Andres Metspalu

List of Publications by Year
in descending order

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356	93,159	492	410
papers	citations	129 h-index	277 g-index

382	382	382	86376
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2020, 581, 434-443.	27.8	6,140
2	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
3	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
4	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	21.4	2,634
5	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681.	21.4	2,224
6	A comprehensive 1000 Genomesâ€“based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	21.4	2,054
7	Genetics of rheumatoid arthritis contributes to biology and drug discovery. Nature, 2014, 506, 376-381.	27.8	1,974
8	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. Nature Genetics, 2018, 50, 1112-1121.	21.4	1,835
9	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
10	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
11	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	21.4	1,748
12	Systematic identification of trans eQTLs as putative drivers of known disease associations. Nature Genetics, 2013, 45, 1238-1243.	21.4	1,544
13	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	21.4	1,439
14	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. Nature Genetics, 2018, 50, 1505-1513.	21.4	1,331
15	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
16	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. Nature Genetics, 2019, 51, 237-244.	21.4	1,307
17	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
18	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	21.4	1,191

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19	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	6.2	1,098
20	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	21.4	959
21	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
22	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
23	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. Nature Genetics, 2016, 48, 624-633.	21.4	870
24	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. Nature Genetics, 2012, 44, 1341-1348.	21.4	848
25	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	21.4	838
26	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, 949-960.	21.4	836
27	Identification of seven loci affecting mean telomere length and their association with disease. Nature Genetics, 2013, 45, 422-427.	21.4	808
28	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	21.4	754
29	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	12.6	750
30	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	21.4	746
31	Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. Nature Genetics, 2015, 47, 1114-1120.	21.4	709
32	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
33	Sequence variants at CHRNB3â€“CHRNA6 and CYP2A6 affect smoking behavior. Nature Genetics, 2010, 42, 448-453.	21.4	649
34	Genome-wide association study identifies eight risk loci and implicates metabo-psychiatric origins for anorexia nervosa. Nature Genetics, 2019, 51, 1207-1214.	21.4	641
35	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. Nature Genetics, 2016, 48, 510-518.	21.4	617
36	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615

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37	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	21.4	578
38	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. Nature Communications, 2016, 7, 11122.	12.8	576
39	Association analyses based on false discovery rate implicate new loci for coronary artery disease. Nature Genetics, 2017, 49, 1385-1391.	21.4	571
40	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	6.2	569
41	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
42	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
43	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
44	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	21.4	520
45	Dating the Origin of the CCR5-Î”32 AIDS-Resistance Allele by the Coalescence of Haplotypes. American Journal of Human Genetics, 1998, 62, 1507-1515.	6.2	507
46	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	21.4	492
47	A Genome-wide Association Study of Lung Cancer Identifies a Region of Chromosome 5p15 Associated with Risk for Adenocarcinoma. American Journal of Human Genetics, 2009, 85, 679-691.	6.2	489
48	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
49	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. Nature Genetics, 2010, 42, 1077-1085.	21.4	445
50	The prevalence of metabolic syndrome and metabolically healthy obesity in Europe: a collaborative analysis of ten large cohort studies. BMC Endocrine Disorders, 2014, 14, 9.	2.2	440
51	Common variants in KCNN3 are associated with lone atrial fibrillation. Nature Genetics, 2010, 42, 240-244.	21.4	438
52	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	12.6	438
53	Coding Variation inANGPTL4,LPL,andSVEP1and the Risk of Coronary Disease. New England Journal of Medicine, 2016, 374, 1134-1144.	27.0	427
54	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426

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55	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
56	Significant Locus and Metabolic Genetic Correlations Revealed in Genome-Wide Association Study of Anorexia Nervosa. American Journal of Psychiatry, 2017, 174, 850-858.	7.2	410
57	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
58	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	27.8	401
59	Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. Nature Genetics, 2013, 45, 314-318.	21.4	398
60	Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. Nature, 2011, 478, 97-102.	27.8	394
61	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	27.8	383
62	A first-generation linkage disequilibrium map of human chromosome 22. Nature, 2002, 418, 544-548.	27.8	376
63	Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. Lancet, The, 2012, 380, 815-823.	13.7	373
64	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	3.5	371
65	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	21.4	365
66	High carrier frequency of the 35delG deafness mutation in European populations. European Journal of Human Genetics, 2000, 8, 19-23.	2.8	363
67	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
68	Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. Nature Genetics, 2014, 46, 736-741.	21.4	360
69	Genomic analyses inform on migration events during the peopling of Eurasia. Nature, 2016, 538, 238-242.	27.8	360
70	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
71	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	21.4	356
72	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494.	3.5	351

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73	A recent bottleneck of Y chromosome diversity coincides with a global change in culture. Genome Research, 2015, 25, 459-466.	5.5	348
74	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
75	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	3.5	331
76	Minisequencing: A Specific Tool for DNA Analysis and Diagnostics on Oligonucleotideâ€‰Arrays. Genome Research, 1997, 7, 606-614.	5.5	324
77	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	27.8	320
78	Cohort Profile: Estonian Biobank of the Estonian Genome Center, University of Tartu. International Journal of Epidemiology, 2015, 44, 1137-1147.	1.9	314
79	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	21.4	310
80	Genome-Wide Association Analyses in 128,266 Individuals Identifies New Morningness and Sleep Duration Loci. PLoS Genetics, 2016, 12, e1006125.	3.5	308
81	Signatures of negative selection in the genetic architecture of human complex traits. Nature Genetics, 2018, 50, 746-753.	21.4	304
82	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. Nature Genetics, 2012, 44, 260-268.	21.4	303
83	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. Nature Genetics, 2015, 47, 1282-1293.	21.4	294
84	Combined Analysis of Genome-wide Association Studies for Crohn Disease and Psoriasis Identifies Seven Shared Susceptibility Loci. American Journal of Human Genetics, 2012, 90, 636-647.	6.2	290
85	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. JAMA Psychiatry, 2015, 72, 642.	11.0	289
86	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
87	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
88	Biomarker Profiling by Nuclear Magnetic Resonance Spectroscopy for the Prediction of All-Cause Mortality: An Observational Study of 17,345 Persons. PLoS Medicine, 2014, 11, e1001606.	8.4	281
89	Genetic Structure of Europeans: A View from the Northâ€“East. PLoS ONE, 2009, 4, e5472.	2.5	279
90	Design of a peptide-based vector, PepFect6, for efficient delivery of siRNA in cell culture and systemically in vivo. Nucleic Acids Research, 2011, 39, 3972-3987.	14.5	262

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91	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
92	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, 7119-7124.	7.1	258
93	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
94	Human Disease-Associated Genetic Variation Impacts Large Intergenic Non-Coding RNA Expression. PLoS Genetics, 2013, 9, e1003201.	3.5	247
95	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. Nature Genetics, 2018, 50, 834-848.	21.4	239
96	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	7.9	235
97	Genome-wide association meta-analysis of human longevity identifies a novel locus conferring survival beyond 90 years of age. Human Molecular Genetics, 2014, 23, 4420-4432.	2.9	227
98	Population genetic differentiation of height and body mass index across Europe. Nature Genetics, 2015, 47, 1357-1362.	21.4	227
99	Genetically Determined Height and Coronary Artery Disease. New England Journal of Medicine, 2015, 372, 1608-1618.	27.0	220
100	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	21.4	218
101	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	2.8	214
102	Influence of common genetic variation on lung cancer risk: meta-analysis of 14 900 cases and 29 485 controls. Human Molecular Genetics, 2012, 21, 4980-4995.	2.9	196
103	Metaâ€analysis of microRNA expression in lung cancer. International Journal of Cancer, 2013, 132, 2884-2893.	5.1	195
104	Defining the Effect of the 16p11.2 Duplication on Cognition, Behavior, and Medical Comorbidities. JAMA Psychiatry, 2016, 73, 20.	11.0	195
105	Dominance Genetic Variation Contributes Little to the Missing Heritability for Human Complex Traits. American Journal of Human Genetics, 2015, 96, 377-385.	6.2	191
106	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.	10.2	191
107	A metabolic profile of all-cause mortality risk identified in an observational study of 44,168 individuals. Nature Communications, 2019, 10, 3346.	12.8	188
108	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183

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109	Association of branchedâ€chain amino acids and other circulating metabolites with risk of incident dementia and Alzheimer's disease: A prospective study in eight cohorts. Alzheimer's and Dementia, 2018, 14, 723-733.	0.8	182
110	Improved imputation accuracy of rare and low-frequency variants using population-specific high-coverage WGS-based imputation reference panel. European Journal of Human Genetics, 2017, 25, 869-876.	2.8	181
111	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. PLoS Medicine, 2013, 10, e1001474.	8.4	178
112	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. Nature Communications, 2015, 6, 7208.	12.8	178
113	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. Behavior Genetics, 2016, 46, 170-182.	2.1	178
114	The Genetic Architecture of Gene Expression in Peripheral Blood. American Journal of Human Genetics, 2017, 100, 228-237.	6.2	178
115	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. Nature Reviews Clinical Oncology, 2020, 17, 687-705.	27.6	178
116	Application of non-HDL cholesterol for population-based cardiovascular risk stratification: results from the Multinational Cardiovascular Risk Consortium. Lancet, The, 2019, 394, 2173-2183.	13.7	177
117	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
118	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
119	Arrayed Primer Extension: Solid-Phase Four-Color DNA Resequencing and Mutation Detection Technology. Genetic Testing and Molecular Biomarkers, 2000, 4, 1-7.	1.7	167
120	Human microRNAs miR-22, miR-138-2, miR-148a, and miR-488 Are Associated with Panic Disorder and Regulate Several Anxiety Candidate Genes and Related Pathways. Biological Psychiatry, 2011, 69, 526-533.	1.3	167
121	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	3.5	166
122	Complementary seminovaginal microbiome in couples. Research in Microbiology, 2015, 166, 440-447.	2.1	164
123	A Genome-Wide Association Study of Upper Aerodigestive Tract Cancers Conducted within the INHANCE Consortium. PLoS Genetics, 2011, 7, e1001333.	3.5	158
124	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
125	Quality, quantity and harmony: the DataSHaPER approach to integrating data across bioclinical studies. International Journal of Epidemiology, 2010, 39, 1383-1393.	1.9	148
126	Age-related profiling of DNA methylation in CD8+ T cells reveals changes in immune response and transcriptional regulator genes. Scientific Reports, 2015, 5, 13107.	3.3	148

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127	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. Journal of the American College of Cardiology, 2019, 73, 58-66.	2.8	147
128	Global implementation of genomic medicine: We are not alone. Science Translational Medicine, 2015, 7, 290ps13.	12.4	146
129	Mutation detection by solid phase primer extension. Human Mutation, 1996, 7, 346-354.	2.5	145
130	Copy Number Variations and Cognitive Phenotypes in Unselected Populations. JAMA - Journal of the American Medical Association, 2015, 313, 2044.	7.4	143
131	Circulating metabolites and general cognitive ability and dementia: Evidence from 11 cohort studies. Alzheimer's and Dementia, 2018, 14, 707-722.	0.8	143
132	Toward a roadmap in global biobanking for health. European Journal of Human Genetics, 2012, 20, 1105-1111.	2.8	139
133	Nine Loci for Ocular Axial Length Identified through Genome-wide Association Studies, Including Shared Loci with Refractive Error. American Journal of Human Genetics, 2013, 93, 264-277.	6.2	139
134	Hidden heritability due to heterogeneity across seven populations. Nature Human Behaviour, 2017, 1, 757-765.	12.0	137
135	Personalized risk prediction for type 2 diabetes: the potential of genetic risk scores. Genetics in Medicine, 2017, 19, 322-329.	2.4	127
136	Association between a 15q25 gene variant, smoking quantity and tobacco-related cancers among 17 000 individuals. International Journal of Epidemiology, 2010, 39, 563-577.	1.9	125
137	Adiposity as a cause of cardiovascular disease: a Mendelian randomization study. International Journal of Epidemiology, 2015, 44, 578-586.	1.9	123
138	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	6.2	123
139	Structural forms of the human amylase locus and their relationships to SNPs, haplotypes and obesity. Nature Genetics, 2015, 47, 921-925.	21.4	120
140	Genotypeâ€“covariate interaction effects and the heritability of adult body mass index. Nature Genetics, 2017, 49, 1174-1181.	21.4	119
141	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. American Journal of Human Genetics, 2018, 102, 1185-1194.	6.2	119
142	Chronotype and sleep duration: The influence of season of assessment. Chronobiology International, 2014, 31, 731-740.	2.0	118
143	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. American Journal of Human Genetics, 2020, 106, 389-404.	6.2	118
144	Linkage Disequilibrium Patterns and tagSNP Transferability among European Populations. American Journal of Human Genetics, 2005, 76, 387-398.	6.2	117

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145	Identification of miRâ€374a as a prognostic marker for survival in patients with earlyâ€stage nonsmall cell lung cancer. Genes Chromosomes and Cancer, 2011, 50, 812-822.	2.8	116
146	Genome-wide analysis of BMI in adolescents and young adults reveals additional insight into the effects of genetic loci over the life course. Human Molecular Genetics, 2013, 22, 3597-3607.	2.9	116
147	A Variant in MCF2L Is Associated with Osteoarthritis. American Journal of Human Genetics, 2011, 89, 446-450.	6.2	115
148	Cell Specific eQTL Analysis without Sorting Cells. PLoS Genetics, 2015, 11, e1005223.	3.5	115
149	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113
150	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
151	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	7.1	110
152	Pathogenic implications for autoimmune mechanisms derived by comparative eQTL analysis of CD4+ versus CD8+ T cells. PLoS Genetics, 2017, 13, e1006643.	3.5	110
153	Assessment of Osteoarthritis Candidate Genes in a Metaâ€Analysis of Nine Genomeâ€Wide Association Studies. Arthritis and Rheumatology, 2014, 66, 940-949.	5.6	108
154	A meta-analysis of genome-wide association studies identifies novel variants associated with osteoarthritis of the hip. Annals of the Rheumatic Diseases, 2014, 73, 2130-2136.	0.9	108
155	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. PLoS Genetics, 2015, 11, e1005035.	3.5	107
156	An Evaluation of the Performance of Tag SNPs Derived from HapMap in a Caucasian Population. PLoS Genetics, 2006, 2, e27.	3.5	105
157	A genome-wide association study of early menopause and the combined impact of identified variants. Human Molecular Genetics, 2013, 22, 1465-1472.	2.9	104
158	Harmonization of Neuroticism and Extraversion phenotypes across inventories and cohorts in the Genetics of Personality Consortium: an application of Item Response Theory. Behavior Genetics, 2014, 44, 295-313.	2.1	103
159	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. Biological Psychiatry, 2021, 90, 611-620.	1.3	103
160	The role of COX-2 and Nrf2/ARE in anti-inflammation and antioxidative stress: Aging and anti-aging. Medical Hypotheses, 2011, 77, 174-178.	1.5	101
161	Reconstructing the Population History of European Romani from Genome-wide Data. Current Biology, 2012, 22, 2342-2349.	3.9	101
162	Genome-Wide Meta-Analysis of Psoriatic Arthritis Identifies Susceptibility Locus at REL. Journal of Investigative Dermatology, 2012, 132, 1133-1140.	0.7	99

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163	Evaluating the arrayed primer extension resequencing assay of TP53 tumor suppressor gene. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 5503-5508.	7.1	98
164	Oral health, dental care and mouthwash associated with upper aerodigestive tract cancer risk in Europe: The ARCAGE study. Oral Oncology, 2014, 50, 616-625.	1.5	98
165	Effects of Metformin on Metabolite Profiles and LDL Cholesterol in Patients With Type 2 Diabetes. Diabetes Care, 2015, 38, 1858-1867.	8.6	97
166	Leukocyte telomere length associates with prospective mortality independent of immune-related parameters and known genetic markers. International Journal of Epidemiology, 2014, 43, 878-886.	1.9	95
167	Genetic Associations of 115 Polymorphisms with Cancers of the Upper Aerodigestive Tract across 10 European Countries: The ARCAGE Project. Cancer Research, 2009, 69, 2956-2965.	0.9	94
168	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
169	Personality traits and eating habits in a large sample of Estonians.. Health Psychology, 2012, 31, 806-814.	1.6	93
170	Ultra-rare disruptive and damaging mutations influence educational attainment in the general population. Nature Neuroscience, 2016, 19, 1563-1565.	14.8	90
171	Epigenetic profiling in CD4+ and CD8+ T cells from Graves' disease patients reveals changes in genes associated with T cell receptor signaling. Journal of Autoimmunity, 2016, 67, 46-56.	6.5	88
172	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. JAMA Psychiatry, 2021, 78, 1258.	11.0	88
173	Does Childhood Trauma Moderate Polygenic Risk for Depression? A Meta-analysis of 5765 Subjects From the Psychiatric Genomics Consortium. Biological Psychiatry, 2018, 84, 138-147.	1.3	87
174	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
175	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
176	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. Biological Psychiatry, 2017, 82, 322-329.	1.3	84
177	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
178	Association study of 90 candidate gene polymorphisms in panic disorder. Psychiatric Genetics, 2005, 15, 17-24.	1.1	83
179	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	7.9	83
180	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	6.2	82

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181	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. PLoS Genetics, 2014, 10, e1004508.	3.5	80
182	Evidence of Inbreeding Depression on Human Height. PLoS Genetics, 2012, 8, e1002655.	3.5	79
183	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. Nature Communications, 2018, 9, 2606.	12.8	79
184	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	12.0	79
185	The Number of Genomic Copies at the 16p11.2 Locus Modulates Language, Verbal Memory, and Inhibition. Biological Psychiatry, 2016, 80, 129-139.	1.3	78
186	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. PLoS Genetics, 2015, 11, e1005230.	3.5	77
187	A Whole-Blood Transcriptome Meta-Analysis Identifies Gene Expression Signatures of Cigarette Smoking. Human Molecular Genetics, 2016, 25, ddw288.	2.9	76
188	Simultaneous Multigene Mutation Detection in Patients With Sensorineural Hearing Loss Through a Novel Diagnostic Microarray: A New Approach for Newborn Screening Follow-up. Pediatrics, 2006, 118, 985-994.	2.1	74
189	Using RNA sequencing for identifying gene imprinting and random monoallelic expression in human placenta. Epigenetics, 2014, 9, 1397-1409.	2.7	74
190	Genetic influence on social outcomes during and after the Soviet era in Estonia. Nature Human Behaviour, 2018, 2, 269-275.	12.0	74
191	Allelic estrogen receptor 1 (ESR1) gene variants predict the outcome of ovarian stimulation in in vitro fertilization. Molecular Human Reproduction, 2007, 13, 521-526.	2.8	71
192	BBMRI-ERIC as a resource for pharmaceutical and life science industries: the development of biobank-based Expert Centres. European Journal of Human Genetics, 2015, 23, 893-900.	2.8	71
193	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	16.3	69
194	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and AlcoholÂUse. Biological Psychiatry, 2019, 85, 946-955.	1.3	69
195	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. Nature Genetics, 2021, 53, 1504-1516.	21.4	69
196	Large scale international replication and meta-analysis study confirms association of the 15q14 locus with myopia. The CREAM consortium. Human Genetics, 2012, 131, 1467-1480.	3.8	67
197	Genome-wide genetic homogeneity between sexes and populations for human height and body mass index. Human Molecular Genetics, 2015, 24, 7445-7449.	2.9	67
198	A Common 16p11.2 Inversion Underlies the Joint Susceptibility to Asthma and Obesity. American Journal of Human Genetics, 2014, 94, 361-372.	6.2	66

#	Article	IF	Citations
199	Sex- and age-interacting eQTLs in human complex diseases. Human Molecular Genetics, 2014, 23, 1947-1956.	2.9	66
200	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. Human Molecular Genetics, 2012, 21, 5329-5343.	2.9	64
201	Genetic characterization of northeastern Italian population isolates in the context of broader European genetic diversity. European Journal of Human Genetics, 2013, 21, 659-665.	2.8	64
202	Sequence variation in nuclear ribosomal small subunit, internal transcribed spacer and large subunit regions of Rhizophagus irregularis and Gigaspora margarita is high and isolateâ€dependent. Molecular Ecology, 2016, 25, 2816-2832.	3.9	64
203	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
204	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	2.5	64
205	Age- and Sex-Specific Causal Effects of Adiposity on Cardiovascular Risk Factors. Diabetes, 2015, 64, 1841-1852.	0.6	63
206	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	12.8	62
207	Methylation Markers of Early-Stage Non-Small Cell Lung Cancer. PLoS ONE, 2012, 7, e39813.	2.5	62
208	Serotonin transporter promoter region polymorphisms do not influence treatment response to escitalopram in patients with major depression. European Neuropsychopharmacology, 2009, 19, 451-456.	0.7	61
209	Differentially expressed genes reflect disease-induced rather than disease-causing changes in the transcriptome. Nature Communications, 2021, 12, 5647.	12.8	61
210	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	6.2	60
211	De Novo SCN8A Mutation Identified by Whole-Exome Sequencing in a Boy With Neonatal Epileptic Encephalopathy, Multiple Congenital Anomalies, and Movement Disorders. Journal of Child Neurology, 2014, 29, NP202-NP206.	1.4	59
212	Genome-wide association study of panic disorder reveals genetic overlap with neuroticism and depression. Molecular Psychiatry, 2021, 26, 4179-4190.	7.9	58
213	Haplotype Sharing Provides Insights into Fine-Scale Population History and Disease in Finland. American Journal of Human Genetics, 2018, 102, 760-775.	6.2	57
214	Reliable Detection of Î²-Thalassemia and G6PD Mutations by a DNA Microarray. Clinical Chemistry, 2002, 48, 2051-2054.	3.2	57
215	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. Human Molecular Genetics, 2014, 23, 2490-2497.	2.9	56
216	Polymorphisms inESR1,ESR2andHSD17B1genes are associated with fertility status in endometriosis. Gynecological Endocrinology, 2011, 27, 425-433.	1.7	53

#	Article	IF	Citations
217	MTHFR and MSX1 contribute to the risk of nonsyndromic cleft lip/palate. European Journal of Oral Sciences, 2010, 118, 213-220.	1.5	52
218	DNA breaks and chromatin structural changes enhance the transcription of autoimmune regulator target genes. Journal of Biological Chemistry, 2017, 292, 6542-6554.	3.4	52
219	The genetic architecture of sporadic and multiple consecutive miscarriage. Nature Communications, 2020, 11, 5980.	12.8	52
220	Interaction of 5-S RNA, 5.8-S RNA and tRNA with Rat-Liver Ribosomal Proteins. FEBS Journal, 1978, 91, 73-81.	0.2	51
221	The DOT1L rs12982744 polymorphism is associated with osteoarthritis of the hip with genome-wide statistical significance in males. Annals of the Rheumatic Diseases, 2013, 72, 1264-1265.	0.9	51
222	Association of Adiposity Genetic Variants With Menarche Timing in 92,105 Women of European Descent. American Journal of Epidemiology, 2013, 178, 451-460.	3.4	51
223	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. JAMA Psychiatry, 2016, 73, 497.	11.0	51
224	Alcohol-related cancers and genetic susceptibility in Europe: the ARCAGE project: study samples and data collection. European Journal of Cancer Prevention, 2009, 18, 76-84.	1.3	50
225	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. American Journal of Human Genetics, 2016, 99, 22-39.	6.2	50
226	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.6	47
227	The ABCA4 2588G>C Stargardt mutation: single origin and increasing frequency from South-West to North-East Europe. European Journal of Human Genetics, 2002, 10, 197-203.	2.8	45
228	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, 481-488.	6.2	45
229	In-solution hybrid capture of bisulfite-converted DNA for targeted bisulfite sequencing of 174 ADME genes. Nucleic Acids Research, 2013, 41, e72-e72.	14.5	43
230	Linking a Population Biobank with National Health Registriesâ€"The Estonian Experience. Journal of Personalized Medicine, 2015, 5, 96-106.	2.5	43
231	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.	1.3	43
232	Genetic variants in COL2A1, COL11A2, and IRF6 contribute risk to nonsyndromic cleft palate. Birth Defects Research Part A: Clinical and Molecular Teratology, 2010, 88, 748-756.	1.6	41
233	Variation in FGF1, FOXE1, and TIMP2genes is associated with nonsyndromic cleft lip with or without cleft palate. Birth Defects Research Part A: Clinical and Molecular Teratology, 2011, 91, 218-225.	1.6	41
234	Lung cancer and DNA repair genes: multilevel association analysis from the International Lung Cancer Consortium. Carcinogenesis, 2012, 33, 1059-1064.	2.8	41

#	Article	IF	Citations
235	Selection for Genetic Variation Inducing Pro-Inflammatory Responses under Adverse Environmental Conditions in a Ghanaian Population. PLoS ONE, 2009, 4, e7795.	2.5	40
236	Feasibility of innovative dietary assessment in epidemiological studies using the approach of combining different assessment instruments. Public Health Nutrition, 2011, 14, 1055-1063.	2.2	40
237	Polygenic prediction of breast cancer: comparison of genetic predictors and implications for risk stratification. BMC Cancer, 2019, 19, 557.	2.6	40
238	Genotyping Microarray for the Detection of More Than 200 CFTR Mutations in Ethnically Diverse Populations. Journal of Molecular Diagnostics, 2005, 7, 375-387.	2.8	39
239	SOS2 and ACP1 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.	6.1	39
240	Comprehensive population-based genome sequencing provides insight into hematopoietic regulatory mechanisms. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E327-E336.	7.1	39
241	Polymorphisms in wolframin (WFS1) gene are possibly related to increased risk for mood disorders. International Journal of Neuropsychopharmacology, 2005, 8, 235-244.	2.1	38
242	Polymorphisms in MMP-2 and MMP-9 promoter regions are associated with endometriosis. Fertility and Sterility, 2010, 94, 1560-1563.	1.0	36
243	The landscape of autosomal-recessive pathogenic variants in European populations reveals phenotype-specific effects. American Journal of Human Genetics, 2021, 108, 608-619.	6.2	36
244	Within-Trait Heterogeneity in Age Group Differences in Personality Domains and Facets: Implications for the Development and Coherence of Personality Traits. PLoS ONE, 2015, 10, e0119667.	2.5	36
245	Imprinted genes and imprinting control regions show predominant intermediate methylation in adult somatic tissues. Epigenomics, 2016, 8, 789-799.	2.1	35
246	Recall by genotype and cascade screening for familial hypercholesterolemia in a population-based biobank from Estonia. Genetics in Medicine, 2019, 21, 1173-1180.	2.4	35
247	Nuclear Import and Nucleolar Accumulation of the Human Ribosomal Protein S7 Depends on both a Minimal Nuclear Localization Sequence and an Adjacent Basic Region. Biochemical and Biophysical Research Communications, 1998, 249, 759-766.	2.1	34
248	Analysis of SNP profiles in patients with major depressive disorder. International Journal of Neuropsychopharmacology, 2006, 9, 167.	2.1	34
249	Genome-wide Study Identifies Association between HLA-Bâˆ—55:01 and Self-Reported Penicillin Allergy. American Journal of Human Genetics, 2020, 107, 612-621.	6.2	34
250	Development of a single tube 640-plex genotyping method for detection of nucleic acid variations on microarrays. Nucleic Acids Research, 2008, 36, e75-e75.	14.5	33
251	Genome-wide meta-analysis of common variant differences between men and women. Human Molecular Genetics, 2012, 21, 4805-4815.	2.9	33
252	Common Variants in Mendelian Kidney Disease Genes and Their Association with Renal Function. Journal of the American Society of Nephrology: JASN, 2013, 24, 2105-2117.	6.1	33

#	Article	IF	Citations
253	Rare Genomic Structural Variants in Complex Disease: Lessons from the Replication of Associations with Obesity. PLoS ONE, 2013, 8, e58048.	2.5	33
254	Locations of several novel 2'-O-methylated nucleotides in human 28S rRNA. BMC Molecular Biology, 2002, 3, 1.	3.0	32
255	Rare coding variants and X-linked loci associated with age at menarche. Nature Communications, 2015, 6, 7756.	12.8	32
256	A Genome-Wide Analysis of Populations from European Russia Reveals a New Pole of Genetic Diversity in Northern Europe. PLoS ONE, 2013, 8, e58552.	2.5	32
257	Whole-exome sequencing identifies a polymorphism in the BMP5 gene associated with SSRI treatment response in major depression. Journal of Psychopharmacology, 2013, 27, 915-920.	4.0	31
258	Mapping the Genetic Architecture of Gene Regulation in Whole Blood. PLoS ONE, 2014, 9, e93844.	2.5	31
259	Ageing with elegans: a research proposal to map healthspan pathways. Biogerontology, 2016, 17, 771-782.	3.9	31
260	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
261	Human ribosomal protein S3a: cloning of the cDNA and primary structure of the protein. Gene, 1992, 119, 313-316.	2.2	30
262	Aromatase gene (CYP19A1) variants, female infertility and ovarian stimulation outcome: a preliminary report. Reproductive BioMedicine Online, 2009, 18, 651-657.	2.4	30
263	Evaluation of the 124-plex SNP typing microarray for forensic testing. Forensic Science International: Genetics, 2009, 4, 43-48.	3.1	29
264	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.	3.5	29
265	Genetic variation in the Estonian population: pharmacogenomics study of adverse drug effects using electronic health records. European Journal of Human Genetics, 2019, 27, 442-454.	2.8	29
266	Location of single-stranded and double-stranded regions in rat liver ribosomal 5S RNA and 5.8S RNA. Nucleic Acids Research, 1981, 9, 5331-5344.	14.5	28
267	Shared genetic risk between eating disorderâ€•and substanceâ€useâ€related phenotypes: Evidence from genomeâ€wide association studies. Addiction Biology, 2021, 26, e12880.	2.6	28
268	Genetic variants in RBFOX3 are associated with sleep latency. European Journal of Human Genetics, 2016, 24, 1488-1495.	2.8	27
269	Harmonising and linking biomedical and clinical data across disparate data archives to enable integrative cross-biobank research. European Journal of Human Genetics, 2016, 24, 521-528.	2.8	27
270	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. Biological Psychiatry, 2020, 87, 419-430.	1.3	27

#	Article	IF	Citations
271	An epigenome-wide association study of metabolic syndrome and its components. Scientific Reports, 2020, 10, 20567.	3.3	27
272	CpG sites associated with NRP1, NRXN2 and miR-29b-2 are hypomethylated in monocytes during ageing. Immunity and Ageing, 2014, 11, 1.	4.2	26
273	Quality Matters: 2016 Annual Conference of the National Infrastructures for Biobanking. Biopreservation and Biobanking, 2017, 15, 270-276.	1.0	26
274	Genomeâ€wide association study and metaâ€analysis in Northern European populations replicate multiple colorectal cancer risk loci. International Journal of Cancer, 2018, 142, 540-546.	5.1	26
275	The ternary complex consisting of rat liver ribosomal 5 S RNA, 5.8 S RNA and protein L5. FEBS Letters, 1980, 119, 81-84.	2.8	25
276	Refining genome-wide linkage intervals using a meta-analysis of genome-wide association studies identifies loci influencing personality dimensions. European Journal of Human Genetics, 2013, 21, 876-882.	2.8	24
277	Occupational irritants and asthma: an Estonian cross-sectional study of 34 000 adults. European Respiratory Journal, 2014, 44, 647-656.	6.7	24
278	Ranking and characterization of established BMI and lipid associated loci as candidates for gene-environment interactions. PLoS Genetics, 2017, 13, e1006812.	3.5	24
279	Variance determines self-observer agreement on the Big Five personality traits. Journal of Research in Personality, 2010, 44, 421-426.	1.7	23
280	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. Genetics, 2019, 212, 905-918.	2.9	23
281	Differences in local population history at the finest level: the case of the Estonian population. European Journal of Human Genetics, 2020, 28, 1580-1591.	2.8	23
282	Whole-genome expression analysis reveals genes associated with treatment response to escitalopram in major depression. European Neuropsychopharmacology, 2016, 26, 1475-1483.	0.7	22
283	The Role of the Fiveâ€“factor Personality Traits in General Selfâ€“rated Health. European Journal of Personality, 2016, 30, 492-504.	3.1	22
284	Roadmap for a precision-medicine initiative in the Nordic region. Nature Genetics, 2019, 51, 924-930.	21.4	22
285	Population distribution and ancestry of the cancer protective MDM2 SNP285 (rs117039649). Oncotarget, 2014, 5, 8223-8234.	1.8	22
286	Manifesto for a European Anxiety Disorders Research Network. European Neuropsychopharmacology, 2010, 20, 426-432.	0.7	21
287	From pharmacogenetics to pharmacometabolomics: SAM modulates TPMT activity. Pharmacogenomics, 2014, 15, 1437-1449.	1.3	20
288	Susceptibility locus for nonâ€syndromic cleft lip with or without cleft palate on chromosome 10q25 confers risk in Estonian patients. European Journal of Oral Sciences, 2010, 118, 317-319.	1.5	19

#	Article	IF	Citations
289	Search for Early Pancreatic Cancer Blood Biomarkers in Five European Prospective Population Biobanks Using Metabolomics. Endocrinology, 2019, 160, 1731-1742.	2.8	19
290	Genotype-first approach to the detection of hereditary breast and ovarian cancer risk, and effects of risk disclosure to biobank participants. European Journal of Human Genetics, 2021, 29, 471-481.	2.8	19
291	Self-Other Agreement in Happiness and Life-Satisfaction: The Role of Personality Traits. Social Indicators Research, 2013, 114, 479-492.	2.7	18
292	Meta-analysis identifies loci affecting levels of the potential osteoarthritis biomarkers sCOMP and uCTX-II with genome wide significance. Journal of Medical Genetics, 2014, 51, 596-604.	3.2	18
293	Coffinâ€“Siris Syndrome with obesity, macrocephaly, hepatomegaly and hyperinsulinism caused by a mutation in the ARID1B gene. European Journal of Human Genetics, 2014, 22, 1327-1329.	2.8	18
294	Genome-wide association meta-analysis of fish and EPA+DHA consumption in 17 US and European cohorts. PLoS ONE, 2017, 12, e0186456.	2.5	18
295	Habitual sleep disturbances and migraine: a Mendelian randomization study. Annals of Clinical and Translational Neurology, 2020, 7, 2370-2380.	3.7	18
296	Thiopurine S-methyltransferase (TPMT) pharmacogenetics: three new mutations and haplotype analysis in the Estonian population. Clinical Chemistry and Laboratory Medicine, 2008, 46, 974-9.	2.3	17
297	Post-translational stabilization of thiopurine S-methyltransferase by S-adenosyl-l-methionine reveals regulation of TPMT*1 and *3C allozymes. Biochemical Pharmacology, 2012, 83, 969-976.	4.4	17
298	Subsequent Event Risk in Individuals With Established Coronary Heart Disease. Circulation Genomic and Precision Medicine, 2019, 12, e002470.	3.6	17
299	Development and validation of two SCORE-based cardiovascular risk prediction models for Eastern Europe: a multicohort study. European Heart Journal, 2020, 41, 3325-3333.	2.2	17
300	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	7.9	17
301	Stratification of Type 2 Diabetes by Age of Diagnosis in the UK Biobank Reveals Subgroup-Specific Genetic Associations and Causal Risk Profiles. Diabetes, 2021, 70, 1816-1825.	0.6	17
302	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	4.4	17
303	The human ribosomal protein S6 gene: isolation, primary structure and location in chromosome 9. Gene, 1992, 121, 387-392.	2.2	16
304	The Estonian Genome Project. Drug Development Research, 2004, 62, 97-101.	2.9	16
305	Arrayed Primer Extension Resequencing of Mutations in the TP53 Tumor Suppressor Gene: Comparison with Denaturing HPLC and Direct Sequencing. Clinical Chemistry, 2005, 51, 1284-1287.	3.2	16
306	Comparison of DNA extraction methods for multiplex polymerase chain reaction. Analytical Biochemistry, 2010, 398, 260-262.	2.4	16

#	Article	IF	Citations
307	Association of Whole-Genome and NETRIN1 Signaling Pathwayâ€“Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. Biological Psychiatry: Cognitive Neuroscience and Neuroimaging, 2019, 4, 91-100.	1.5	16
308	Phantom epistasis between unlinked loci. Nature, 2021, 596, E1-E3.	27.8	16
309	The blood metabolome of incident kidney cancer: A caseâ€“control study nested within the MetKid consortium. PLoS Medicine, 2021, 18, e1003786.	8.4	16
310	Identification of lung cancer histology-specific variants applying Bayesian framework variant prioritization approaches within the TRICL and ILCCO consortia. Carcinogenesis, 2015, 36, 1314-1326.	2.8	15
311	Phenylalanine Hydroxylase Gene Mutation R408W Is Present on 84% of Estonian Phenylketonuria Chromosomes. European Journal of Human Genetics, 1996, 4, 296-300.	2.8	15
312	History of the Diagnosis of a Sexually Transmitted Disease is Linked to Normal Variation in Personality Traits. Journal of Sexual Medicine, 2012, 9, 2861-2867.	0.6	14
313	Cis-epistasis at the LPA locus and risk of cardiovascular diseases. Cardiovascular Research, 2022, 118, 1088-1102.	3.8	14
314	A novel snoRNA (U73) is encoded within the introns of the human and mouse ribosomal protein S3a genes. Gene, 1998, 210, 255-263.	2.2	13
315	Association study of sporadic Parkinson's disease genetic risk factors in patients from Russia by APEX technology. Neuroscience Letters, 2006, 405, 212-216.	2.1	13
316	Noncoding RET variants explain the strong association with Hirschsprung disease in patients without rare coding sequence variant. European Journal of Medical Genetics, 2019, 62, 229-234.	1.3	13
317	PAIRUP-MS: Pathway analysis and imputation to relate unknowns in profiles from mass spectrometry-based metabolite data. PLoS Computational Biology, 2019, 15, e1006734.	3.2	13
318	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
319	Hemani et al. reply. Nature, 2014, 514, E5-E6.	27.8	12
320	Reporting incidental findings of genomic disorder-associated copy number variants to unselected biobank participants. Personalized Medicine, 2016, 13, 303-314.	1.5	12
321	Integrating untargeted metabolomics, genetically informed causal inference, and pathway enrichment to define the obesity metabolome. International Journal of Obesity, 2020, 44, 1596-1606.	3.4	12
322	Gut metagenome associations with extensive digital health data in a volunteer-based Estonian microbiome cohort. Nature Communications, 2022, 13, 869.	12.8	12
323	Sequence Variants and the Risk of Head and Neck Cancer: Pooled Analysis in the INHANCE Consortium. Frontiers in Oncology, 2011, 1, 13.	2.8	11
324	Analysis of Polymorphisms in the SRD5A2 Gene and Semen Parameters in Estonian Men. Journal of Andrology, 2010, 31, 372-378.	2.0	10

#	Article	IF	Citations
325	Metabolomic Fingerprints in Large Population Cohorts: Impact of Preanalytical Heterogeneity. Clinical Chemistry, 2021, 67, 1153-1155.	3.2	10
326	Reliable detection of beta-thalassemia and G6PD mutations by a DNA microarray. Clinical Chemistry, 2002, 48, 2051-4.	3.2	10
327	The relationship between the Five-Factor Model personality traits and peptic ulcer disease in a large population-based adult sample. Scandinavian Journal of Psychology, 2015, 56, 693-699.	1.5	9
328	Haplotype Phasing and Inheritance of Copy Number Variants in Nuclear Families. PLoS ONE, 2015, 10, e0122713.	2.5	9
329	Identifying pathways modulating sleep duration: from genomics to transcriptomics. Scientific Reports, 2017, 7, 4555.	3.3	9
330	A parallel SNP array study of genomic aberrations associated with mental retardation in patients and general population in Estonia. European Journal of Medical Genetics, 2011, 54, 136-143.	1.3	8
331	De novo exonic mutation in MYH7 gene leading to exon skipping in a patient with early onset muscular weakness and fiber-type disproportion. Neuromuscular Disorders, 2016, 26, 236-239.	0.6	8
332	MixFit: Methodology for Computing Ancestry-Related Genetic Scores at the Individual Level and Its Application to the Estonian and Finnish Population Studies. PLoS ONE, 2017, 12, e0170325.	2.5	7
333	Severe CF manifestation with anaemia and failure to thrive in a 394delTT homozygous patient. Journal of Cystic Fibrosis, 2004, 3, 58-60.	0.7	6
334	ROS1 Asp2213Asn polymorphism is not associated with coronary artery disease in a Greek case-control study. Clinical Chemistry and Laboratory Medicine, 2009, 47, 1471-3.	2.3	6
335	Analysis of Allele and Haplotype Diversity Across 25 Genomic Regions in Three Eastern European Populations. Human Heredity, 2009, 68, 35-44.	0.8	6
336	Exome analysis in an Estonian multiplex family with neural tube defectsâ€”a case report. Child's Nervous System, 2017, 33, 1575-1581.	1.1	6
337	Viva Europa, a Land of Excellence in Research and Innovation for Health and Wellbeing. Progress in Preventive Medicine (New York, N Y), 2017, 2, e006.	0.7	6
338	Human basonuclin 2 up-regulates a cascade set of interferon-stimulated genes with anti-cancerous properties in a lung cancer model. Cancer Cell International, 2017, 17, 18.	4.1	6
339	Estimating the performance of three cardiovascular disease risk scores: the Estonian Biobank cohort study. Journal of Epidemiology and Community Health, 2019, 73, 272-277.	3.7	6
340	Advances in Genomic Discovery and Implications for Personalized Prevention and Medicine: Estonia as Example. Journal of Personalized Medicine, 2021, 11, 358.	2.5	6
341	Association analysis of juvenile idiopathic arthritis genetic susceptibility factors in Estonian patients. Clinical Rheumatology, 2021, 40, 4157-4165.	2.2	6
342	Structural characterization of the mouse ribosomal protein S6-encoding gene. Gene, 1996, 175, 241-245.	2.2	5

#	Article	IF	Citations
343	Mutation 985A>G in the MCAD gene shows low incidence in Estonian population. Human Mutation, 2000, 15, 293-294.	2.5	5
344	High-density genotyping and linkage disequilibrium in the human genome using chromosome 22 as a model. Current Opinion in Chemical Biology, 2002, 6, 24-30.	6.1	5
345	Giving and Withholding of Information following Genomic Screening: Challenges Identified in a Study of Primary Care Physicians in Estonia. Journal of Genetic Counseling, 2012, 21, 591-604.	1.6	5
346	Cumulative Small Effect Genetic Markers and the Risk of Colorectal Cancer in Poland, Estonia, Lithuania, and Latvia. Gastroenterology Research and Practice, 2015, 2015, 1-10.	1.5	5
347	Genome-Wide Association Scan of Serum Urea in European Populations Identifies Two Novel Loci. American Journal of Nephrology, 2019, 49, 193-202.	3.1	5
348	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. Circulation Genomic and Precision Medicine, 2020, 13, e002769.	3.6	5
349	Spectrum and frequency of CHEK2 variants in breast cancer affected and general population in the Baltic states region, initial results and literature review. European Journal of Medical Genetics, 2022, 65, 104477.	1.3	5
350	Isolation and characterization of the mouse ribosomal protein S7 gene. IUBMB Life, 1998, 46, 287-295.	3.4	3
351	5 S RNA and 5.8 S RNA build up eukaryotic subribosomal domains active in tRNA binding. FEBS Letters, 1981, 136, 255-258.	2.8	2
352	Gene Expression-Based Approaches in Differentiation of Metastases and Second Primary Tumour. Case Reports in Oncology, 2010, 3, 255-261.	0.7	2
353	Ancient Haplotypes at the 15q24.2 Microdeletion Region Are Linked to Brain Expression of MAN2C1 and Children's Intelligence. PLoS ONE, 2016, 11, e0157739.	2.5	2
354	The ABCA4 2588G>C Stargardt mutation: single origin and increasing frequency from South-West to North-East Europe. , 0, .		1
355	Oligonucleotide Array for Mutation Analysis in Familial Breast Cancer. Disease Markers, 1999, 15, 117-117.	1.3	0
356	P2-030: NSCLC gene expression study in Estonia. Journal of Thoracic Oncology, 2007, 2, S493-S494.	1.1	0