

# Tnu Esko

## List of Publications by Year in Descending Order

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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.

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	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology.. <i>Nature Communications</i> , <b>2022</b> , 13, 634	17.4	3
293	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. <i>Biological Psychiatry</i> , <b>2022</b> , 91, 102-117	7.9	11
292	Mapping genomic loci implicates genes and synaptic biology in schizophrenia.. <i>Nature</i> , <b>2022</b> ,	50.4	35
291	Using genetic variation to disentangle the complex relationship between food intake and health outcomes. <i>PLoS Genetics</i> , <b>2022</b> , 18, e1010162	6	0
290	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
289	Genomic analysis of diet composition finds novel loci and associations with health and lifestyle. <i>Molecular Psychiatry</i> , <b>2021</b> , 26, 2056-2069	15.1	25
288	Electronic health record-based genome-wide meta-analysis provides insights on the genetic architecture of non-alcoholic fatty liver disease. <i>Cell Reports Medicine</i> , <b>2021</b> , 2, 100437	18	4
287	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. <i>Nature Genetics</i> , <b>2021</b> , 53, 1504-1516	36.3	7
286	Multivariate genome-wide analysis of immunoglobulin G N-glycosylation identifies new loci pleiotropic with immune function. <i>Human Molecular Genetics</i> , <b>2021</b> , 30, 1259-1270	5.6	0
285	Multi-ancestry genome-wide gene-sleep interactions identify novel loci for blood pressure. <i>Molecular Psychiatry</i> , <b>2021</b> ,	15.1	3
284	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> , <b>2021</b> , 114, 290-294	2.3	2
283	Predicting COVID-19 Transmission to Inform the Management of Mass Events: Model-Based Approach. <i>JMIR Public Health and Surveillance</i> , <b>2021</b> , 7, e30648	11.4	0
282	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
281	Genome-wide analyses of smoking behaviors in schizophrenia: Findings from the Psychiatric Genomics Consortium. <i>Journal of Psychiatric Research</i> , <b>2021</b> , 137, 215-224	5.2	3
280	Resource profile and user guide of the Polygenic Index Repository. <i>Nature Human Behaviour</i> , <b>2021</b> ,	12.8	5
279	Shared genetic risk between eating disorder- and substance-use-related phenotypes: Evidence from genome-wide association studies. <i>Addiction Biology</i> , <b>2021</b> , 26, e12880	4.6	12
278	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , <b>2021</b> , 12, 24	17.4	30

277	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , <b>2021</b> , 596, 393-397	50.4	28
276	The genomics of heart failure: design and rationale of the HERMES consortium. <i>ESC Heart Failure</i> , <b>2021</b> ,	3.7	1
275	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
274	Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors. <i>Biological Psychiatry</i> , <b>2021</b> ,	7.9	11
273	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. <i>Cell</i> , <b>2021</b> , 184, 4784-4818.e17	50.4	27
272	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
271	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
270	Polymorphic Inversions Underlie the Shared Genetic Susceptibility of Obesity-Related Diseases. <i>American Journal of Human Genetics</i> , <b>2020</b> , 106, 846-858	11	3
269	The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , <b>2020</b> , 581, 434-443	50.4	2278
268	Integrating untargeted metabolomics, genetically informed causal inference, and pathway enrichment to define the obesity metabolome. <i>International Journal of Obesity</i> , <b>2020</b> , 44, 1596-1606	5.5	4
267	A structural variation reference for medical and population genetics. <i>Nature</i> , <b>2020</b> , 581, 444-451	50.4	223
266	The effect of LRRK2 loss-of-function variants in humans. <i>Nature Medicine</i> , <b>2020</b> , 26, 869-877	50.5	47
265	Genetic and In Vitro Inhibition of and Calcific Aortic Valve Stenosis. <i>JACC Basic To Translational Science</i> , <b>2020</b> , 5, 649-661	8.7	18
264	A genome-wide cross-phenotype meta-analysis of the association of blood pressure with migraine. <i>Nature Communications</i> , <b>2020</b> , 11, 3368	17.4	22
263	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
262	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
261	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
260	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

259	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , <b>2020</b> , 182, 1214-1231.e11	56.2	96
258	Development and validation of two SCORE-based cardiovascular risk prediction models for Eastern Europe: a multicohort study. <i>European Heart Journal</i> , <b>2020</b> , 41, 3325-3333	9.5	6
257	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. <i>Nature Genetics</i> , <b>2020</b> , 52, 1314-1332	36.3	26
256	Differences in local population history at the finest level: the case of the Estonian population. <i>European Journal of Human Genetics</i> , <b>2020</b> , 28, 1580-1591	5.3	8
255	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. <i>Circulation Genomic and Precision Medicine</i> , <b>2020</b> , 13, e002769	5.2	1
254	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. <i>International Journal of Epidemiology</i> , <b>2020</b> , 49, 1022-1031	7.8	15
253	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , <b>2019</b> , 188, 1033-1054	3.8	39
252	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
251	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. <i>Genetics</i> , <b>2019</b> , 212, 905-918	4	13
250	Genome-wide association study identifies 30 loci associated with bipolar disorder. <i>Nature Genetics</i> , <b>2019</b> , 51, 793-803	36.3	662
249	Roadmap for a precision-medicine initiative in the Nordic region. <i>Nature Genetics</i> , <b>2019</b> , 51, 924-930	36.3	12
248	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. <i>Human Molecular Genetics</i> , <b>2019</b> , 28, 2615-2633	5.6	14
247	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
246	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
245	Analytical strategies to include the X-chromosome in variance heterogeneity analyses: Evidence for trait-specific polygenic variance structure. <i>Genetic Epidemiology</i> , <b>2019</b> , 43, 815-830	2.6	4
244	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , <b>2019</b> , 10, 4957	17.4	40
243	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
242	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

241	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
240	Improved polygenic prediction by Bayesian multiple regression on summary statistics. <i>Nature Communications</i> , <b>2019</b> , 10, 5086	17.4	114
239	PAIRUP-MS: Pathway analysis and imputation to relate unknowns in profiles from mass spectrometry-based metabolite data. <i>PLoS Computational Biology</i> , <b>2019</b> , 15, e1006734	5	9
238	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
237	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
236	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
235	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
234	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
233	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
232	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
231	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
230	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
229	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
228	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
227	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
226	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. <i>Nature Communications</i> , <b>2018</b> , 9, 3391	17.4	90
225	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. <i>Cell</i> , <b>2018</b> , 173, 1705-1715.e16	56.2	360
224	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , <b>2018</b> , 50, 1225-1233	36.3	277

223	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
222	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
221	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
220	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
219	Reply to 'Misestimation of heritability and prediction accuracy of male-pattern baldness'. <i>Nature Communications</i> , <b>2018</b> , 9, 2538	17.4	
218	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
217	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , <b>2017</b> , 542, 186-190	50.4	412
216	Metabolomic profiles as reliable biomarkers of dietary composition. <i>American Journal of Clinical Nutrition</i> , <b>2017</b> , 105, 547-554	7	56
215	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
214	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
213	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
212	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
211	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. <i>Scientific Reports</i> , <b>2017</b> , 7, 45040	4.9	70
210	Large scale meta-analysis characterizes genetic architecture for common psoriasis associated variants. <i>Nature Communications</i> , <b>2017</b> , 8, 15382	17.4	136
209	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , <b>2017</b> , 66, 2888-2902	29.0	414
208	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , <b>2017</b> , 66, 2019-2032	0.9	29
207	and Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. <i>Journal of the American Society of Nephrology: JASN</i> , <b>2017</b> , 28, 981-994	12.7	30
206	Comprehensive population-based genome sequencing provides insight into hematopoietic regulatory mechanisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E327-E336	11.5	30

205	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
204	The Genetic Architecture of Gene Expression in Peripheral Blood. <i>American Journal of Human Genetics</i> , <b>2017</b> , 100, 228-237	11	98
203	SNP-Based Heritability Estimates of Common and Specific Variance in Self- and Informant-Reported Neuroticism Scales. <i>Journal of Personality</i> , <b>2017</b> , 85, 906-919	4.4	5
202	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , <b>2017</b> , 49, 1758-1766	36.6	310
201	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
200	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475 000 Individuals. <i>Circulation: Cardiovascular Genetics</i> , <b>2017</b> , 10,		33
199	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
198	Hidden heritability due to heterogeneity across seven populations. <i>Nature Human Behaviour</i> , <b>2017</b> , 1, 757-765	12.8	94
197	Genetic correlations reveal the shared genetic architecture of transcription in human peripheral blood. <i>Nature Communications</i> , <b>2017</b> , 8, 483	17.4	10
196	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
195	Constraints on eQTL Fine Mapping in the Presence of Multisite Local Regulation of Gene Expression. <i>G3: Genes, Genomes, Genetics</i> , <b>2017</b> , 7, 2533-2544	3.2	17
194	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
193	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
192	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
191	An epigenome-wide association study meta-analysis of educational attainment. <i>Molecular Psychiatry</i> , <b>2017</b> , 22, 1680-1690	15.1	46
190	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , <b>2017</b> , 4, 170179	8.2	22
189	Exome-wide association study reveals novel psoriasis susceptibility locus at TNFSF15 and rare protective alleles in genes contributing to type I IFN signalling. <i>Human Molecular Genetics</i> , <b>2017</b> , 26, 4307-4313	5.6	25
188	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

187	MixFit: Methodology for Computing Ancestry-Related Genetic Scores at the Individual Level and Its Application to the Estonian and Finnish Population Studies. <i>PLoS ONE</i> , <b>2017</b> , 12, e0170325	3.7	6
186	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
185	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
184	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
183	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
182	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , <b>2016</b> , 68, 1435-1448	15.1	76
181	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
180	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
179	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
178	The Role of the Five-factor Personality Traits in General Self-rated Health. <i>European Journal of Personality</i> , <b>2016</b> , 30, 492-504	5.1	9
177	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
176	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , <b>2016</b> , 48, 1462-1472	36.3	198
175	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
174	Autosomal genetic control of human gene expression does not differ across the sexes. <i>Genome Biology</i> , <b>2016</b> , 17, 248	18.3	10
173	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
172	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
171	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
170	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



169	Testing the role of predicted gene knockouts in human anthropometric trait variation. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 2082-2092	5.6	7
168	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
167	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
166	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
165	Ancient Haplotypes at the 15q24.2 Microdeletion Region Are Linked to Brain Expression of MAN2C1 and Children's Intelligence. <i>PLoS ONE</i> , <b>2016</b> , 11, e0157739	3.7	0
164	The genetic architecture of type 2 diabetes. <i>Nature</i> , <b>2016</b> , 536, 41-47	50.4	704
163	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
162	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
161	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
160	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
159	Genome-wide association study of serum coenzyme Q10 levels identifies susceptibility loci linked to neuronal diseases. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 2881-2891	5.6	10
158	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , <b>2016</b> , 533, 539-42	50.4	850
157	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
156	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
155	Biological interpretation of genome-wide association studies using predicted gene functions. <i>Nature Communications</i> , <b>2015</b> , 6, 5890	17.4	489
154	Age- and sex-specific causal effects of adiposity on cardiovascular risk factors. <i>Diabetes</i> , <b>2015</b> , 64, 1841-529		50
153	Cell Specific eQTL Analysis without Sorting Cells. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005223	6	81
152	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , <b>2015</b> , 523, 459-463	50.4	119

151	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
150	A meta-analysis of gene expression signatures of blood pressure and hypertension. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005035	6	83
149	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
148	The impact of low-frequency and rare variants on lipid levels. <i>Nature Genetics</i> , <b>2015</b> , 47, 589-97	36.3	229
147	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
146	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
145	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
144	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
143	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
142	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , <b>2015</b> , 6, 8570	17.4	335
141	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
140	Population genetic differentiation of height and body mass index across Europe. <i>Nature Genetics</i> , <b>2015</b> , 47, 1357-62	36.3	186
139	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
138	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
137	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
136	RegScan: a GWAS tool for quick estimation of allele effects on continuous traits and their combinations. <i>Briefings in Bioinformatics</i> , <b>2015</b> , 16, 39-44	13.4	25
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133	Haplotype phasing and inheritance of copy number variants in nuclear families. <i>PLoS ONE</i> , <b>2015</b> , 10, e0132713	6	220
132	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
131	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
130	Functional Impact and Evolution of a Novel Human Polymorphic Inversion That Disrupts a Gene and Creates a Fusion Transcript. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005495	6	18
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128	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
127	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
126	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
125	Enhanced meta-analysis and replication studies identify five new psoriasis susceptibility loci. <i>Nature Communications</i> , <b>2015</b> , 6, 7001	17.4	122
124	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
123	Rare coding variants and X-linked loci associated with age at menarche. <i>Nature Communications</i> , <b>2015</b> , 6, 7756	17.4	23
122	Genetic variants of inducible costimulator are associated with allergic asthma susceptibility. <i>Journal of Allergy and Clinical Immunology</i> , <b>2015</b> , 135, 556-8	11.5	3
121	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , <b>2015</b> , 518, 187-196	50.4	920
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114	Detection and replication of epistasis influencing transcription in humans. <i>Nature</i> , <b>2014</b> , 508, 249-53	50.4	149
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112	Genetics of rheumatoid arthritis contributes to biology and drug discovery. <i>Nature</i> , <b>2014</b> , 506, 376-81	50.4	1426
111	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
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109	Replicability and robustness of genome-wide-association studies for behavioral traits. <i>Psychological Science</i> , <b>2014</b> , 25, 1975-86	7.9	75
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106	A genome-wide association study of anorexia nervosa. <i>Molecular Psychiatry</i> , <b>2014</b> , 19, 1085-94	15.1	224
105	Quality control and conduct of genome-wide association meta-analyses. <i>Nature Protocols</i> , <b>2014</b> , 9, 1192-218	28.8	278
104	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
103	Sex- and age-interacting eQTLs in human complex diseases. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 1947-56	5.6	48
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99	Mediation analysis demonstrates that trans-eQTLs are often explained by cis-mediation: a genome-wide analysis among 1,800 South Asians. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004818	6	56
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94	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
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91	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
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89	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , <b>2013</b> , 45, 1274-1283	36.3	1904
88	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
87	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
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81	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
80	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

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78	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
77	The DOT1L rs12982744 polymorphism is associated with osteoarthritis of the hip with genome-wide statistical significance in males. <i>Annals of the Rheumatic Diseases</i> , <b>2013</b> , 72, 1264-5	2.4	48
76	Human disease-associated genetic variation impacts large intergenic non-coding RNA expression. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003201	6	209
75	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
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57	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
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52	Genome-wide association and functional follow-up reveals new loci for kidney function. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002584	6	143
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38	Common variants in KCNN3 are associated with lone atrial fibrillation. <i>Nature Genetics</i> , <b>2010</b> , 42, 240-4	36.3	362
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36	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
35	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
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32	Genome-wide study identifies association between HLA-B*55:01 and penicillin allergy		2
31	Haplotype sharing provides insights into fine-scale population history and disease in Finland		2
30	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals		4
29	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries		1
28	Improved polygenic prediction by Bayesian multiple regression on summary statistics		2
27	Genome-wide association study provides new insights into the genetic architecture and pathogenesis of heart failure		2
26	Genetic Associations with Subjective Well-Being Also Implicate Depression and Neuroticism		7



25	Mega-analysis of 31,396 individuals from 6 countries uncovers strong gene-environment interaction for human fertility	7
24	Constraints on eQTL fine mapping in the presence of multi-site local regulation of gene expression	1
23	Novel blood pressure locus and gene discovery using GWAS and expression datasets from blood and the kidney	1
22	Widespread signatures of negative selection in the genetic architecture of human complex traits	7
21	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depressive disorder	21
20	Genome-wide association study identifies 30 Loci Associated with Bipolar Disorder	28
19	Genetic analysis of over one million people identifies 535 novel loci for blood pressure	4
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14	Dissecting the shared genetic architecture of suicide attempt, psychiatric disorders and known risk factors	2
13	Identifying tissues implicated in Anorexia Nervosa using Transcriptomic Imputation	1
12	Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution	1
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