> , <b>2016</b> , 48, 624-33	36.3	602
270	Common variants associated with plasma triglycerides and risk for coronary artery disease. <i>Nature Genetics</i> , <b>2013</b> , 45, 1345-52	36.3	597
269	Sequence variants at CHRN3-CHRNA6 and CYP2A6 affect smoking behavior. <i>Nature Genetics</i> , <b>2010</b> , 42, 448-53	36.3	582
268	GWAS of 126,559 individuals identifies genetic variants associated with educational attainment. <i>Science</i> , <b>2013</b> , 340, 1467-71	33.3	563
267	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , <b>2017</b> , 49, 27-35	36.3	530
266	Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. <i>Nature Genetics</i> , <b>2015</b> , 47, 1114-20	36.3	522
265	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. <i>Nature Genetics</i> , <b>2019</b> , 51, 237-244	36.3	516
264	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , <b>2013</b> , 45, 145-54	36.3	505
263	Biological interpretation of genome-wide association studies using predicted gene functions. <i>Nature Communications</i> , <b>2015</b> , 6, 5890	17.4	489
262	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , <b>2013</b> , 45, 501-12	36.3	437
261	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , <b>2017</b> , 66, 2888-2902	29.0	414
260	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , <b>2017</b> , 542, 186-190	50.4	412

259	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. <i>Nature Genetics</i> , <b>2016</b> , 48, 510-8	36.3	404
258	A new highly penetrant form of obesity due to deletions on chromosome 16p11.2. <i>Nature</i> , <b>2010</b> , 463, 671-5	50.4	403
257	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , <b>2014</b> , 514, 92-97	50.4	401
256	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , <b>2018</b> , 50, 1412-1425	36.3	386
255	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. <i>Nature Genetics</i> , <b>2010</b> , 42, 1077-85	36.3	372
254	Genome-wide association analysis identifies variation in vitamin D receptor and other host factors influencing the gut microbiota. <i>Nature Genetics</i> , <b>2016</b> , 48, 1396-1406	36.3	369
253	Common variants in KCNN3 are associated with lone atrial fibrillation. <i>Nature Genetics</i> , <b>2010</b> , 42, 240-4	36.3	362
252	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. <i>Cell</i> , <b>2018</b> , 173, 1705-1715.e16	56.2	360
251	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. <i>Nature Genetics</i> , <b>2016</b> , 48, 856-66	36.3	355
250	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , <b>2011</b> , 43, 1005-11	36.3	338
249	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , <b>2015</b> , 6, 8570	17.4	335
248	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. <i>Nature Communications</i> , <b>2016</b> , 7, 11122	17.4	335
247	New gene functions in megakaryopoiesis and platelet formation. <i>Nature</i> , <b>2011</b> , 480, 201-8	50.4	330
246	Coding Variation in ANGPTL4, LPL, and SVEP1 and the Risk of Coronary Disease. <i>New England Journal of Medicine</i> , <b>2016</b> , 374, 1134-44	59.2	325
245	Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. <i>Nature</i> , <b>2011</b> , 478, 97-102	50.4	322
244	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , <b>2017</b> , 49, 403-415	36.3	313
243	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , <b>2017</b> , 49, 1758-1766	36.3	310
242	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , <b>2012</b> , 490, 267-72	50.4	304

241	Genome-wide association study identifies eight risk loci and implicates metabo-psychiatric origins for anorexia nervosa. <i>Nature Genetics</i> , <b>2019</b> , 51, 1207-1214	36.3	303
240	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , <b>2016</b> , 7, 10023	17.4	295
239	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , <b>2015</b> , 47, 1415-25	36.3	292
238	Quality control and conduct of genome-wide association meta-analyses. <i>Nature Protocols</i> , <b>2014</b> , 9, 1192-218	28.8	278
237	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , <b>2018</b> , 50, 1225-1233	36.3	277
236	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003500	6	277
235	Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. <i>Lancet, The</i> , <b>2012</b> , 380, 815-23	40	275
234	Meta-analysis of genome-wide association studies for personality. <i>Molecular Psychiatry</i> , <b>2012</b> , 17, 337-49	15.1	274
233	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. <i>Nature Genetics</i> , <b>2019</b> , 51, 245-257	36.3	259
232	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , <b>2017</b> , 49, 834-841	36.3	257
231	Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , <b>2012</b> , 492, 369-75	50.4	257
230	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , <b>2016</b> , 48, 1171-1184	36.3	251
229	Distribution and medical impact of loss-of-function variants in the Finnish founder population. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004494	6	243
228	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. <i>Nature Genetics</i> , <b>2012</b> , 44, 260-8	36.3	243
227	Genetic structure of Europeans: a view from the North-East. <i>PLoS ONE</i> , <b>2009</b> , 4, e5472	3.7	237
226	The impact of low-frequency and rare variants on lipid levels. <i>Nature Genetics</i> , <b>2015</b> , 47, 589-97	36.3	229
225	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , <b>2015</b> , 47, 1294-1303	36.3	226
224	A genome-wide association study of anorexia nervosa. <i>Molecular Psychiatry</i> , <b>2014</b> , 19, 1085-94	15.1	224

223	Combined analysis of genome-wide association studies for Crohn disease and psoriasis identifies seven shared susceptibility loci. <i>American Journal of Human Genetics</i> , <b>2012</b> , 90, 636-47	11	224
222	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. <i>Nature Genetics</i> , <b>2015</b> , 47, 1282-1293	36.3	223
221	A structural variation reference for medical and population genetics. <i>Nature</i> , <b>2020</b> , 581, 444-451	50.4	223
220	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. <i>JAMA Psychiatry</i> , <b>2015</b> , 72, 642-50	14.5	222
219	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005378	6	220
218	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , <b>2013</b> , 45, 621-31	36.3	219
217	Genome-wide association and genetic functional studies identify autism susceptibility candidate 2 gene (AUTS2) in the regulation of alcohol consumption. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 7119-24	11.5	218
216	Human disease-associated genetic variation impacts large intergenic non-coding RNA expression. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003201	6	209
215	Biomarker profiling by nuclear magnetic resonance spectroscopy for the prediction of all-cause mortality: an observational study of 17,345 persons. <i>PLoS Medicine</i> , <b>2014</b> , 11, e1001606	11.6	206
214	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , <b>2016</b> , 48, 1462-1472	36.3	198
213	Population genetic differentiation of height and body mass index across Europe. <i>Nature Genetics</i> , <b>2015</b> , 47, 1357-62	36.3	186
212	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , <b>2018</b> , 50, 26-41	36.3	186
211	Genome-wide Association Analysis of Psoriatic Arthritis and Cutaneous Psoriasis Reveals Differences in Their Genetic Architecture. <i>American Journal of Human Genetics</i> , <b>2015</b> , 97, 816-36	11	185
210	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , <b>2016</b> , 48, 1151-1161	36.3	181
209	Common genetic variants associated with cognitive performance identified using the proxy-phenotype method. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 13790-4	11.5	181
208	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , <b>2016</b> , 7, 10495	17.4	180
207	Signatures of negative selection in the genetic architecture of human complex traits. <i>Nature Genetics</i> , <b>2018</b> , 50, 746-753	36.3	178
206	Cohort Profile: Estonian Biobank of the Estonian Genome Center, University of Tartu. <i>International Journal of Epidemiology</i> , <b>2015</b> , 44, 1137-47	7.8	175

205	Unraveling the polygenic architecture of complex traits using blood eQTL metaanalysis		175
204	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , <b>2015</b> , 20, 647-656	15.1	167
203	KLB is associated with alcohol drinking, and its gene product Klotho is necessary for FGF21 regulation of alcohol preference. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 14372-14377	11.5	150
202	Detection and replication of epistasis influencing transcription in humans. <i>Nature</i> , <b>2014</b> , 508, 249-53	50.4	149
201	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , <b>2017</b> , 69, 823-836	15.1	146
200	The role of adiposity in cardiometabolic traits: a Mendelian randomization analysis. <i>PLoS Medicine</i> , <b>2013</b> , 10, e1001474	11.6	144
199	Genome-wide association and functional follow-up reveals new loci for kidney function. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002584	6	143
198	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. <i>Nature Communications</i> , <b>2020</b> , 11, 163	17.4	140
197	Dominance genetic variation contributes little to the missing heritability for human complex traits. <i>American Journal of Human Genetics</i> , <b>2015</b> , 96, 377-85	11	138
196	Large scale meta-analysis characterizes genetic architecture for common psoriasis associated variants. <i>Nature Communications</i> , <b>2017</b> , 8, 15382	17.4	136
195	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. <i>Nature Communications</i> , <b>2015</b> , 6, 7208	17.4	126
194	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. <i>Behavior Genetics</i> , <b>2016</b> , 46, 170-82	3.2	122
193	Enhanced meta-analysis and replication studies identify five new psoriasis susceptibility loci. <i>Nature Communications</i> , <b>2015</b> , 6, 7001	17.4	122
192	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. <i>Nature Communications</i> , <b>2014</b> , 5, 4926	17.4	121
191	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , <b>2015</b> , 523, 459-463	50.4	119
190	Improved polygenic prediction by Bayesian multiple regression on summary statistics. <i>Nature Communications</i> , <b>2019</b> , 10, 5086	17.4	114
189	A K(ATP) channel gene effect on sleep duration: from genome-wide association studies to function in <i>Drosophila</i> . <i>Molecular Psychiatry</i> , <b>2013</b> , 18, 122-32	15.1	113
188	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , <b>2017</b> , 8, 14977	17.4	105

187	Genome-wide analysis of BMI in adolescents and young adults reveals additional insight into the effects of genetic loci over the life course. <i>Human Molecular Genetics</i> , <b>2013</b> , 22, 3597-607	5.6	103
186	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006528	6	103
185	A variant in MCF2L is associated with osteoarthritis. <i>American Journal of Human Genetics</i> , <b>2011</b> , 89, 446-50		102
184	Genome-wide association study of lifetime cannabis use based on a large meta-analytic sample of 32 330 subjects from the International Cannabis Consortium. <i>Translational Psychiatry</i> , <b>2016</b> , 6, e769	8.6	102
183	The Genetic Architecture of Gene Expression in Peripheral Blood. <i>American Journal of Human Genetics</i> , <b>2017</b> , 100, 228-237	11	98
182	Adiposity as a cause of cardiovascular disease: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , <b>2015</b> , 44, 578-86	7.8	97
181	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , <b>2020</b> , 182, 1214-1231.e11	56.2	96
180	A meta-analysis of genome-wide association studies identifies novel variants associated with osteoarthritis of the hip. <i>Annals of the Rheumatic Diseases</i> , <b>2014</b> , 73, 2130-6	2.4	95
179	Hidden heritability due to heterogeneity across seven populations. <i>Nature Human Behaviour</i> , <b>2017</b> , 1, 757-765	12.8	94
178	Structural forms of the human amylase locus and their relationships to SNPs, haplotypes and obesity. <i>Nature Genetics</i> , <b>2015</b> , 47, 921-5	36.3	92
177	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 13366-13371	11.5	90
176	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. <i>Nature Communications</i> , <b>2018</b> , 9, 3391	17.4	90
175	Genome-wide meta-analysis of psoriatic arthritis identifies susceptibility locus at REL. <i>Journal of Investigative Dermatology</i> , <b>2012</b> , 132, 1133-40	4.3	89
174	Assessment of osteoarthritis candidate genes in a meta-analysis of nine genome-wide association studies. <i>Arthritis and Rheumatology</i> , <b>2014</b> , 66, 940-9	9.5	88
173	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. <i>Journal of the American College of Cardiology</i> , <b>2019</b> , 73, 58-66	15.1	86
172	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. <i>Hypertension</i> , <b>2017</b> ,	8.5	85
171	Insights into the genetic architecture of osteoarthritis from stage 1 of the arcOGEN study. <i>Annals of the Rheumatic Diseases</i> , <b>2011</b> , 70, 864-7	2.4	85
170	Meta-analysis of genome-wide association studies identifies common variants in CTNNA2 associated with excitement-seeking. <i>Translational Psychiatry</i> , <b>2011</b> , 1, e49	8.6	84



169	A meta-analysis of gene expression signatures of blood pressure and hypertension. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005035	6	83
168	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. <i>Nature Genetics</i> , <b>2021</b> , 53, 817-829	36.3	83
167	Improved imputation accuracy of rare and low-frequency variants using population-specific high-coverage WGS-based imputation reference panel. <i>European Journal of Human Genetics</i> , <b>2017</b> , 25, 869-876	5.3	82
166	A genome-wide association study of early menopause and the combined impact of identified variants. <i>Human Molecular Genetics</i> , <b>2013</b> , 22, 1465-72	5.6	82
165	Genomics of 1 million parent lifespans implicates novel pathways and common diseases and distinguishes survival chances. <i>ELife</i> , <b>2019</b> , 8,	8.9	82
164	Cell Specific eQTL Analysis without Sorting Cells. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005223	6	81
163	Harmonization of Neuroticism and Extraversion phenotypes across inventories and cohorts in the Genetics of Personality Consortium: an application of Item Response Theory. <i>Behavior Genetics</i> , <b>2014</b> , 44, 295-313	3.2	80
162	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. <i>Nature Communications</i> , <b>2017</b> , 8, 910	17.4	78
161	Genotype-covariate interaction effects and the heritability of adult body mass index. <i>Nature Genetics</i> , <b>2017</b> , 49, 1174-1181	36.3	78
160	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , <b>2016</b> , 68, 1435-1448	15.1	76
159	Pathogenic implications for autoimmune mechanisms derived by comparative eQTL analysis of CD4+ versus CD8+ T cells. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006643	6	75
158	Replicability and robustness of genome-wide-association studies for behavioral traits. <i>Psychological Science</i> , <b>2014</b> , 25, 1975-86	7.9	75
157	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. <i>Scientific Reports</i> , <b>2017</b> , 7, 45040	4.9	70
156	Personality traits and eating habits in a large sample of Estonians. <i>Health Psychology</i> , <b>2012</b> , 31, 806-14	5	69
155	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. <i>Biological Psychiatry</i> , <b>2017</b> , 82, 322-329	7.9	68
154	Ultra-rare disruptive and damaging mutations influence educational attainment in the general population. <i>Nature Neuroscience</i> , <b>2016</b> , 19, 1563-1565	25.5	63
153	Evidence of inbreeding depression on human height. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002655	6	62
152	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. <i>American Journal of Human Genetics</i> , <b>2016</b> , 99, 40-55	11	61

151	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. <i>Nature Metabolism</i> , <b>2020</b> , 2, 1135-1148	14.6	61
150	Genetic signature to provide robust risk assessment of psoriatic arthritis development in psoriasis patients. <i>Nature Communications</i> , <b>2018</b> , 9, 4178	17.4	61
149	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. <i>Nature Genetics</i> , <b>2021</b> , 53, 1300-1310	36.3	60
148	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , <b>2019</b> , 51, 636-648	36.3	59
147	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , <b>2018</b> , 102, 375-400	11	59
146	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005230	6	59
145	A whole-blood transcriptome meta-analysis identifies gene expression signatures of cigarette smoking. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 4611-4623	5.6	58
144	Targeted Application of Human Genetic Variation Can Improve Red Blood Cell Production from Stem Cells. <i>Cell Stem Cell</i> , <b>2016</b> , 18, 73-78	18	57
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140	Variants near CHRNA3/5 and APOE have age- and sex-related effects on human lifespan. <i>Nature Communications</i> , <b>2016</b> , 7, 11174	17.4	55
139	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. <i>Human Molecular Genetics</i> , <b>2012</b> , 21, 5329-43	5.6	54
138	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. <i>Nature Communications</i> , <b>2018</b> , 9, 2606	17.4	53
137	Age- and sex-specific causal effects of adiposity on cardiovascular risk factors. <i>Diabetes</i> , <b>2015</b> , 64, 1841-529	5.29	50
136	Genetic characterization of northeastern Italian population isolates in the context of broader European genetic diversity. <i>European Journal of Human Genetics</i> , <b>2013</b> , 21, 659-65	5.3	50
135	Genome-wide genetic homogeneity between sexes and populations for human height and body mass index. <i>Human Molecular Genetics</i> , <b>2015</b> , 24, 7445-9	5.6	49
134	Meta-analysis of gene-level associations for rare variants based on single-variant statistics. <i>American Journal of Human Genetics</i> , <b>2013</b> , 93, 236-48	11	49

133	Sex- and age-interacting eQTLs in human complex diseases. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 1947-56.6	5.6	48
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131	Association of adiposity genetic variants with menarche timing in 92,105 women of European descent. <i>American Journal of Epidemiology</i> , <b>2013</b> , 178, 451-60	3.8	48
130	The effect of LRRK2 loss-of-function variants in humans. <i>Nature Medicine</i> , <b>2020</b> , 26, 869-877	50.5	47
129	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. <i>American Journal of Human Genetics</i> , <b>2016</b> , 99, 8-21	11	47
128	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , <b>2016</b> , 7, 13357	17.4	46
127	A common 16p11.2 inversion underlies the joint susceptibility to asthma and obesity. <i>American Journal of Human Genetics</i> , <b>2014</b> , 94, 361-72	11	46
126	An epigenome-wide association study meta-analysis of educational attainment. <i>Molecular Psychiatry</i> , <b>2017</b> , 22, 1680-1690	15.1	46
125	Novel approach identifies SNPs in SLC2A10 and KCNK9 with evidence for parent-of-origin effect on body mass index. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004508	6	45
124	Genome-wide Analysis of Body Proportion Classifies Height-Associated Variants by Mechanism of Action and Implicates Genes Important for Skeletal Development. <i>American Journal of Human Genetics</i> , <b>2015</b> , 96, 695-708	11	44
123	Gene-based meta-analysis of genome-wide association studies implicates new loci involved in obesity. <i>Human Molecular Genetics</i> , <b>2015</b> , 24, 6849-60	5.6	44
122	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , <b>2019</b> , 51, 452-469	36.3	44
121	Genetic influence on social outcomes during and after the Soviet era in Estonia. <i>Nature Human Behaviour</i> , <b>2018</b> , 2, 269-275	12.8	42
120	Common Variant Burden Contributes to the Familial Aggregation of Migraine in 1,589 Families. <i>Neuron</i> , <b>2018</b> , 98, 743-753.e4	13.9	42
119	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. <i>American Journal of Human Genetics</i> , <b>2016</b> , 99, 22-39	11	42
118	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , <b>2019</b> , 10, 376	17.4	41
117	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , <b>2019</b> , 10, 4957	17.4	40
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115	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25,000 subjects. <i>Molecular Psychiatry</i> , <b>2015</b> , 20, 735-43	15.1	39
114	Glycosylation of immunoglobulin G is regulated by a large network of genes pleiotropic with inflammatory diseases. <i>Science Advances</i> , <b>2020</b> , 6, eaax0301	14.3	38
113	GWAS for male-pattern baldness identifies 71 susceptibility loci explaining 38% of the risk. <i>Nature Communications</i> , <b>2017</b> , 8, 1584	17.4	37
112	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 2490-7	5.6	35
111	Mapping genomic loci implicates genes and synaptic biology in schizophrenia.. <i>Nature</i> , <b>2022</b> ,	50.4	35
110	Haplotype Sharing Provides Insights into Fine-Scale Population History and Disease in Finland. <i>American Journal of Human Genetics</i> , <b>2018</b> , 102, 760-775	11	34
109	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475 000 Individuals. <i>Circulation: Cardiovascular Genetics</i> , <b>2017</b> , 10,		33
108	Allele-specific expression changes dynamically during T cell activation in HLA and other autoimmune loci. <i>Nature Genetics</i> , <b>2020</b> , 52, 247-253	36.3	33
107	Molecular genetic overlap between migraine and major depressive disorder. <i>European Journal of Human Genetics</i> , <b>2018</b> , 26, 1202-1216	5.3	32
106	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , <b>2018</b> , 13, e0198166	3.7	31
105	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. <i>Nature Communications</i> , <b>2019</b> , 10, 5121	17.4	31
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93	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , <b>2021</b> , 53, 1311-1321	36.3	27
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51	Mega-analysis of 31,396 individuals from 6 countries uncovers strong gene-environment interaction for human fertility		7
50	Widespread signatures of negative selection in the genetic architecture of human complex traits		7
49	Genomic and phenomic insights from an atlas of genetic effects on DNA methylation		7
48	Human loss-of-function variants suggest that partial LRRK2 inhibition is a safe therapeutic strategy for Parkinson disease		7
47	Habitual sleep disturbances and migraine: a Mendelian randomization study. <i>Annals of Clinical and Translational Neurology</i> , <b>2020</b> , 7, 2370-2380	5.3	6
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32	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4
31	Allele-specific expression changes dynamically during T cell activation in HLA and other autoimmune loci		4
30	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. <i>Molecular Psychiatry</i> , <b>2021</b> , 26, 2111-2125	15.1	3
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26	The Polygenic and Monogenic Basis of Blood Traits and Diseases		3



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22	Genome-wide study identifies association between HLA-B*55:01 and penicillin allergy		2
21	Haplotype sharing provides insights into fine-scale population history and disease in Finland		2
20	Improved polygenic prediction by Bayesian multiple regression on summary statistics		2
19	Genome-wide association study provides new insights into the genetic architecture and pathogenesis of heart failure		2
18	Dissecting the shared genetic architecture of suicide attempt, psychiatric disorders and known risk factors		2
17	The effect of X-linked dosage compensation on complex trait variation		2
16	Safe management of full-capacity live/mass events in COVID-19 will require mathematical, epidemiological and economic modelling. <i>Journal of the Royal Society of Medicine</i> , 2021, 114, 290-294	2.3	2
15	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries		1
14	Constraints on eQTL fine mapping in the presence of multi-site local regulation of gene expression		1
13	Novel blood pressure locus and gene discovery using GWAS and expression datasets from blood and the kidney		1
12	Identifying tissues implicated in Anorexia Nervosa using Transcriptomic Imputation		1
11	Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution		1
10	Genomic underpinnings of lifespan allow prediction and reveal basis in modern risks		1
9	Multi-ancestry analysis of gene-sleep interactions in 126,926 individuals identifies multiple novel blood lipid loci that contribute to our understanding of sleep-associated adverse blood lipid profile		1
8	Genomic analyses for age at menarche identify 389 independent signals and indicate BMI-independent effects of puberty timing on cancer susceptibility		1

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