

# Andres Metspalu

## List of Publications by Year in descending order

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Version: 2024-02-01

356  
papers

93,159  
citations

492

129  
h-index

410

277  
g-index

382  
all docs

382  
docs citations

382  
times ranked

86376  
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>Cis</i>-epistasis at the <i>LPA</i> locus and risk of cardiovascular diseases. Cardiovascular Research, 2022, 118, 1088-1102.	3.8	14
2	Gut metagenome associations with extensive digital health data in a volunteer-based Estonian microbiome cohort. Nature Communications, 2022, 13, 869.	12.8	12
3	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
4	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	4.4	17
5	Genome-wide association study of panic disorder reveals genetic overlap with neuroticism and depression. Molecular Psychiatry, 2021, 26, 4179-4190.	7.9	58
6	Shared genetic risk between eating disorder and substance use related phenotypes: Evidence from genome-wide association studies. Addiction Biology, 2021, 26, e12880.	2.6	28
7	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	12.0	79
8	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
9	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
10	Multi-ancestry genome-wide gene-sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
11	Advances in Genomic Discovery and Implications for Personalized Prevention and Medicine: Estonia as Example. Journal of Personalized Medicine, 2021, 11, 358.	2.5	6
12	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
13	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. Biological Psychiatry, 2021, 90, 611-620.	1.3	103
14	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
15	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
16	Association analysis of juvenile idiopathic arthritis genetic susceptibility factors in Estonian patients. Clinical Rheumatology, 2021, 40, 4157-4165.	2.2	6
17	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
18	Metabolomic Fingerprints in Large Population Cohorts: Impact of Preanalytical Heterogeneity. Clinical Chemistry, 2021, 67, 1153-1155.	3.2	10

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19	Phantom epistasis between unlinked loci. <i>Nature</i> , 2021, 596, E1-E3.	27.8	16
20	The blood metabolome of incident kidney cancer: A case-control study nested within the MetKid consortium. <i>PLoS Medicine</i> , 2021, 18, e1003786.	8.4	16
21	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	21.4	218
22	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. <i>JAMA Psychiatry</i> , 2021, 78, 1258.	11.0	88
23	Differentially expressed genes reflect disease-induced rather than disease-causing changes in the transcriptome. <i>Nature Communications</i> , 2021, 12, 5647.	12.8	61
24	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.	21.4	69
25	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. <i>Molecular Psychiatry</i> , 2020, 25, 2392-2409.	7.9	83
26	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. <i>Biological Psychiatry</i> , 2020, 87, 419-430.	1.3	27
27	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	17
28	The genetic architecture of sporadic and multiple consecutive miscarriage. <i>Nature Communications</i> , 2020, 11, 5980.	12.8	52
29	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.	2.8	23
30	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002769.	3.6	5
31	An epigenome-wide association study of metabolic syndrome and its components. <i>Scientific Reports</i> , 2020, 10, 20567.	3.3	27
32	Habitual sleep disturbances and migraine: a Mendelian randomization study. <i>Annals of Clinical and Translational Neurology</i> , 2020, 7, 2370-2380.	3.7	18
33	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.	7.9	17
34	The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2020, 581, 434-443.	27.8	6,140
35	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.	3.4	12
36	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. <i>Nature Reviews Clinical Oncology</i> , 2020, 17, 687-705.	27.6	178

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37	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. <i>American Journal of Human Genetics</i> , 2020, 106, 389-404.	6.2	118
38	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.	6.2	34
39	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.	1.3	13
40	A metabolic profile of all-cause mortality risk identified in an observational study of 44,168 individuals. <i>Nature Communications</i> , 2019, 10, 3346.	12.8	188
41	Genome-wide association study identifies eight risk loci and implicates metabo-psychiatric origins for anorexia nervosa. <i>Nature Genetics</i> , 2019, 51, 1207-1214.	21.4	641
42	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	12.8	84
43	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. <i>Nature Communications</i> , 2019, 10, 5121.	12.8	62
44	Leveraging European infrastructures to access 1 million human genomes by 2022. <i>Nature Reviews Genetics</i> , 2019, 20, 693-701.	16.3	69
45	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	21.4	251
46	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019, 188, 1033-1054.	3.4	85
47	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376.	12.8	64
48	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. <i>Genetics</i> , 2019, 212, 905-918.	2.9	23
49	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	21.4	549
50	Search for Early Pancreatic Cancer Blood Biomarkers in Five European Prospective Population Biobanks Using Metabolomics. <i>Endocrinology</i> , 2019, 160, 1731-1742.	2.8	19
51	Polygenic prediction of breast cancer: comparison of genetic predictors and implications for risk stratification. <i>BMC Cancer</i> , 2019, 19, 557.	2.6	40
52	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.	1.3	43
53	Subsequent Event Risk in Individuals With Established Coronary Heart Disease. <i>Circulation Genomic and Precision Medicine</i> , 2019, 12, e002470.	3.6	17
54	Genome-wide association study identifies 30 loci associated with bipolar disorder. <i>Nature Genetics</i> , 2019, 51, 793-803.	21.4	1,191

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55	Genome-Wide Association Scan of Serum Urea in European Populations Identifies Two Novel Loci. <i>American Journal of Nephrology</i> , 2019, 49, 193-202.	3.1	5
56	Roadmap for a precision-medicine initiative in the Nordic region. <i>Nature Genetics</i> , 2019, 51, 924-930.	21.4	22
57	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	31
58	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.	21.4	112
59	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.	13.7	177
60	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.	1.5	16
61	Genetic variation in the Estonian population: pharmacogenomics study of adverse drug effects using electronic health records. <i>European Journal of Human Genetics</i> , 2019, 27, 442-454.	2.8	29
62	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.	3.7	6
63	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.	3.2	13
64	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.	2.8	147
65	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.	21.4	1,307
66	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.	1.3	69
67	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.	2.4	35
68	Association of branched-chain amino acids and other circulating metabolites with risk of incident dementia and Alzheimer's disease: A prospective study in eight cohorts. <i>Alzheimer's and Dementia</i> , 2018, 14, 723-733.	0.8	182
69	Signatures of negative selection in the genetic architecture of human complex traits. <i>Nature Genetics</i> , 2018, 50, 746-753.	21.4	304
70	Genetic influence on social outcomes during and after the Soviet era in Estonia. <i>Nature Human Behaviour</i> , 2018, 2, 269-275.	12.0	74
71	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018, 50, 559-571.	21.4	356
72	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.	6.2	123

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73	Circulating metabolites and general cognitive ability and dementia: Evidence from 11 cohort studies. <i>Alzheimer's and Dementia</i> , 2018, 14, 707-722.	0.8	143
74	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	21.4	2,224
75	Haplotype Sharing Provides Insights into Fine-Scale Population History and Disease in Finland. <i>American Journal of Human Genetics</i> , 2018, 102, 760-775.	6.2	57
76	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.	5.1	26
77	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.	1.3	87
78	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.	21.4	1,331
79	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	21.4	924
80	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. <i>Nature Genetics</i> , 2018, 50, 834-848.	21.4	239
81	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. <i>American Journal of Human Genetics</i> , 2018, 102, 1185-1194.	6.2	119
82	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.	21.4	1,835
83	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. <i>Nature Communications</i> , 2018, 9, 2606.	12.8	79
84	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.	2.5	94
85	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , 2017, 49, 403-415.	21.4	492
86	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	27.8	544
87	DNA breaks and chromatin structural changes enhance the transcription of autoimmune regulator target genes. <i>Journal of Biological Chemistry</i> , 2017, 292, 6542-6554.	3.4	52
88	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.	2.8	214
89	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.	2.8	181
90	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.	21.4	426

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91	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.	7.2	410
92	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, 14977.	12.8	169
93	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017, 66, 2888-2902.	0.6	615
94	A Low-Frequency Inactivating <i>AKT2</i> Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017, 66, 2019-2032.	0.6	47
95	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.	6.1	39
96	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, E327-E336.	7.1	39
97	Quality Matters: 2016 Annual Conference of the National Infrastructures for Biobanking, Biopreservation and Biobanking, 2017, 15, 270-276.	1.0	26
98	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.	1.3	84
99	The Genetic Architecture of Gene Expression in Peripheral Blood. <i>American Journal of Human Genetics</i> , 2017, 100, 228-237.	6.2	178
100	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766.	21.4	470
101	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</i> , The, 2017, 16, 898-907.	10.2	191
102	Hidden heritability due to heterogeneity across seven populations. <i>Nature Human Behaviour</i> , 2017, 1, 757-765.	12.0	137
103	Exome analysis in an Estonian multiplex family with neural tube defects—a case report. <i>Child's Nervous System</i> , 2017, 33, 1575-1581.	1.1	6
104	Association analyses based on false discovery rate implicate new loci for coronary artery disease. <i>Nature Genetics</i> , 2017, 49, 1385-1391.	21.4	571
105	Genotype-covariate interaction effects and the heritability of adult body mass index. <i>Nature Genetics</i> , 2017, 49, 1174-1181.	21.4	119
106	Viva Europa, a Land of Excellence in Research and Innovation for Health and Wellbeing. <i>Progress in Preventive Medicine (New York, N Y)</i> , 2017, 2, e006.	0.7	6
107	Identifying pathways modulating sleep duration: from genomics to transcriptomics. <i>Scientific Reports</i> , 2017, 7, 4555.	3.3	9
108	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, 18.	4.1	6

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109	Personalized risk prediction for type 2 diabetes: the potential of genetic risk scores. <i>Genetics in Medicine</i> , 2017, 19, 322-329.	2.4	127
110	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , 2017, 49, 27-35.	21.4	838
111	Genome-wide association meta-analysis of fish and EPA+DHA consumption in 17 US and European cohorts. <i>PLoS ONE</i> , 2017, 12, e0186456.	2.5	18
112	Pathogenic implications for autoimmune mechanisms derived by comparative eQTL analysis of CD4+ versus CD8+ T cells. <i>PLoS Genetics</i> , 2017, 13, e1006643.	3.5	110
113	Genome-wide physical activity interactions in adiposity – A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	3.5	158
114	Ranking and characterization of established BMI and lipid associated loci as candidates for gene-environment interactions. <i>PLoS Genetics</i> , 2017, 13, e1006812.	3.5	24
115	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.	2.5	7
116	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	27.8	952
117	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. <i>American Journal of Human Genetics</i> , 2016, 99, 8-21.	6.2	60
118	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 isolate-dependent. <i>Molecular Ecology</i> , 2016, 25, 2816-2832.	3.9	64
119	Coding Variation in <i>ANGPTL4</i> , <i>LPL</i> and <i>SVEP1</i> and the Risk of Coronary Disease. <i>New England Journal of Medicine</i> , 2016, 374, 1134-1144.	27.0	427
120	Ageing with elegans: a research proposal to map healthspan pathways. <i>Biogerontology</i> , 2016, 17, 771-782.	3.9	31
121	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. <i>Nature Genetics</i> , 2016, 48, 624-633.	21.4	870
122	Genetic variants in <i>RBFOX3</i> are associated with sleep latency. <i>European Journal of Human Genetics</i> , 2016, 24, 1488-1495.	2.8	27
123	Imprinted genes and imprinting control regions show predominant intermediate methylation in adult somatic tissues. <i>Epigenomics</i> , 2016, 8, 789-799.	2.1	35
124	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	27.8	1,204
125	Whole-genome expression analysis reveals genes associated with treatment response to escitalopram in major depression. <i>European Neuropsychopharmacology</i> , 2016, 26, 1475-1483.	0.7	22
126	Ultra-rare disruptive and damaging mutations influence educational attainment in the general population. <i>Nature Neuroscience</i> , 2016, 19, 1563-1565.	14.8	90



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127	Whole-Exome Sequencing Identifies Loci Associated with Blood Cell Traits and Reveals a Role for Alternative GF11B Splice Variants in Human Hematopoiesis. <i>American Journal of Human Genetics</i> , 2016, 99, 481-488.	6.2	45
128	A Whole-Blood Transcriptome Meta-Analysis Identifies Gene Expression Signatures of Cigarette Smoking. <i>Human Molecular Genetics</i> , 2016, 25, ddw288.	2.9	76
129	Genomic analyses inform on migration events during the peopling of Eurasia. <i>Nature</i> , 2016, 538, 238-242.	27.8	360
130	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1435-1448.	2.8	113
131	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016, 48, 1151-1161.	21.4	261
132	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.	21.4	362
133	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. <i>Nature Communications</i> , 2016, 7, 11122.	12.8	576
134	The Role of the Five-factor Personality Traits in General Self-rated Health. <i>European Journal of Personality</i> , 2016, 30, 492-504.	3.1	22
135	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016, 48, 1462-1472.	21.4	284
136	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13366-13371.	7.1	110
137	Reporting incidental findings of genomic disorder-associated copy number variants to unselected biobank participants. <i>Personalized Medicine</i> , 2016, 13, 303-314.	1.5	12
138	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. <i>Nature Genetics</i> , 2016, 48, 856-866.	21.4	520
139	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. <i>American Journal of Human Genetics</i> , 2016, 99, 40-55.	6.2	82
140	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. <i>American Journal of Human Genetics</i> , 2016, 99, 22-39.	6.2	50
141	The Number of Genomic Copies at the 16p11.2 Locus Modulates Language, Verbal Memory, and Inhibition. <i>Biological Psychiatry</i> , 2016, 80, 129-139.	1.3	78
142	De novo exonic mutation in MYH7 gene leading to exon skipping in a patient with early onset muscular weakness and fiber-type disproportion. <i>Neuromuscular Disorders</i> , 2016, 26, 236-239.	0.6	8
143	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. <i>Science</i> , 2016, 351, 1166-1171.	12.6	438
144	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. <i>JAMA Psychiatry</i> , 2016, 73, 497.	11.0	51

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145	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016, 7, 10023.	12.8	412
146	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. <i>Nature Genetics</i> , 2016, 48, 510-518.	21.4	617
147	Harmonising and linking biomedical and clinical data across disparate data archives to enable integrative cross-biobank research. <i>European Journal of Human Genetics</i> , 2016, 24, 521-528.	2.8	27
148	Defining the Effect of the 16p11.2 Duplication on Cognition, Behavior, and Medical Comorbidities. <i>JAMA Psychiatry</i> , 2016, 73, 20.	11.0	195
149	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. <i>Behavior Genetics</i> , 2016, 46, 170-182.	2.1	178
150	Epigenetic profiling in CD4+ and CD8+ T cells from Graves' disease patients reveals changes in genes associated with T cell receptor signaling. <i>Journal of Autoimmunity</i> , 2016, 67, 46-56.	6.5	88
151	Genome-Wide Association Analyses in 128,266 Individuals Identifies New Morningness and Sleep Duration Loci. <i>PLoS Genetics</i> , 2016, 12, e1006125.	3.5	308
152	Ancient Haplotypes at the 15q24.2 Microdeletion Region Are Linked to Brain Expression of MAN2C1 and Children's Intelligence. <i>PLoS ONE</i> , 2016, 11, e0157739.	2.5	2
153	Age-related profiling of DNA methylation in CD8+ T cells reveals changes in immune response and transcriptional regulator genes. <i>Scientific Reports</i> , 2015, 5, 13107.	3.3	148
154	The relationship between the Five-Factor Model personality traits and peptic ulcer disease in a large population-based adult sample. <i>Scandinavian Journal of Psychology</i> , 2015, 56, 693-699.	1.5	9
155	Linking a Population Biobank with National Health Registries—The Estonian Experience. <i>Journal of Personalized Medicine</i> , 2015, 5, 96-106.	2.5	43
156	Haplotype Phasing and Inheritance of Copy Number Variants in Nuclear Families. <i>PLoS ONE</i> , 2015, 10, e0122713.	2.5	9
157	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	3.5	331
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