

# Andres Metspalu

## List of Articles by Year in descending order

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506

PR articles

105,755

PR citations

202

141

PR h-index

179

311

g-index

532

documents

119757

doc citations

201

152

h-index

155613

citing authors

#	ARTICLE	IF	CITATIONS
1	Distinct Genetic Risk Profile in Aortic Stenosis Compared With Coronary Artery Disease. <i>JAMA Cardiology</i> , 2025, 10, 145.	11.2	3
2	Altered IL-6 signalling and risk of tuberculosis: a multi-ancestry mendelian randomisation study. <i>Lancet Microbe</i> , The, 2025, 6, 100922.	12.3	20
3	A large-scale genome-wide association study on female genital tract polyps highlights role of DNA repair, cell proliferation, and cell growth. <i>Human Reproduction</i> , 2025, 40, 750-763.	1.0	4
4	GWAS meta-analysis of psoriasis identifies new susceptibility alleles impacting disease mechanisms and therapeutic targets. <i>Nature Communications</i> , 2025, 16, .	13.7	35
5	Atlas of genetic and phenotypic associations across 42 female reproductive health diagnoses. <i>Nature Medicine</i> , 2025, 31, 1626-1634.	33.0	11
6	The Estonian Biobank's journey from biobanking to personalized medicine. <i>Nature Communications</i> , 2025, 16, .	13.7	32
7	Genome-wide analyses identify 25 infertility loci and relationships with reproductive traits across the allele frequency spectrum. <i>Nature Genetics</i> , 2025, 57, 1107-1118.	25.2	9
8	Genome-wide analyses identify 30 loci associated with obsessive-compulsive disorder. <i>Nature Genetics</i> , 2025, 57, 1389-1401.	25.2	27
9	Pleiotropic and sex-specific genetic mechanisms of circulating metabolic markers. <i>Nature Communications</i> , 2025, 16, .	13.7	3
10	Transcriptome analysis reveals involvement of thiopurine S-methyltransferase in oxidation-reduction processes. <i>European Journal of Pharmaceutical Sciences</i> , 2024, 192, 106616.	4.3	1
11	Distinct and shared genetic architectures of gestational diabetes mellitus and type 2 diabetes. <i>Nature Genetics</i> , 2024, 56, 377-382.	25.2	66
12	Rare copy-number variants as modulators of common disease susceptibility. <i>Genome Medicine</i> , 2024, 16, .	9.6	41
13	Genetic drivers of heterogeneity in type 2 diabetes pathophysiology. <i>Nature</i> , 2024, 627, 347-357.	37.9	383
14	Body mass index stratified meta-analysis of genome-wide association studies of polycystic ovary syndrome in women of European ancestry. <i>BMC Genomics</i> , 2024, 25, .	3.3	19
15	Prioritization of Kidney Cell Types Highlights Myofibroblast Cells in Regulating Human Blood Pressure. <i>Kidney International Reports</i> , 2024, 9, 1849-1859.	2.5	3
16	Genetic determinants of plasma protein levels in the Estonian population. <i>Scientific Reports</i> , 2024, 14, .	3.4	7
17	Genome-wide analysis in over 1 million individuals of European ancestry yields improved polygenic risk scores for blood pressure traits. <i>Nature Genetics</i> , 2024, 56, 778-791.	25.2	142
18	Genome-wide meta-analyses of restless legs syndrome yield insights into genetic architecture, disease biology and risk prediction. <i>Nature Genetics</i> , 2024, 56, 1090-1099.	25.2	40

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19	Shared Genetic Architecture Between Schizophrenia and Anorexia Nervosa: A Cross-trait Genome-Wide Analysis. <i>Schizophrenia Bulletin</i> , 2024, 50, 1255-1265.	3.9	10
20	Genetic drivers and cellular selection of female mosaic X chromosome loss. <i>Nature</i> , 2024, 631, 134-141.	37.9	32
21	SMIM1 absence is associated with reduced energy expenditure and excess weight. <i>Med</i> , 2024, 5, 1083-1095.e6.	7.0	5
22	Distinct genetic liability profiles define clinically relevant patient strata across common diseases. <i>Nature Communications</i> , 2024, 15, .	13.7	6
23	Characterising the genetic architecture of changes in adiposity during adulthood using electronic health records. <i>Nature Communications</i> , 2024, 15, .	13.7	11
24	Uncovering the shared genetic components of thyroid disorders and reproductive health. <i>European Journal of Endocrinology</i> , 2024, 191, 211-222.	4.0	5
25	Metadata for Data discoverability and Study replicability in observational Studies (MINERVA): Development and Pilot of a Metadata List and Catalogue in Europe. <i>Pharmacoepidemiology and Drug Safety</i> , 2024, 33, .	1.9	9
26	Genetic architecture reconciles linkage and association studies of complex traits. <i>Nature Genetics</i> , 2024, 56, 2352-2360.	25.2	10
27	High SHBG and Low Bioavailable Testosterone are Strongly Causally Associated with Increased Forearm Fracture Risk in Women: An MR Study Leveraging Novel Female-Specific Data. <i>Calcified Tissue International</i> , 2024, 115, 648-660.	2.8	0
28	Socio-demographic and genetic risk factors for drug adherence and persistence across 5 common medication classes. <i>Nature Communications</i> , 2024, 15, .	13.7	12
29	Genome-wide meta-analysis conducted in three large biobanks expands the genetic landscape of lumbar disc herniations. <i>Nature Communications</i> , 2024, 15, .	13.7	6
30	Use of Estonian Biobank data and participant recall to improve Wilson's disease management. <i>European Journal of Human Genetics</i> , 2024, 33, 1499-1508.	3.0	1
31	Long-range regulatory effects of Neandertal DNA in modern humans. <i>Genetics</i> , 2023, 223, .	4.2	6
32	Genome-wide screen of otosclerosis in population biobanks: 27 loci and shared associations with skeletal structure. <i>Nature Communications</i> , 2023, 14, .	13.7	9
33	Rare variant analyses across multiethnic cohorts identify novel genes for refractive error. <i>Communications Biology</i> , 2023, 6, .	4.4	7
34	FinnGen provides genetic insights from a well-phenotyped isolated population. <i>Nature</i> , 2023, 613, 508-518.	37.9	3,207
35	Genetic Risk Score for Intracranial Aneurysms: Prediction of Subarachnoid Hemorrhage and Role in Clinical Heterogeneity. <i>Stroke</i> , 2023, 54, 810-818.	6.0	25
36	Migraine, inflammatory bowel disease and celiac disease: A Mendelian randomization study. <i>Headache</i> , 2023, 63, 642-651.	3.0	10

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37	A new polygenic score for refractive error improves detection of children at risk of high myopia but not the prediction of those at risk of myopic macular degeneration. <i>EBioMedicine</i> , 2023, 91, 104551.	9.7	22
38	Genome-wide analysis identifies genetic effects on reproductive success and ongoing natural selection at the FADS locus. <i>Nature Human Behaviour</i> , 2023, 7, 790-801.	9.1	38
39	Genome-wide meta-analysis identifies novel loci conferring risk of acne vulgaris. <i>European Journal of Human Genetics</i> , 2023, 32, 1136-1143.	3.0	24
40	Genome-wide association study of obstructive sleep apnoea in the Million Veteran Program uncovers genetic heterogeneity by sex. <i>EBioMedicine</i> , 2023, 90, 104536.	9.7	48
41	Using brain cell-type-specific protein interactomes to interpret neurodevelopmental genetic signals in schizophrenia. <i>IScience</i> , 2023, 26, 106701.	3.6	10
42	Nationwide health, socio-economic and genetic predictors of COVID-19 vaccination status in Finland. <i>Nature Human Behaviour</i> , 2023, 7, 1069-1083.	9.1	35
43	Dissecting the genetic heterogeneity of gastric cancer. <i>EBioMedicine</i> , 2023, 92, 104616.	9.7	25
44	Genome-wide association analysis identifies ancestry-specific genetic variation associated with acute response to metformin and glipizide in SUGAR-MGH. <i>Diabetologia</i> , 2023, 66, 1260-1272.	7.6	10
45	Schizophrenia-associated somatic copy-number variants from 12,834 cases reveal recurrent NRXN1 and ABCB11 disruptions. <i>Cell Genomics</i> , 2023, 3, 100356.	6.8	28
46	Genetics of circulating inflammatory proteins identifies drivers of immune-mediated disease risk and therapeutic targets. <i>Nature Immunology</i> , 2023, 24, 1540-1551.	23.6	609
47	European and multi-ancestry genome-wide association meta-analysis of atopic dermatitis highlights importance of systemic immune regulation. <i>Nature Communications</i> , 2023, 14, .	13.7	95
48	Global Effect of Modifiable Risk Factors on Cardiovascular Disease and Mortality. <i>New England Journal of Medicine</i> , 2023, 389, 1273-1285.	34.6	614
49	HLA allele-calling using multi-ancestry whole-exome sequencing from the UK Biobank identifies 129 novel associations in 11 autoimmune diseases. <i>Communications Biology</i> , 2023, 6, .	4.4	22
50	Inferring compound heterozygosity from large-scale exome sequencing data. <i>Nature Genetics</i> , 2023, 56, 152-161.	25.2	27
51	A genomic mutational constraint map using variation in 76,156 human genomes. <i>Nature</i> , 2023, 625, 92-100.	37.9	1,024
52	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. <i>Biological Psychiatry</i> , 2022, 91, 102-117.	5.4	119
53	Cis-epistasis at the LPA locus and risk of cardiovascular diseases. <i>Cardiovascular Research</i> , 2022, 118, 1088-1102.	5.5	25
54	Identifying the Common Genetic Basis of Antidepressant Response. <i>Biological Psychiatry Global Open Science</i> , 2022, 2, 115-126.	2.7	107

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55	Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors. <i>Biological Psychiatry</i> , 2022, 91, 313-327.	5.4	221
56	Interaction Testing and Polygenic Risk Scoring to Estimate the Association of Common Genetic Variants With Treatment Resistance in Schizophrenia. <i>JAMA Psychiatry</i> , 2022, 79, 260.	12.4	92
57	Impact of the pre-examination phase on multicenter metabolomic studies. <i>New Biotechnology</i> , 2022, 68, 37-47.	4.7	28
58	Elucidating the relationship between migraine risk and brain structure using genetic data. <i>Brain</i> , 2022, 145, 3214-3224.	8.4	30
59	Gut metagenome associations with extensive digital health data in a volunteer-based Estonian microbiome cohort. <i>Nature Communications</i> , 2022, 13, .	13.7	56
60	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. <i>Nature Genetics</i> , 2022, 54, 437-449.	25.2	536
61	Spectrum and frequency of CHEK2 variants in breast cancer affected and general population in the Baltic states region, initial results and literature review. <i>European Journal of Medical Genetics</i> , 2022, 65, 104477.	1.6	10
62	Whole-genome sequencing reveals host factors underlying critical COVID-19. <i>Nature</i> , 2022, 607, 97-103.	37.9	298
63	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022, 604, 502-508.	37.9	2,335
64	The individual and global impact of copy-number variants on complex human traits. <i>American Journal of Human Genetics</i> , 2022, 109, 647-668.	6.5	79
65	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. <i>Nature Genetics</i> , 2022, 54, 560-572.	25.2	616
66	Genome-wide association meta-analysis identifies 48 risk variants and highlights the role of the stria vascularis in hearing loss. <i>American Journal of Human Genetics</i> , 2022, 109, 1077-1091.	6.5	65
67	Advancing our understanding of genetic risk factors and potential personalized strategies for pelvic organ prolapse. <i>Nature Communications</i> , 2022, 13, .	13.7	31
68	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022, 5, .	4.4	31
69	Contribution of schizophrenia polygenic burden to longitudinal phenotypic variance in 22q11.2 deletion syndrome. <i>Molecular Psychiatry</i> , 2022, 27, 4191-4200.	7.8	19
70	Do Biobank Recall Studies Matter? Long-Term Follow-Up of Research Participants With Familial Hypercholesterolemia. <i>Frontiers in Genetics</i> , 2022, 13, .	2.3	8
71	Precise, Genotype-First Breast Cancer Prevention: Experience With Transferring Monogenic Findings From a Population Biobank to the Clinical Setting. <i>Frontiers in Genetics</i> , 2022, 13, .	2.3	11
72	Inframe insertion and splice site variants in MFGE8 associate with protection against coronary atherosclerosis. <i>Communications Biology</i> , 2022, 5, .	4.4	15

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73	A first update on mapping the human genetic architecture of COVID-19. <i>Nature</i> , 2022, 608, E1-E10.	37.9	144
74	Genetic and modifiable risk factors combine multiplicatively in common disease. <i>Clinical Research in Cardiology</i> , 2022, 112, 247-257.	2.8	19
75	A cross-disorder dosage sensitivity map of the human genome. <i>Cell</i> , 2022, 185, 3041-3055.e25.	33.7	313
76	Genome-wide association analyses of physical activity and sedentary behavior provide insights into underlying mechanisms and roles in disease prevention. <i>Nature Genetics</i> , 2022, 54, 1332-1344.	25.2	196
77	Stroke genetics informs drug discovery and risk prediction across ancestries. <i>Nature</i> , 2022, 611, 115-123.	37.9	489
78	Lessons learned during the process of reporting individual genomic results to participants of a population-based biobank. <i>European Journal of Human Genetics</i> , 2022, 31, 1048-1056.	3.0	16
79	Neandertal introgression partitions the genetic landscape of neuropsychiatric disorders and associated behavioral phenotypes. <i>Translational Psychiatry</i> , 2022, 12, .	5.2	19
80	ANGPTL7, a therapeutic target for increased intraocular pressure and glaucoma. <i>Communications Biology</i> , 2022, 5, .	4.4	20
81	A saturated map of common genetic variants associated with human height. <i>Nature</i> , 2022, 610, 704-712.	37.9	687
82	Assessment of the genetic and clinical determinants of hip fracture risk: Genome-wide association and Mendelian randomization study. <i>Cell Reports Medicine</i> , 2022, 3, 100776.	6.6	32
83	Prioritizing autoimmunity risk variants for functional analyses by fine-mapping mutations under natural selection. <i>Nature Communications</i> , 2022, 13, .	13.7	12
84	Effectiveness and feasibility of cardiovascular disease personalized prevention on high polygenic risk score subjects: a randomized controlled pilot study. <i>European Heart Journal Open</i> , 2022, 2, .	2.5	20
85	Genetic diversity fuels gene discovery for tobacco and alcohol use. <i>Nature</i> , 2022, 612, 720-724.	37.9	410
86	Shared genetic risk between eating disorder and substance use related phenotypes: Evidence from genome-wide association studies. <i>Addiction Biology</i> , 2021, 26, .	2.6	54
87	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021, 12, .	13.7	132
88	Model-based assessment of replicability for genome-wide association meta-analysis. <i>Nature Communications</i> , 2021, 12, .	13.7	36
89	Multi-ancestry genome-wide gene-sleep interactions identify novel loci for blood pressure. <i>Molecular Psychiatry</i> , 2021, 26, 6293-6304.	7.8	22
90	Advances in Genomic Discovery and Implications for Personalized Prevention and Medicine: Estonia as Example. <i>Journal of Personalized Medicine</i> , 2021, 11, 358.	2.4	14

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91	The landscape of autosomal-recessive pathogenic variants in European populations reveals phenotype-specific effects. <i>American Journal of Human Genetics</i> , 2021, 108, 608-619.	6.5	62
92	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. <i>Biological Psychiatry</i> , 2021, 90, 611-620.	5.4	182
93	Stratification of Type 2 Diabetes by Age of Diagnosis in the UK Biobank Reveals Subgroup-Specific Genetic Associations and Causal Risk Profiles. <i>Diabetes</i> , 2021, 70, 1816-1825.	4.2	29
94	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	25.2	650
95	Genome-wide association study identifies five risk loci for pernicious anemia. <i>Nature Communications</i> , 2021, 12, .	13.7	52
96	Evaluation of Shared Genetic Susceptibility to High and Low Myopia and Hyperopia. <i>JAMA Ophthalmology</i> , 2021, 139, 601.	6.1	47
97	Association analysis of juvenile idiopathic arthritis genetic susceptibility factors in Estonian patients. <i>Clinical Rheumatology</i> , 2021, 40, 4157-4165.	2.2	7
98	Mapping the human genetic architecture of COVID-19. <i>Nature</i> , 2021, 600, 472-477.	37.9	871
99	Identification of 371 genetic variants for age at first sex and birth linked to externalising behaviour. <i>Nature Human Behaviour</i> , 2021, 5, 1717-1730.	9.1	140
100	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	37.9	343
101	Metabolomic Fingerprints in Large Population Cohorts: Impact of Preanalytical Heterogeneity. <i>Clinical Chemistry</i> , 2021, 67, 1153-1155.	1.1	13
102	Phantom epistasis between unlinked loci. <i>Nature</i> , 2021, 596, E1-E3.	37.9	32
103	The blood metabolome of incident kidney cancer: A case-control study nested within the MetKid consortium. <i>PLoS Medicine</i> , 2021, 18, e1003786.	8.1	35
104	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	25.2	436
105	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. <i>JAMA Psychiatry</i> , 2021, 78, 1258.	12.4	169
106	Worldwide trends in hypertension prevalence and progress in treatment and control from 1990 to 2019: a pooled analysis of 1201 population-representative studies with 104 million participants. <i>Lancet</i> , 2021, 398, 957-980.	62.3	2,827
107	Differentially expressed genes reflect disease-induced rather than disease-causing changes in the transcriptome. <i>Nature Communications</i> , 2021, 12, .	13.7	111
108	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. <i>Nature Genetics</i> , 2021, 53, 1504-1516.	25.2	153

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109	Mendelian Randomization Identifies the Potential Causal Impact of Dietary Patterns on Circulating Blood Metabolites. <i>Frontiers in Genetics</i> , 2021, 12, .	2.3	10
110	SARS-CoV-2 susceptibility and COVID-19 disease severity are associated with genetic variants affecting gene expression in a variety of tissues. <i>Cell Reports</i> , 2021, 37, 110020.	6.3	37
111	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. <i>Biological Psychiatry</i> , 2020, 87, 419-430.	5.4	34
112	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. <i>Biological Psychiatry</i> , 2020, 88, 169-184.	5.4	191
113	Development and validation of two SCORE-based cardiovascular risk prediction models for Eastern Europe: a multicohort study. <i>European Heart Journal</i> , 2020, 41, 3325-3333.	2.2	24
114	The genetic architecture of sporadic and multiple consecutive miscarriage. <i>Nature Communications</i> , 2020, 11, .	13.7	97
115	Differences in local population history at the finest level: the case of the Estonian population. <i>European Journal of Human Genetics</i> , 2020, 28, 1580-1591.	3.0	40
116	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, .	2.9	10
117	An epigenome-wide association study of metabolic syndrome and its components. <i>Scientific Reports</i> , 2020, 10, .	3.4	40
118	Cerebral small vessel disease genomics and its implications across the lifespan. <i>Nature Communications</i> , 2020, 11, .	13.7	179
119	Habitual sleep disturbances and migraine: a Mendelian randomization study. <i>Annals of Clinical and Translational Neurology</i> , 2020, 7, 2370-2380.	3.8	36
120	Height and body-mass index trajectories of school-aged children and adolescents from 1985 to 2019 in 200 countries and territories: a pooled analysis of 2181 population-based studies with 65 million participants. <i>Lancet, The</i> , 2020, 396, 1511-1524.	62.3	343
121	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. <i>Molecular Psychiatry</i> , 2020, 26, 2111-2125.	7.8	23
122	A phenome-wide association and Mendelian Randomisation study of polygenic risk for depression in UK Biobank. <i>Nature Communications</i> , 2020, 11, .	13.7	112
123	Evaluating drug targets through human loss-of-function genetic variation. <i>Nature</i> , 2020, 581, 459-464.	37.9	167
124	The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2020, 581, 434-443.	37.9	8,804
125	Integrating untargeted metabolomics, genetically informed causal inference, and pathway enrichment to define the obesity metabolome. <i>International Journal of Obesity</i> , 2020, 44, 1596-1606.	3.0	26
126	Characterising the loss-of-function impact of 5â€™ untranslated region variants in 15,708 individuals. <i>Nature Communications</i> , 2020, 11, .	13.7	151

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127	Landscape of multi-nucleotide variants in 125,748 human exomes and 15,708 genomes. <i>Nature Communications</i> , 2020, 11, .	13.7	125
128	A structural variation reference for medical and population genetics. <i>Nature</i> , 2020, 581, 444-451.	37.9	921
129	Transcript expression-aware annotation improves rare variant interpretation. <i>Nature</i> , 2020, 581, 452-458.	37.9	182
130	The effect of LRRK2 loss-of-function variants in humans. <i>Nature Medicine</i> , 2020, 26, 869-877.	33.0	105
131	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. <i>Nature Reviews Clinical Oncology</i> , 2020, 17, 687-705.	70.8	331
132	Genome-wide association meta-analysis of corneal curvature identifies novel loci and shared genetic influences across axial length and refractive error. <i>Communications Biology</i> , 2020, 3, .	4.4	35
133	Association of polygenic score for major depression with response to lithium in patients with bipolar disorder. <i>Molecular Psychiatry</i> , 2020, 26, 2457-2470.	7.8	72
134	A genome-wide cross-phenotype meta-analysis of the association of blood pressure with migraine. <i>Nature Communications</i> , 2020, 11, .	13.7	78
135	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. <i>American Journal of Human Genetics</i> , 2020, 106, 389-404.	6.5	162
136	Genome-wide gene-environment analyses of major depressive disorder and reported lifetime traumatic experiences in UK Biobank. <i>Molecular Psychiatry</i> , 2020, 25, 1430-1446.	7.8	178
137	Genetic identification of cell types underlying brain complex traits yields insights into the etiology of Parkinson's disease. <i>Nature Genetics</i> , 2020, 52, 482-493.	25.2	343
138	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. <i>International Journal of Epidemiology</i> , 2020, 49, 1022-1031.	4.9	46
139	Genome-wide association study identifies 48 common genetic variants associated with handedness. <i>Nature Human Behaviour</i> , 2020, 5, 59-70.	9.1	126
140	Genotype-first approach to the detection of hereditary breast and ovarian cancer risk, and effects of risk disclosure to biobank participants. <i>European Journal of Human Genetics</i> , 2020, 29, 471-481.	3.0	36
141	Genome-wide Study Identifies Association between HLA-B*55:01 and Self-Reported Penicillin Allergy. <i>American Journal of Human Genetics</i> , 2020, 107, 612-621.	6.5	54
142	Identification of ALK in Thinness. <i>Cell</i> , 2020, 181, 1246-1262.e22.	33.7	103
143	COVID-19 and beyond: A call for action and audacious solidarity to all the citizens and nations, it is humanity's fight. <i>F1000Research</i> , 2020, 9, 1130.	0.5	3
144	Noncoding RET variants explain the strong association with Hirschsprung disease in patients without rare coding sequence variant. <i>European Journal of Medical Genetics</i> , 2019, 62, 229-234.	1.6	17

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145	A metabolic profile of all-cause mortality risk identified in an observational study of 44,168 individuals. <i>Nature Communications</i> , 2019, 10, .	13.7	295
146	Metabolomics reveals a link between homocysteine and lipid metabolism and leukocyte telomere length: the ENGAGE consortium. <i>Scientific Reports</i> , 2019, 9, .	3.4	17
147	Genome-wide association study identifies eight risk loci and implicates metabo-psychiatric origins for anorexia nervosa. <i>Nature Genetics</i> , 2019, 51, 1207-1214.	25.2	987
148	The effect of X-linked dosage compensation on complex trait variation. <i>Nature Communications</i> , 2019, 10, .	13.7	66
149	Genome-wide association study of panic disorder reveals genetic overlap with neuroticism and depression. <i>Molecular Psychiatry</i> , 2019, 26, 4179-4190.	7.8	131
150	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, .	13.7	117
151	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. <i>Nature Communications</i> , 2019, 10, .	13.7	82
152	Leveraging European infrastructures to access 1 million human genomes by 2022. <i>Nature Reviews Genetics</i> , 2019, 20, 693-701.	47.0	83
153	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	25.2	363
154	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019, 188, 1033-1054.	3.3	110
155	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, .	13.7	84
156	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. <i>Genetics</i> , 2019, 212, 905-918.	4.2	31
157	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	25.2	796
158	Search for Early Pancreatic Cancer Blood Biomarkers in Five European Prospective Population Biobanks Using Metabolomics. <i>Endocrinology</i> , 2019, 160, 1731-1742.	2.5	25
159	Integrated analysis of environmental and genetic influences on cord blood DNA methylation in new-borns. <i>Nature Communications</i> , 2019, 10, .	13.7	126
160	Polygenic prediction of breast cancer: comparison of genetic predictors and implications for risk stratification. <i>BMC Cancer</i> , 2019, 19, .	2.9	48
161	Associations Between Attention-Deficit/Hyperactivity Disorder and Various Eating Disorders: A Swedish Nationwide Population Study Using Multiple Genetically Informative Approaches. <i>Biological Psychiatry</i> , 2019, 86, 577-586.	5.4	61
162	Subsequent Event Risk in Individuals With Established Coronary Heart Disease. <i>Circulation Genomic and Precision Medicine</i> , 2019, 12, .	2.9	19

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163	Association of Chromosome 9p21 With Subsequent Coronary Heart Disease Events. <i>Circulation Genomic and Precision Medicine</i> , 2019, 12, .	2.9	30
164	Genome-wide association study identifies 30 loci associated with bipolar disorder. <i>Nature Genetics</i> , 2019, 51, 793-803.	25.2	1,478
165	Genetic Overlap Between Alzheimer's Disease and Bipolar Disorder Implicates the MARK2 and VAC14 Genes. <i>Frontiers in Neuroscience</i> , 2019, 13, .	2.7	56
166	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> , 2019, 28, 2615-2633.	2.9	44
167	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019, 51, 636-648.	25.2	133
168	Population-based identity-by-descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2019, 180, 223-231.	1.5	4
169	Improved polygenic prediction by Bayesian multiple regression on summary statistics. <i>Nature Communications</i> , 2019, 10, .	13.7	473
170	Application of non-HDL cholesterol for population-based cardiovascular risk stratification: results from the Multinational Cardiovascular Risk Consortium. <i>Lancet, The</i> , 2019, 394, 2173-2183.	62.3	247
171	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. <i>Cell</i> , 2019, 179, 1469-1482.e11.	33.7	1,304
172	Association of Whole-Genome and NETRIN1 Signaling Pathway-Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. <i>Biological Psychiatry: Cognitive Neuroscience and Neuroimaging</i> , 2019, 4, 91-100.	1.2	18
173	Estimating the performance of three cardiovascular disease risk scores: the Estonian Biobank cohort study. <i>Journal of Epidemiology and Community Health</i> , 2019, 73, 272-277.	2.9	7
174	PAIRUP-MS: Pathway analysis and imputation to relate unknowns in profiles from mass spectrometry-based metabolite data. <i>PLoS Computational Biology</i> , 2019, 15, e1006734.	3.1	20
175	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. <i>Journal of the American College of Cardiology</i> , 2019, 73, 58-66.	2.3	180
176	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> , 2019, 51, 237-244.	25.2	1,819
177	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol Use. <i>Biological Psychiatry</i> , 2019, 85, 946-955.	5.4	84
178	Recall by genotype and cascade screening for familial hypercholesterolemia in a population-based biobank from Estonia. <i>Genetics in Medicine</i> , 2019, 21, 1173-1180.	4.2	47
179	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. <i>Molecular Psychiatry</i> , 2019, 25, 2392-2409.	7.8	107
180	Bipolar multiplex families have an increased burden of common risk variants for psychiatric disorders. <i>Molecular Psychiatry</i> , 2019, 26, 1286-1298.	7.8	46

#	ARTICLE	IF	CITATIONS
181	Signatures of negative selection in the genetic architecture of human complex traits. <i>Nature Genetics</i> , 2018, 50, 746-753.	25.2	402
182	Genetic influence on social outcomes during and after the Soviet era in Estonia. <i>Nature Human Behaviour</i> , 2018, 2, 269-275.	9.1	104
183	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018, 50, 559-571.	25.2	429
184	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> , 2018, 102, 375-400.	6.5	156
185	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	25.2	2,886
186	Contributions of mean and shape of blood pressure distribution to worldwide trends and variations in raised blood pressure: a pooled analysis of 1018 population-based measurement studies with 88.6 million participants. <i>International Journal of Epidemiology</i> , 2018, 47, 872-883i.	4.9	76
187	Haplotype Sharing Provides Insights into Fine-Scale Population History and Disease in Finland. <i>American Journal of Human Genetics</i> , 2018, 102, 760-775.	6.5	67
188	Genome-wide association study and meta-analysis in Northern European populations replicate multiple colorectal cancer risk loci. <i>International Journal of Cancer</i> , 2018, 142, 540-546.	4.3	30
189	Does Childhood Trauma Moderate Polygenic Risk for Depression? A Meta-analysis of 5765 Subjects From the Psychiatric Genomics Consortium. <i>Biological Psychiatry</i> , 2018, 84, 138-147.	5.4	112
190	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. <i>Nature Communications</i> , 2018, 9, .	13.7	108
191	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. <i>Nature Genetics</i> , 2018, 50, 1505-1513.	25.2	1,673
192	Genes reveal traces of common recent demographic history for most of the Uralic-speaking populations. <i>Genome Biology</i> , 2018, 19, .	8.1	103
193	Circulating metabolic biomarkers of renal function in diabetic and non-diabetic populations. <i>Scientific Reports</i> , 2018, 8, .	3.4	54
194	Applying polygenic risk scoring for psychiatric disorders to a large family with bipolar disorder and major depressive disorder. <i>Communications Biology</i> , 2018, 1, .	4.4	20
195	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	25.2	1,300
196	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. <i>Nature Genetics</i> , 2018, 50, 834-848.	25.2	324
197	Age at first birth in women is genetically associated with increased risk of schizophrenia. <i>Scientific Reports</i> , 2018, 8, .	3.4	20
198	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. <i>Nature Genetics</i> , 2018, 50, 1112-1121.	25.2	2,406

#	ARTICLE	IF	CITATIONS
199	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. <i>Nature Communications</i> , 2018, 9, .	13.7	770
200	Analysis of shared heritability in common disorders of the brain. <i>Science</i> , 2018, 360, .	36.2	1,340
201	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. <i>Nature Communications</i> , 2018, 9, .	13.7	105
202	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. <i>Cell</i> , 2018, 173, 1705-1715.e16.	33.7	755
203	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. <i>Nature Communications</i> , 2018, 9, .	13.7	408
204	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018, 13, e0198166.	2.3	114
205	Genetic variation in the Estonian population: pharmacogenomics study of adverse drug effects using electronic health records. <i>European Journal of Human Genetics</i> , 2018, 27, 442-454.	3.0	40
206	Genetic evidence of assortative mating in humans. <i>Nature Human Behaviour</i> , 2017, 1, .	9.1	308
207	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , 2017, 49, 403-415.	25.2	573
208	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	37.9	612
209	DNA breaks and chromatin structural changes enhance the transcription of autoimmune regulator target genes. <i>Journal of Biological Chemistry</i> , 2017, 292, 6542-6554.	2.2	63
210	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2017, 69, 823-836.	2.3	243
211	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> , 2017, 25, 869-876.	3.0	247
212	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> , 2017, 49, 834-841.	25.2	514
213	Significant Locus and Metabolic Genetic Correlations Revealed in Genome-Wide Association Study of Anorexia Nervosa. <i>American Journal of Psychiatry</i> , 2017, 174, 850-858.	8.8	512
214	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, .	13.7	198
215	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. <i>Scientific Reports</i> , 2017, 7, .	3.4	108
216	A genome-wide association study of anorexia nervosa suggests a risk locus implicated in dysregulated leptin signaling. <i>Scientific Reports</i> , 2017, 7, .	3.4	30

#	ARTICLE	IF	CITATIONS
217	Large scale meta-analysis characterizes genetic architecture for common psoriasis associated variants. <i>Nature Communications</i> , 2017, 8, .	13.7	333
218	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017, 66, 2888-2902.	4.2	717
219	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017, 66, 2019-2032.	4.2	51
220	Genetic correlation between amyotrophic lateral sclerosis and schizophrenia. <i>Nature Communications</i> , 2017, 8, .	13.7	140
221	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 981-994.	0.4	44
222	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> , 2017, 114, .	7.5	45
223	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. <i>Biological Psychiatry</i> , 2017, 82, 322-329.	5.4	91
224	The Genetic Architecture of Gene Expression in Peripheral Blood. <i>American Journal of Human Genetics</i> , 2017, 100, 228-237.	6.5	224
225	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766.	25.2	543
226	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. <i>Nature Communications</i> , 2017, 8, .	13.7	85
227	Worldwide trends in body-mass index, underweight, overweight, and obesity from 1975 to 2016: a pooled analysis of 2416 population-based measurement studies in 128.9 million children, adolescents, and adults. <i>Lancet, The</i> , 2017, 390, 2627-2642.	62.3	6,316
228	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. <i>Nature Communications</i> , 2017, 8, .	13.7	163
229	Identification of novel risk loci for restless legs syndrome in genome-wide association studies in individuals of European ancestry: a meta-analysis. <i>Lancet Neurology, The</i> , 2017, 16, 898-907.	17.9	237
230	Hidden heritability due to heterogeneity across seven populations. <i>Nature Human Behaviour</i> , 2017, 1, 757-765.	9.1	158
231	Genetic correlations reveal the shared genetic architecture of transcription in human peripheral blood. <i>Nature Communications</i> , 2017, 8, .	13.7	25
232	Exome analysis in an Estonian multiplex family with neural tube defects—a case report. <i>Child's Nervous System</i> , 2017, 33, 1575-1581.	0.9	7
233	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. <i>Hypertension</i> , 2017, 70, .	6.6	143
234	Association analyses based on false discovery rate implicate new loci for coronary artery disease. <i>Nature Genetics</i> , 2017, 49, 1385-1391.	25.2	679

#	ARTICLE	IF	CITATIONS
235	Constraints on eQTL Fine Mapping in the Presence of Multisite Local Regulation of Gene Expression. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2533-2544.	1.9	27
236	Hair Cortisol in Twins: Heritability and Genetic Overlap with Psychological Variables and Stress-System Genes. <i>Scientific Reports</i> , 2017, 7, .	3.4	63
237	Genotypeâ€œcovariate interaction effects and the heritability of adult body mass index. <i>Nature Genetics</i> , 2017, 49, 1174-1181.	25.2	159
238	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. <i>Nature Communications</i> , 2017, 8, .	13.7	192
239	Identifying pathways modulating sleep duration: from genomics to transcriptomics. <i>Scientific Reports</i> , 2017, 7, .	3.4	10
240	Human basonuclin 2 up-regulates a cascade set of interferon-stimulated genes with anti-cancerous properties in a lung cancer model. <i>Cancer Cell International</i> , 2017, 17, .	5.3	11
241	Worldwide trends in blood pressure from 1975 to 2015: a pooled analysis of 1479 population-based measurement studies with 19Â1 million participants. <i>Lancet, The</i> , 2017, 389, 37-55.	62.3	2,027
242	Personalized risk prediction for type 2 diabetes: the potential of genetic risk scores. <i>Genetics in Medicine</i> , 2017, 19, 322-329.	4.2	145
243	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, .	5.7	36
244	Genome-wide association meta-analysis of fish and EPA+DHA consumption in 17 US and European cohorts. <i>PLoS ONE</i> , 2017, 12, e0186456.	2.3	20
245	Pathogenic implications for autoimmune mechanisms derived by comparative eQTL analysis of CD4+ versus CD8+ T cells. <i>PLoS Genetics</i> , 2017, 13, e1006643.	3.2	129
246	An interaction map of circulating metabolites, immune gene networks, and their genetic regulation. <i>Genome Biology</i> , 2017, 18, .	8.1	56
247	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	3.2	181
248	Ranking and characterization of established BMI and lipid associated loci as candidates for gene-environment interactions. <i>PLoS Genetics</i> , 2017, 13, e1006812.	3.2	30
249	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> , 2017, 12, e0170325.	2.3	9
250	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	37.9	1,051
251	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. <i>American Journal of Human Genetics</i> , 2016, 99, 8-21.	6.5	66
252	Sequence variation in nuclear ribosomal small subunit, internal transcribed spacer and large subunit regions of <i>Rhizophagus irregularis</i> and <i>Gigaspora margarita</i> is high and isolateâ€œdependent. <i>Molecular Ecology</i> , 2016, 25, 2816-2832.	3.7	72

#	ARTICLE	IF	CITATIONS
253	Coding Variation in ANGPTL4, LPL, and SVEP1 and the Risk of Coronary Disease. <i>New England Journal of Medicine</i> , 2016, 374, 1134-1144.	34.6	481
254	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. <i>Nature Genetics</i> , 2016, 48, 624-633.	25.2	1,005
255	Genetic variants in RBFOX3 are associated with sleep latency. <i>European Journal of Human Genetics</i> , 2016, 24, 1488-1495.	3.0	33
256	Imprinted Genes and Imprinting Control Regions Show Predominant Intermediate Methylation in Adult Somatic Tissues. <i>Epigenomics</i> , 2016, 8, 789-799.	2.2	46
257	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	37.9	1,361
258	Whole-genome expression analysis reveals genes associated with treatment response to escitalopram in major depression. <i>European Neuropsychopharmacology</i> , 2016, 26, 1475-1483.	1.0	26
259	Ultra-rare disruptive and damaging mutations influence educational attainment in the general population. <i>Nature Neuroscience</i> , 2016, 19, 1563-1565.	17.0	108
260	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, .	13.7	90
261	Genomic analyses inform on migration events during the peopling of Eurasia. <i>Nature</i> , 2016, 538, 238-242.	37.9	414
262	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1435-1448.	2.3	132
263	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016, 48, 1151-1161.	25.2	298
264	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016, 48, 1171-1184.	25.2	410
265	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. <i>Scientific Reports</i> , 2016, 6, .	3.4	30
266	Meta-analysis of gene-environment-wide association scans accounting for education level identifies additional loci for refractive error. <i>Nature Communications</i> , 2016, 7, .	13.7	128
267	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. <i>Nature Communications</i> , 2016, 7, .	13.7	745
268	Childhood gene-environment interactions and age-dependent effects of genetic variants associated with refractive error and myopia: The CREAM Consortium. <i>Scientific Reports</i> , 2016, 6, .	3.4	93
269	The Role of the Five-factor Personality Traits in General Self-rated Health. <i>European Journal of Personality</i> , 2016, 30, 492-504.	2.9	27
270	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016, 48, 1462-1472.	25.2	323

#	ARTICLE	IF	CITATIONS
271	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	7.5	125
272	Autosomal genetic control of human gene expression does not differ across the sexes. Genome Biology, 2016, 17, .	8.1	17
273	Reporting incidental findings of genomic disorder-associated copy number variants to unselected biobank participants. Personalized Medicine, 2016, 13, 303-314.	1.3	15
274	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	25.2	632
275	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	6.5	90
276	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.	6.5	58
277	The Number of Genomic Copies at the 16p11.2 Locus Modulates Language, Verbal Memory, and Inhibition. Biological Psychiatry, 2016, 80, 129-139.	5.4	89
278	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.	0.7	9
279	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	36.2	506
280	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. JAMA Psychiatry, 2016, 73, 497.	12.4	59
281	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, .	13.7	493
282	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. Nature Genetics, 2016, 48, 510-518.	25.2	728
283	Defining the Effect of the 16p11.2 Duplication on Cognition, Behavior, and Medical Comorbidities. JAMA Psychiatry, 2016, 73, 20.	12.4	239
284	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.	6.6	108
285	Evidence for three genetic loci involved in both anorexia nervosa risk and variation of body mass index. Molecular Psychiatry, 2016, 22, 192-201.	7.8	70
286	Metabolites of milk intake: a metabolomic approach in UK twins with findings replicated in two European cohorts. European Journal of Nutrition, 2016, 56, 2379-2391.	3.4	32
287	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2016, 49, 27-35.	25.2	1,026
288	Genome-Wide Association Analyses in 128,266 Individuals Identifies New Morningness and Sleep Duration Loci. PLoS Genetics, 2016, 12, e1006125.	3.2	374

#	ARTICLE	IF	CITATIONS
289	Ancient Haplotypes at the 15q24.2 Microdeletion Region Are Linked to Brain Expression of MAN2C1 and Children's Intelligence. PLoS ONE, 2016, 11, e0157739.	2.3	3
290	Extensive alterations of the whole-blood transcriptome are associated with body mass index: results of an mRNA profiling study involving two large population-based cohorts. BMC Medical Genomics, 2015, 8, .	1.7	45
291	Age-related profiling of DNA methylation in CD8+ T cells reveals changes in immune response and transcriptional regulator genes. Scientific Reports, 2015, 5, .	3.4	179
292	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.	2.0	12
293	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. Obstetrical and Gynecological Survey, 2015, 70, 758-762.	0.5	0
294	Linking a Population Biobank with National Health Registries—The Estonian Experience. Journal of Personalized Medicine, 2015, 5, 96-106.	2.4	64
295	Haplotype Phasing and Inheritance of Copy Number Variants in Nuclear Families. PLoS ONE, 2015, 10, e0122713.	2.3	9
296	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.	3.2	393
297	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. PLoS Genetics, 2015, 11, e1005230.	3.2	84
298	Adiposity as a cause of cardiovascular disease: a Mendelian randomization study. International Journal of Epidemiology, 2015, 44, 578-586.	4.9	136
299	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. JAMA Psychiatry, 2015, 72, 642.	12.4	320
300	Copy Number Variations and Cognitive Phenotypes in Unselected Populations. JAMA - Journal of the American Medical Association, 2015, 313, 2044.	16.6	173
301	Enhanced meta-analysis and replication studies identify five new psoriasis susceptibility loci. Nature Communications, 2015, 6, .	13.7	174
302	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. Nature Communications, 2015, 6, .	13.7	209
303	Rare coding variants and X-linked loci associated with age at menarche. Nature Communications, 2015, 6, .	13.7	39
304	Genetic variants of inducible costimulator are associated with allergic asthma susceptibility. Journal of Allergy and Clinical Immunology, 2015, 135, 556-558.e13.	6.1	4
305	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	37.9	1,561
306	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	37.9	4,431

#	ARTICLE	IF	CITATIONS
307	Dominance Genetic Variation Contributes Little to the Missing Heritability for Human Complex Traits. <i>American Journal of Human Genetics</i> , 2015, 96, 377-385.	6.5	217
308	Cohort Profile: Estonian Biobank of the Estonian Genome Center, University of Tartu. <i>International Journal of Epidemiology</i> , 2015, 44, 1137-1147.	4.9	444
309	Age- and Sex-Specific Causal Effects of Adiposity on Cardiovascular Risk Factors. <i>Diabetes</i> , 2015, 64, 1841-1852.	4.2	71
310	Cell Specific eQTL Analysis without Sorting Cells. <i>PLoS Genetics</i> , 2015, 11, e1005223.	3.2	129
311	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	37.9	198
312	Structural forms of the human amylase locus and their relationships to SNPs, haplotypes and obesity. <i>Nature Genetics</i> , 2015, 47, 921-925.	25.2	138
313	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. <i>PLoS Genetics</i> , 2015, 11, e1005035.	3.2	125
314	The impact of low-frequency and rare variants on lipid levels. <i>Nature Genetics</i> , 2015, 47, 589-597.	25.2	347
315	A recent bottleneck of Y chromosome diversity coincides with a global change in culture. <i>Genome Research</i> , 2015, 25, 459-466.	4.6	423
316	Genetically Determined Height and Coronary Artery Disease. <i>New England Journal of Medicine</i> , 2015, 372, 1608-1618.	34.6	244
317	Complementary seminovaginal microbiome in couples. <i>Research in Microbiology</i> , 2015, 166, 440-447.	3.0	210
318	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , 2015, 97, 576-592.	6.5	1,332
319	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015, 47, 1294-1303.	25.2	417
320	Identification of lung cancer histology-specific variants applying Bayesian framework variant prioritization approaches within the TRICL and ILCCO consortia. <i>Carcinogenesis</i> , 2015, 36, 1314-1326.	2.8	16
321	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. <i>Nature Genetics</i> , 2015, 47, 1282-1293.	25.2	335
322	Genome-wide genetic homogeneity between sexes and populations for human height and body mass index. <i>Human Molecular Genetics</i> , 2015, 24, 7445-7449.	2.9	75
323	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015, 6, .	13.7	686
324	Effects of Metformin on Metabolite Profiles and LDL Cholesterol in Patients With Type 2 Diabetes. <i>Diabetes Care</i> , 2015, 38, 1858-1867.	6.2	118

#	ARTICLE	IF	CITATIONS
325	Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. <i>Nature Genetics</i> , 2015, 47, 1114-1120.	25.2	809
326	Population genetic differentiation of height and body mass index across Europe. <i>Nature Genetics</i> , 2015, 47, 1357-1362.	25.2	243
327	A comprehensive 1000 Genomesâ€‘based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , 2015, 47, 1121-1130.	25.2	2,461
328	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015, 47, 1415-1425.	25.2	408
329	Harmonising and linking biomedical and clinical data across disparate data archives to enable integrative cross-biobank research. <i>European Journal of Human Genetics</i> , 2015, 24, 521-528.	3.0	31
330	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. <i>Behavior Genetics</i> , 2015, 46, 170-182.	1.3	207
331	Within-Trait Heterogeneity in Age Group Differences in Personality Domains and Facets: Implications for the Development and Coherence of Personality Traits. <i>PLoS ONE</i> , 2015, 10, e0119667.	2.3	43
332	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. <i>PLoS ONE</i> , 2015, 10, e0119752.	2.3	71
333	Mapping the Genetic Architecture of Gene Regulation in Whole Blood. <i>PLoS ONE</i> , 2014, 9, e93844.	2.3	32
334	De Novo SCN8A Mutation Identified by Whole-Exome Sequencing in a Boy With Neonatal Epileptic Encephalopathy, Multiple Congenital Anomalies, and Movement Disorders. <i>Journal of Child Neurology</i> , 2014, 29, NP202-NP206.	1.6	63
335	From Pharmacogenetics to Pharmacometabolomics: SAM Modulates TPMT Activity. <i>Pharmacogenomics</i> , 2014, 15, 1437-1449.	1.5	24
336	Meta-analysis identifies loci affecting levels of the potential osteoarthritis biomarkers sCOMP and uCTX-II with genome wide significance. <i>Journal of Medical Genetics</i> , 2014, 51, 596-604.	3.8	22
337	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. <i>PLoS Genetics</i> , 2014, 10, e1004508.	3.2	85
338	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. <i>PLoS Genetics</i> , 2014, 10, e1004494.	3.2	387
339	Assessment of Osteoarthritis Candidate Genes in a Metaâ€‘Analysis of Nine Genomeâ€‘Wide Association Studies. <i>Arthritis and Rheumatology</i> , 2014, 66, 940-949.	6.2	116
340	A meta-analysis of genome-wide association studies identifies novel variants associated with osteoarthritis of the hip. <i>Annals of the Rheumatic Diseases</i> , 2014, 73, 2130-2136.	6.9	113
341	Using RNA sequencing for identifying gene imprinting and random monoallelic expression in human placenta. <i>Epigenetics</i> , 2014, 9, 1397-1409.	3.0	80
342	Occupational irritants and asthma: an Estonian cross-sectional study of 34 000 adults. <i>European Respiratory Journal</i> , 2014, 44, 647-656.	8.7	25

#	ARTICLE	IF	CITATIONS
343	Leukocyte telomere length associates with prospective mortality independent of immune-related parameters and known genetic markers. <i>International Journal of Epidemiology</i> , 2014, 43, 878-886.	4.9	99
344	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. <i>Human Molecular Genetics</i> , 2014, 23, 2490-2497.	2.9	65
345	Biomarker Profiling by Nuclear Magnetic Resonance Spectroscopy for the Prediction of All-Cause Mortality: An Observational Study of 17,345 Persons. <i>PLoS Medicine</i> , 2014, 11, e1001606.	8.1	342
346	Copper Metabolism Domain-Containing 1 Represses Genes That Promote Inflammation and Protects Mice From Colitis and Colitis-Associated Cancer. <i>Gastroenterology</i> , 2014, 147, 184-195.e3.	0.9	41
347	The prevalence of metabolic syndrome and metabolically healthy obesity in Europe: a collaborative analysis of ten large cohort studies. <i>BMC Endocrine Disorders</i> , 2014, 14, .	2.9	519
348	A Common 16p11.2 Inversion Underlies the Joint Susceptibility to Asthma and Obesity. <i>American Journal of Human Genetics</i> , 2014, 94, 361-372.	6.5	70
349	Chronotype and sleep duration: The influence of season of assessment. <i>Chronobiology International</i> , 2014, 31, 731-740.	1.9	139
350	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. <i>Nature Communications</i> , 2014, 5, .	13.7	244
351	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. <i>American Journal of Human Genetics</i> , 2014, 95, 535-552.	6.5	627
352	A metabolic view on menopause and ageing. <i>Nature Communications</i> , 2014, 5, .	13.7	249
353	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	37.9	620
354	Genome-wide association meta-analysis of human longevity identifies a novel locus conferring survival beyond 90 years of age. <i>Human Molecular Genetics</i> , 2014, 23, 4420-4432.	2.9	257
355	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	25.2	1,965
356	Harmonization of Neuroticism and Extraversion phenotypes across inventories and cohorts in the Genetics of Personality Consortium: an application of Item Response Theory. <i>Behavior Genetics</i> , 2014, 44, 295-313.	1.3	115
357	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014, 46, 234-244.	25.2	1,030
358	Sex- and age-interacting eQTLs in human complex diseases. <i>Human Molecular Genetics</i> , 2014, 23, 1947-1956.	2.9	78
359	Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. <i>Nature Genetics</i> , 2014, 46, 736-741.	25.2	423
360	Oral health, dental care and mouthwash associated with upper aerodigestive tract cancer risk in Europe: The ARCAGE study. <i>Oral Oncology</i> , 2014, 50, 616-625.	2.4	109

#	ARTICLE	IF	CITATIONS
361	BBMRI-ERIC as a resource for pharmaceutical and life science industries: the development of biobank-based Expert Centres. <i>European Journal of Human Genetics</i> , 2014, 23, 893-900.	3.0	79
362	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2014, 20, 647-656.	7.8	266
363	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. <i>American Journal of Human Genetics</i> , 2013, 93, 236-248.	6.5	65
364	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013, 45, 1274-1283.	25.2	2,993
365	Common variants associated with plasma triglycerides and risk for coronary artery disease. <i>Nature Genetics</i> , 2013, 45, 1345-1352.	25.2	833
366	Systematic identification of trans eQTLs as putative drivers of known disease associations. <i>Nature Genetics</i> , 2013, 45, 1238-1243.	25.2	1,672
367	Nine Loci for Ocular Axial Length Identified through Genome-wide Association Studies, Including Shared Loci with Refractive Error. <i>American Journal of Human Genetics</i> , 2013, 93, 264-277.	6.5	154
368	Common Variants in Mendelian Kidney Disease Genes and Their Association with Renal Function. <i>Journal of the American Society of Nephrology: JASN</i> , 2013, 24, 2105-2117.	0.4	35
369	Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. <i>Nature Genetics</i> , 2013, 45, 314-318.	25.2	439
370	Identification of seven loci affecting mean telomere length and their association with disease. <i>Nature Genetics</i> , 2013, 45, 422-427.	25.2	901
371	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013, 45, 501-512.	25.2	645
372	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013, 45, 621-631.	25.2	308
373	Meta-analysis of microRNA expression in lung cancer. <i>International Journal of Cancer</i> , 2013, 132, 2884-2893.	4.3	200
374	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> , 2013, 22, 3597-3607.	2.9	126
375	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> , 2013, 72, 1264-1265.	6.9	54
376	Human Disease-Associated Genetic Variation Impacts Large Intergenic Non-Coding RNA Expression. <i>PLoS Genetics</i> , 2013, 9, e1003201.	3.2	264
377	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. <i>PLoS Genetics</i> , 2013, 9, e1003500.	3.2	416
378	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. <i>PLoS Medicine</i> , 2013, 10, e1001474.	8.1	192

#	ARTICLE	IF	CITATIONS
379	A genome-wide association study of early menopause and the combined impact of identified variants. <i>Human Molecular Genetics</i> , 2013, 22, 1465-1472.	2.9	119
380	Association of Adiposity Genetic Variants With Menarche Timing in 92,105 Women of European Descent. <i>American Journal of Epidemiology</i> , 2013, 178, 451-460.	3.3	57
381	In-solution hybrid capture of bisulfite-converted DNA for targeted bisulfite sequencing of 174 ADME genes. <i>Nucleic Acids Research</i> , 2013, 41, e72-e72.	15.5	43
382	Whole-exome sequencing identifies a polymorphism in the BMP5 gene associated with SSRI treatment response in major depression. <i>Journal of Psychopharmacology</i> , 2013, 27, 915-920.	4.8	32
383	Genetics of rheumatoid arthritis contributes to biology and drug discovery. <i>Nature</i> , 2013, 506, 376-381.	37.9	2,269
384	Rare Genomic Structural Variants in Complex Disease: Lessons from the Replication of Associations with Obesity. <i>PLoS ONE</i> , 2013, 8, e58048.	2.3	36
385	A Genome-Wide Analysis of Populations from European Russia Reveals a New Pole of Genetic Diversity in Northern Europe. <i>PLoS ONE</i> , 2013, 8, e58552.	2.3	38
386	Personality traits and eating habits in a large sample of Estonians.. <i>Health Psychology</i> , 2012, 31, 806-814.	1.6	110
387	Evidence of Inbreeding Depression on Human Height. <i>PLoS Genetics</i> , 2012, 8, e1002655.	3.2	93
388	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. <i>PLoS Genetics</i> , 2012, 8, e1002584.	3.2	182
389	Influence of common genetic variation on lung cancer risk: meta-analysis of 14 900 cases and 29 485 controls. <i>Human Molecular Genetics</i> , 2012, 21, 4980-4995.	2.9	216
390	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. <i>Human Molecular Genetics</i> , 2012, 21, 5329-5343.	2.9	65
391	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , 2012, 44, 991-1005.	25.2	803
392	Lung cancer and DNA repair genes: multilevel association analysis from the International Lung Cancer Consortium. <i>Carcinogenesis</i> , 2012, 33, 1059-1064.	2.8	43
393	History of the Diagnosis of a Sexually Transmitted Disease is Linked to Normal Variation in Personality Traits. <i>Journal of Sexual Medicine</i> , 2012, 9, 2861-2867.	0.5	16
394	Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. <i>Lancet, The</i> , 2012, 380, 815-823.	62.3	405
395	Large scale international replication and meta-analysis study confirms association of the 15q14 locus with myopia. The CREAM consortium. <i>Human Genetics</i> , 2012, 131, 1467-1480.	2.9	68
396	Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , 2012, 492, 369-375.	37.9	339

#	ARTICLE	IF	CITATIONS
397	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012, 44, 981-990.	25.2	1,863
398	Genome-wide meta-analysis of common variant differences between men and women. <i>Human Molecular Genetics</i> , 2012, 21, 4805-4815.	2.9	38
399	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012, 490, 267-272.	37.9	426
400	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. <i>Nature Genetics</i> , 2012, 44, 1341-1348.	25.2	950
401	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. <i>Nature Genetics</i> , 2012, 44, 260-268.	25.2	343
402	Toward a roadmap in global biobanking for health. <i>European Journal of Human Genetics</i> , 2012, 20, 1105-1111.	3.0	151
403	Combined Analysis of Genome-wide Association Studies for Crohn Disease and Psoriasis Identifies Seven Shared Susceptibility Loci. <i>American Journal of Human Genetics</i> , 2012, 90, 636-647.	6.5	332
404	Genome-Wide Meta-Analysis of Psoriatic Arthritis Identifies Susceptibility Locus at REL. <i>Journal of Investigative Dermatology</i> , 2012, 132, 1133-1140.	2.3	109
405	Giving and Withholding of Information following Genomic Screening: Challenges Identified in a Study of Primary Care Physicians in Estonia. <i>Journal of Genetic Counseling</i> , 2012, 21, 591-604.	1.7	7
406	Post-translational stabilization of thiopurine S-methyltransferase by S-adenosyl-L-methionine reveals regulation of TPMT*1 and *3C allozymes. <i>Biochemical Pharmacology</i> , 2012, 83, 969-976.	5.1	19
407	Longevity candidate genes and their association with personality traits in the elderly. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2012, 159B, 192-200.	1.5	14
408	Self-Other Agreement in Happiness and Life-Satisfaction: The Role of Personality Traits. <i>Social Indicators Research</i> , 2012, 114, 479-492.	2.4	20
409	Genetic characterization of northeastern Italian population isolates in the context of broader European genetic diversity. <i>European Journal of Human Genetics</i> , 2012, 21, 659-665.	3.0	68
410	Large-scale association analysis identifies new risk loci for coronary artery disease. <i>Nature Genetics</i> , 2012, 45, 25-33.	25.2	1,557
411	Refining genome-wide linkage intervals using a meta-analysis of genome-wide association studies identifies loci influencing personality dimensions. <i>European Journal of Human Genetics</i> , 2012, 21, 876-882.	3.0	25
412	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2012, 45, 145-154.	25.2	776
413	Methylation Markers of Early-Stage Non-Small Cell Lung Cancer. <i>PLoS ONE</i> , 2012, 7, e39813.	2.3	65
414	Systems medicine and integrated care to combat chronic noncommunicable diseases. <i>Genome Medicine</i> , 2011, 3, 43.	9.6	185

#	ARTICLE	IF	CITATIONS
415	Polymorphisms in ESR1, ESR2 and HSD17B1 genes are associated with fertility status in endometriosis. <i>Gynecological Endocrinology</i> , 2011, 27, 425-433.	1.8	55
416	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. <i>Biological Psychiatry</i> , 2011, 69, 526-533.	5.4	176
417	Design of a peptide-based vector, PepFect6, for efficient delivery of siRNA in cell culture and systemically in vivo. <i>Nucleic Acids Research</i> , 2011, 39, 3972-3987.	15.5	278
418	Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. <i>Nature</i> , 2011, 478, 97-102.	37.9	439
419	New gene functions in megakaryopoiesis and platelet formation. <i>Nature</i> , 2011, 480, 201-208.	37.9	426
420	Comprehensive catalog of European biobanks. <i>Nature Biotechnology</i> , 2011, 29, 795-797.	29.8	86
421	A parallel SNP array study of genomic aberrations associated with mental retardation in patients and general population in Estonia. <i>European Journal of Medical Genetics</i> , 2011, 54, 136-143.	1.6	9
422	The role of COX-2 and Nrf2/ARE in anti-inflammation and antioxidative stress: Aging and anti-aging. <i>Medical Hypotheses</i> , 2011, 77, 174-178.	0.7	112
423	Sequence Variants and the Risk of Head and Neck Cancer: Pooled Analysis in the INHANCE Consortium. <i>Frontiers in Oncology</i> , 2011, 1, .	2.6	12
424	A Genome-Wide Association Study of Upper Aerodigestive Tract Cancers Conducted within the INHANCE Consortium. <i>PLoS Genetics</i> , 2011, 7, e1001333.	3.2	169
425	Identification of miR-374a as a prognostic marker for survival in patients with early-stage non-small cell lung cancer. <i>Genes Chromosomes and Cancer</i> , 2011, 50, 812-822.	3.0	126
426	Variation in FGF1, FOXE1, and TIMP2 genes is associated with nonsyndromic cleft lip with or without cleft palate. <i>Birth Defects Research Part A: Clinical and Molecular Teratology</i> , 2011, 91, 218-225.	1.9	43
427	Genome-wide association and genetic functional studies identify autism susceptibility candidate 2 gene (TJ ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50 262 Td ( AUTS2) Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50 260	7.5	260
428	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011, 43, 1005-1011.	25.2	421
429	A Genome-Wide Screen for Interactions Reveals a New Locus on 4p15 Modifying the Effect of Waist-to-Hip Ratio on Total Cholesterol. <i>PLoS Genetics</i> , 2011, 7, e1002333.	3.2	30
430	Susceptibility locus for nonsyndromic cleft lip with or without cleft palate on chromosome 10q25 confers risk in Estonian patients. <i>European Journal of Oral Sciences</i> , 2010, 118, 317-319.	1.7	21
431	Variance determines self-observer agreement on the Big Five personality traits. <i>Journal of Research in Personality</i> , 2010, 44, 421-426.	2.3	26
432	Genetic variants in COL2A1, COL11A2, and IRF6 contribute risk to nonsyndromic cleft palate. <i>Birth Defects Research Part A: Clinical and Molecular Teratology</i> , 2010, 88, 748-756.	1.9	48

#	ARTICLE	IF	CITATIONS
433	Comparison of DNA extraction methods for multiplex polymerase chain reaction. <i>Analytical Biochemistry</i> , 2010, 398, 260-262.	2.4	16
434	Fibrinogen beta variants confer protection against coronary artery disease in a Greek case-control study. <i>BMC Medical Genetics</i> , 2010, 11, .	1.8	27
435	Molecular diagnosis of Down syndrome using quantitative APEX microarrays. <i>Prenatal Diagnosis</i> , 2010, 30, 1170-1177.	2.3	1
436	MTHFR and MSX1 contribute to the risk of nonsyndromic cleft lip/palate. <i>European Journal of Oral Sciences</i> , 2010, 118, 213-220.	1.7	55
437	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	37.9	1,875
438	Common variants in KCNN3 are associated with lone atrial fibrillation. <i>Nature Genetics</i> , 2010, 42, 240-244.	25.2	462
439	Sequence variants at CHRN3, CHRNA6 and CYP2A6 affect smoking behavior. <i>Nature Genetics</i> , 2010, 42, 448-453.	25.2	672
440	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> , 2010, 42, 949-960.	25.2	899
441	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	25.2	2,774
442	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 1077-1085.	25.2	476
443	Quality, quantity and harmony: the DataSHaPER approach to integrating data across bioclinical studies. <i>International Journal of Epidemiology</i> , 2010, 39, 1383-1393.	4.9	164
444	Association between a 15q25 gene variant, smoking quantity and tobacco-related cancers among 17 000 individuals. <i>International Journal of Epidemiology</i> , 2010, 39, 563-577.	4.9	125
445	Analysis of Polymorphisms in the SRD5A2 Gene and Semen Parameters in Estonian Men. <i>Journal of Andrology</i> , 2010, 31, 372-378.	2.1	10
446	Manifesto for a European Anxiety Disorders Research Network. <i>European Neuropsychopharmacology</i> , 2010, 20, 426-432.	1.0	21
447	Genetic Structure of Europeans: A View from the North-East. <i>PLoS ONE</i> , 2009, 4, e5472.	2.3	297
448	Selection for Genetic Variation Inducing Pro-Inflammatory Responses under Adverse Environmental Conditions in a Ghanaian Population. <i>PLoS ONE</i> , 2009, 4, e7795.	2.3	41
449	ROS1 Asp2213Asn polymorphism is not associated with coronary artery disease in a Greek case-control study. <i>Clinical Chemistry and Laboratory Medicine</i> , 2009, 47, .	2.3	9
450	Replication of novel susceptibility locus for nonsyndromic cleft lip with or without cleft palate on chromosome 8q24 in Estonian and Lithuanian patients. <i>American Journal of Medical Genetics, Part A</i> , 2009, 149A, 2551-2553.	1.6	36

#	ARTICLE	IF	CITATIONS
451	Aromatase gene (CYP19A1) variants, female infertility and ovarian stimulation outcome: a preliminary report. <i>Reproductive BioMedicine Online</i> , 2009, 18, 651-657.	2.7	31
452	Serotonin transporter promoter region polymorphisms do not influence treatment response to escitalopram in patients with major depression. <i>European Neuropsychopharmacology</i> , 2009, 19, 451-456.	1.0	67
453	Evaluation of the 124-plex SNP typing microarray for forensic testing. <i>Forensic Science International: Genetics</i> , 2009, 4, 43-48.	2.2	32
454	Alcohol-related cancers and genetic susceptibility in Europe: the ARCAGE project: study samples and data collection. <i>European Journal of Cancer Prevention</i> , 2009, 18, 76-84.	2.0	54
455	Thiopurine S-methyltransferase (TPMT) pharmacogenetics: three new mutations and haplotype analysis in the Estonian population. <i>Clinical Chemistry and Laboratory Medicine</i> , 2008, 46, .	2.3	19
456	Development of a single tube 640-plex genotyping method for detection of nucleic acid variations on microarrays. <i>Nucleic Acids Research</i> , 2008, 36, e75-e75.	15.5	34
457	Allelic estrogen receptor 1 (ESR1) gene variants predict the outcome of ovarian stimulation in in vitro fertilization. <i>Molecular Human Reproduction</i> , 2007, 13, 521-526.	2.9	73
458	Evaluating the performance of commercial whole-genome marker sets for capturing common genetic variation. <i>BMC Genomics</i> , 2007, 8, 159.	3.3	29
459	Analysis of SNP profiles in patients with major depressive disorder. <i>International Journal of Neuropsychopharmacology</i> , 2006, 9, 167.	2.7	43
460	Association study of sporadic Parkinson's disease genetic risk factors in patients from Russia by APEX technology. <i>Neuroscience Letters</i> , 2006, 405, 212-216.	1.9	13
461	An Evaluation of the Performance of Tag SNPs Derived from HapMap in a Caucasian Population. <i>PLoS Genetics</i> , 2006, 2, e27.	3.2	109
462	Simultaneous Multigene Mutation Detection in Patients With Sensorineural Hearing Loss Through a Novel Diagnostic Microarray: A New Approach for Newborn Screening Follow-up. <i>Pediatrics</i> , 2006, 118, 985-994.	4.5	75
463	Association study of 90 candidate gene polymorphisms in panic disorder. <i>Psychiatric Genetics</i> , 2005, 15, 17-24.	1.3	84
464	Arrayed Primer Extension Resequencing of Mutations in the TP53 Tumor Suppressor Gene: Comparison with Denaturing HPLC and Direct Sequencing. <i>Clinical Chemistry</i> , 2005, 51, 1284-1287.	1.1	16
465	Polymorphisms in wolframin (WFS1) gene are possibly related to increased risk for mood disorders. <i>International Journal of Neuropsychopharmacology</i> , 2005, 8, 235-244.	2.7	43
466	Linkage Disequilibrium Patterns and tagSNP Transferability among European Populations. <i>American Journal of Human Genetics</i> , 2005, 76, 387-398.	6.5	117
467	Genotyping Microarray for the Detection of More Than 200 CFTR Mutations in Ethnically Diverse Populations. <i>Journal of Molecular Diagnostics</i> , 2005, 7, 375-387.	2.5	41
468	Severe CF manifestation with anaemia and failure to thrive in a 394delTT homozygous patient. <i>Journal of Cystic Fibrosis</i> , 2004, 3, 58-60.	0.8	7

#	ARTICLE	IF	CITATIONS
469	The ABCA4 2588G>C Stargardt mutation: single origin and increasing frequency from South-West to North-East Europe. <i>European Journal of Human Genetics</i> , 2002, 10, 197-203.	3.0	46
470	Evaluating the arrayed primer extension resequencing assay of TP53 tumor suppressor gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 5503-5508.	7.5	100
471	Genes, technology and public dialogue in Tartu, Estonia. <i>Trends in Biotechnology</i> , 2002, 20, 51-52.	8.7	1
472	High-density genotyping and linkage disequilibrium in the human genome using chromosome 22 as a model. <i>Current Opinion in Chemical Biology</i> , 2002, 6, 24-30.	5.8	5
473	Title is missing!. <i>BMC Molecular Biology</i> , 2002, 3, 1.	4.0	36
474	A first-generation linkage disequilibrium map of human chromosome 22. <i>Nature</i> , 2002, 418, 544-548.	37.9	382
475	Title is missing!. , 2002, .		1
476	Reliable Detection of $\beta$ -Thalassemia and G6PD Mutations by a DNA Microarray. <i>Clinical Chemistry</i> , 2002, 48, 2051-2054.	1.1	59
477	Mutation 985A>G in the MCAD gene shows low incidence in Estonian population. <i>Human Mutation</i> , 2000, 15, 293-294.	4.5	5
478	High carrier frequency of the 35delG deafness mutation in European populations. <i>European Journal of Human Genetics</i> , 2000, 8, 19-23.	3.0	374
479	Unravelling Genetic Data by Arrayed Primer Extension. <i>Clinical Chemistry and Laboratory Medicine</i> , 2000, 38, .	2.3	52
480	Arrayed Primer Extension: Solid-Phase Four-Color DNA Resequencing and Mutation Detection Technology. <i>Genetic Testing and Molecular Biomarkers</i> , 2000, 4, 1-7.	1.5	169
481	U82, a novel snoRNA identified from the fifth intron of human and mouse nucleolin gene. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1999, 1446, 426-430.	3.4	5
482	Isolation and characterization of the mouse ribosomal protein S7 gene. <i>IUBMB Life</i> , 1998, 46, 287-295.	2.9	3
483	A novel snoRNA (U73) is encoded within the introns of the human and mouse ribosomal protein S3a genes. <i>Gene</i> , 1998, 210, 255-263.	2.3	13
484	Dating the Origin of the CCR5- $\Delta$ 32 AIDS-Resistance Allele by the Coalescence of Haplotypes. <i>American Journal of Human Genetics</i> , 1998, 62, 1507-1515.	6.5	518
485	Nuclear Import and Nucleolar Accumulation of the Human Ribosomal Protein S7 Depends on both a Minimal Nuclear Localization Sequence and an Adjacent Basic Region. <i>Biochemical and Biophysical Research Communications</i> , 1998, 249, 759-766.	2.1	34
486	Minisequencing: A Specific Tool for DNA Analysis and Diagnostics on Oligonucleotide Arrays. <i>Genome Research</i> , 1997, 7, 606-614.	4.6	326

#	ARTICLE	IF	CITATIONS
487	Structural characterization of the mouse ribosomal protein S6-encoding gene. <i>Gene</i> , 1996, 175, 241-245.	2.3	5
488	Mutation detection by solid phase primer extension. <i>Human Mutation</i> , 1996, 7, 346-354.	4.5	146
489	The human ribosomal protein S7-encoding gene: isolation, structure and localization in 2p25. <i>Gene</i> , 1995, 165, 297-302.	2.3	16
490	Human ribosomal protein S3a: cloning of the cDNA and primary structure of the protein. <i>Gene</i> , 1992, 119, 313-316.	2.3	30
491	The human ribosomal protein S6 gene: isolation, primary structure and location in chromosome 9. <i>Gene</i> , 1992, 121, 387-392.	2.3	16
492	5 S RNA and 5.8 S RNA build up eukaryotic subribosomal domains active in tRNA binding. <i>FEBS Letters</i> , 1981, 136, 255-258.	2.7	2
493	Location of single-stranded and double-stranded regions in rat liver ribosomal 5S RNA and 5.8S RNA. <i>Nucleic Acids Research</i> , 1981, 9, 5331-5344.	15.5	28
494	The ternary complex consisting of rat liver ribosomal 5 S RNA, 5.8 S RNA and protein L5. <i>FEBS Letters</i> , 1980, 119, 81-84.	2.7	25
495	Interaction of 5-S RNA, 5.8-S RNA and tRNA with Rat-Liver Ribosomal Proteins. <i>FEBS Journal</i> , 1978, 91, 73-81.	0.2	51
496	A Whole-Blood Transcriptome Meta-Analysis Identifies Gene Expression Signatures of Cigarette Smoking. <i>Human Molecular Genetics</i> , 0, , ddw288.	2.9	81
497	Heterogeneous contributions of change in population distribution of body mass index to change in obesity and underweight. <i>ELife</i> , 0, 10, .	1.6	64
498	Title is missing!. , 0, .		4
499	Polygenic prediction of body mass index and obesity through the life course and across ancestries. <i>Nature Medicine</i> , 0, 31, 3151-3168.	33.0	10
500	Parent-of-origin effects on complex traits in up to 236,781 individuals. <i>Nature</i> , 0, 646, 647-656.	37.9	8
501	Characterization of prevalent genetic variants in the Estonian Biobank body-mass index GWAS. <i>Nature Communications</i> , 0, 16, .	13.7	1
502	Cohort Profiles: Personality Measurements at the Estonian Biobank of the Estonian Genome Center, University of Tartu. <i>Personality Science</i> , 0, 6, .	2.0	1
503	Genome-wide association study identifies ABCG1 as a susceptibility locus for tick-borne encephalitis. <i>IScience</i> , 0, 28, 114017.	3.6	0
504	Genetic effects on migration behavior contribute to increasing spatial differentiation at trait-associated loci in Estonia. <i>IScience</i> , 0, 28, 114013.	3.6	1

#	ARTICLE	IF	CITATIONS
505	Genome-wide association study and polygenic risk prediction of hypothyroidism. Nature Genetics, 0, 57, 3007-3015.	25.2	0
506	Genome-wide meta-analyses of non-response to antidepressants provide insights into underlying molecular genetics and suggest potential pharmacotherapies. Molecular Psychiatry, 0, , .	7.8	0