Lili Milani

List of Publications by Year in Descending Order

164 papers	22,431 citations	58 h-index	149 g-index
190 ext. papers	31,223 ext. citations	15.6 avg, IF	5.21 L-index

#	Paper	IF	Citations
164	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. *Biological Psychiatry*, **2022**, 91, 102-117	7.9	11
163	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals.. *Nature Genetics*, **2022**,	36.3	7
162	Mapping genomic loci implicates genes and synaptic biology in schizophrenia.. *Nature*, **2022**,	50.4	35
161	Rare coding variants in ten genes confer substantial risk for schizophrenia.. *Nature*, **2022**,	50.4	16
160	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases.. *Nature Communications*, **2022**, 13, 2408	17.4	1
159	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. *Molecular Psychiatry*, **2021**, 26, 2111-2125	15.1	3
158	Association of polygenic score for major depression with response to lithium in patients with bipolar disorder. *Molecular Psychiatry*, **2021**, 26, 2457-2470	15.1	17
157	Response to comment on "Evaluating the cardiovascular safety of sclerostin inhibition using evidence from meta-analysis of clinical trials and human genetics". *Science Translational Medicine*, **2021**, 13, eabf4530	17.5	
156	Cohort Profile: COVIDMENT: COVID-19 cohorts on mental health across six nations.. *International Journal of Epidemiology*, **2021**,	7.8	2
155	Multi-ancestry genome-wide gene-sleep interactions identify novel loci for blood pressure. *Molecular Psychiatry*, **2021**,	15.1	3
154	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. *Biological Psychiatry*, **2021**, 90, 611-620	7.9	17
153	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. *Nature Genetics*, **2021**, 53, 817-829	36.3	83
152	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. *Genome Biology*, **2021**, 22, 194	18.3	14
151	Genome-wide association study identifies five risk loci for pernicious anemia. *Nature Communications*, **2021**, 12, 3761	17.4	4
150	Resource profile and user guide of the Polygenic Index Repository. *Nature Human Behaviour*, **2021**,	12.8	5
149	Genome-wide association study identifies 48 common genetic variants associated with handedness. *Nature Human Behaviour*, **2021**, 5, 59-70	12.8	33
148	Genetic insights into biological mechanisms governing human ovarian ageing. *Nature*, **2021**, 596, 393-397	50.4	28

147	Genetic regulation of spermine oxidase activity and cancer risk: a Mendelian randomization study. *Scientific Reports*, **2021**, 11, 17463	4.9	0
146	Identifying the Common Genetic Basis of Antidepressant Response. *Biological Psychiatry Global Open Science*, **2021**,		4
145	Genomic Insights into Myasthenia Gravis Identify Distinct Immunological Mechanisms in Early and Late Onset Disease. *Annals of Neurology*, **2021**, 90, 455-463	9.4	3
144	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. *Nature Genetics*, **2021**, 53, 1311-1321	36.3	27
143	Rare genetic variability in human drug target genes modulates drug response and can guide precision medicine. *Science Advances*, **2021**, 7, eabi6856	14.3	3
142	The Genetic Architecture of Depression in Individuals of East Asian Ancestry: A Genome-Wide Association Study. *JAMA Psychiatry*, **2021**, 78, 1258-1269	14.5	7
141	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. *Nature Genetics*, **2021**, 53, 1300-1310	36.3	60
140	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. *Nature Communications*, **2021**, 12, 7173	17.4	1
139	Meta-analyses identify DNA methylation associated with kidney function and damage. *Nature Communications*, **2021**, 12, 7174	17.4	0
138	Habitual sleep disturbances and migraine: a Mendelian randomization study. *Annals of Clinical and Translational Neurology*, **2020**, 7, 2370-2380	5.3	6
137	The effect of LRRK2 loss-of-function variants in humans. *Nature Medicine*, **2020**, 26, 869-877	50.5	47
136	Identification, Heritability, and Relation With Gene Expression of Novel DNA Methylation Loci for Blood Pressure. *Hypertension*, **2020**, 76, 195-205	8.5	12
135	A genome-wide cross-phenotype meta-analysis of the association of blood pressure with migraine. *Nature Communications*, **2020**, 11, 3368	17.4	22
134	Evaluating the cardiovascular safety of sclerostin inhibition using evidence from meta-analysis of clinical trials and human genetics. *Science Translational Medicine*, **2020**, 12,	17.5	27
133	Monocytes present age-related changes in phospholipid concentration and decreased energy metabolism. *Aging Cell*, **2020**, 19, e13127	9.9	23
132	Genome-wide gene-environment analyses of major depressive disorder and reported lifetime traumatic experiences in UK Biobank. *Molecular Psychiatry*, **2020**, 25, 1430-1446	15.1	47
131	Implications of secondary findings for clinical contexts **2020**, 155-201		2
130	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. *Biological Psychiatry*, **2020**, 88, 169-184	7.9	57

129	Variation near MTNR1A associates with early development and interacts with seasons. *Journal of Sleep Research*, **2020**, 29, e12925	5.8	
128	Longitudinal proteomic profiling reveals increased early inflammation and sustained apoptosis proteins in severe COVID-19. *Scientific Reports*, **2020**, 10, 20533	4.9	34
127	Differences in local population history at the finest level: the case of the Estonian population. *European Journal of Human Genetics*, **2020**, 28, 1580-1591	5.3	8
126	A data-driven medication score predicts 10-year mortality among aging adults. *Scientific Reports*, **2020**, 10, 15760	4.9	1
125	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. *Circulation Genomic and Precision Medicine*, **2020**, 13, e002769	5.2	1
124	An epigenome-wide association study of metabolic syndrome and its components. *Scientific Reports*, **2020**, 10, 20567	4.9	14
123	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. *Biological Psychiatry*, **2020**, 87, 419-430	7.9	9
122	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. *International Journal of Epidemiology*, **2020**, 49, 1022-1031	7.8	15
121	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. *American Journal of Epidemiology*, **2019**, 188, 1033-1054	3.8	39
120	Genome-wide association study identifies 30 loci associated with bipolar disorder. *Nature Genetics*, **2019**, 51, 793-803	36.3	662
119	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. *Human Molecular Genetics*, **2019**, 28, 2615-2633	5.6	14
118	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. *Nature Genetics*, **2019**, 51, 636-648	36.3	59
117	Population-based identity-by-descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2019**, 180, 223-231	3.5	2
116	A distinctive DNA methylation pattern in insufficient sleep. *Scientific Reports*, **2019**, 9, 1193	4.9	17
115	A genetics-led approach defines the drug target landscape of 30 immune-related traits. *Nature Genetics*, **2019**, 51, 1082-1091	36.3	85
114	Translating pharmacogenomics into clinical decisions: do not let the perfect be the enemy of the good. *Human Genomics*, **2019**, 13, 39	6.8	63
113	Associations of autozygosity with a broad range of human phenotypes. *Nature Communications*, **2019**, 10, 4957	17.4	40
112	Association of Whole-Genome and NETRIN1 Signaling Pathway-Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. *Biological Psychiatry: Cognitive Neuroscience and Neuroimaging*, **2019**, 4, 91-100	3.4	12

111	Genetic variation in the Estonian population: pharmacogenomics study of adverse drug effects using electronic health records. *European Journal of Human Genetics*, **2019**, 27, 442-454	5.3	13
110	Translating genotype data of 44,000 biobank participants into clinical pharmacogenetic recommendations: challenges and solutions. *Genetics in Medicine*, **2019**, 21, 1345-1354	8.1	37
109	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. *American Journal of Human Genetics*, **2018**, 102, 375-400	11	59
108	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. *Nature Genetics*, **2018**, 50, 668-681	36.3	1301
107	IgG glycosylation and DNA methylation are interconnected with smoking. *Biochimica Et Biophysica Acta - General Subjects*, **2018**, 1862, 637-648	4	25
106	Genetic risk scores and family history as predictors of schizophrenia in Nordic registers. *Psychological Medicine*, **2018**, 48, 1201-1208	6.9	18
105	Does Childhood Trauma Moderate Polygenic Risk for Depression? A Meta-analysis of 5765 Subjects From the Psychiatric Genomics Consortium. *Biological Psychiatry*, **2018**, 84, 138-147	7.9	48
104	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. *Nature Genetics*, **2018**, 50, 1112-1121	36.3	950
103	Global genetic diversity of human apolipoproteins and effects on cardiovascular disease risk. *Journal of Lipid Research*, **2018**, 59, 1987-2000	6.3	11
102	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. *PLoS ONE*, **2018**, 13, e0198166	3.7	31
101	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
100	Association of maternal prenatal smoking GFI1-locus and cardio-metabolic phenotypes in 18,212 adults. *EBioMedicine*, **2018**, 38, 206-216	8.8	19
99	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. *Nature Genetics*, **2018**, 50, 1412-1425	36.3	386
98	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. *American Journal of Human Genetics*, **2018**, 102, 1185-1194	11	55
97	Whole-exome sequencing identifies a potential TTN mutation in a multiplex family with inguinal hernia. *Hernia: the Journal of Hernias and Abdominal Wall Surgery*, **2017**, 21, 95-100	3.2	3
96	DNA breaks and chromatin structural changes enhance the transcription of autoimmune regulator target genes. *Journal of Biological Chemistry*, **2017**, 292, 6542-6554	5.4	21
95	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. *Nature Genetics*, **2017**, 49, 834-841	36.3	257
94	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. *Diabetes*, **2017**, 66, 2019-2032	0.9	29

93	Comprehensive population-based genome sequencing provides insight into hematopoietic regulatory mechanisms. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, E327-E336	11.5	30
92	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. *Nature*, **2017**, 541, 81-86	50.4	511
91	Homocysteine levels associate with subtle changes in leukocyte DNA methylation: an epigenome-wide analysis. *Epigenomics*, **2017**, 9, 1403-1422	4.4	4
90	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. *Nature Communications*, **2017**, 8, 910	17.4	78
89	Pathogenic implications for autoimmune mechanisms derived by comparative eQTL analysis of CD4+ versus CD8+ T cells. *PLoS Genetics*, **2017**, 13, e1006643	6	75
88	An interaction map of circulating metabolites, immune gene networks, and their genetic regulation. *Genome Biology*, **2017**, 18, 146	18.3	27
87	Neuregulin signaling pathway in smoking behavior. *Translational Psychiatry*, **2017**, 7, e1212	8.6	5
86	Genotype-covariate interaction effects and the heritability of adult body mass index. *Nature Genetics*, **2017**, 49, 1174-1181	36.3	78
85	Polymorphic variation in TPMT is the principal determinant of TPMT phenotype: A meta-analysis of three genome-wide association studies. *Clinical Pharmacology and Therapeutics*, **2017**, 101, 684-695	6.1	27
84	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. *Nature Genetics*, **2017**, 49, 27-35	36.3	530
83	An epigenome-wide association study meta-analysis of educational attainment. *Molecular Psychiatry*, **2017**, 22, 1680-1690	15.1	46
82	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
81	Variants in calcium voltage-gated channel subunit Alpha1 C-gene (CACNA1C) are associated with sleep latency in infants. *PLoS ONE*, **2017**, 12, e0180652	3.7	8
80	Pharmacogenomic Biomarkers for Improved Drug Therapy-Recent Progress and Future Developments. *AAPS Journal*, **2017**, 20, 4	3.7	78
79	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	15.5	61
78	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. *Nature Communications*, **2016**, 7, 13357	17.4	46
77	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. *Nature Genetics*, **2016**, 48, 1462-1472	36.3	198
76	Genetic variants linked to education predict longevity. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 13366-13371	11.5	90

75	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. *Nature Genetics*, **2016**, 48, 856-66	36.3	355
74	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
73	Sequence variation in nuclear ribosomal small subunit, internal transcribed spacer and large subunit regions of Rhizophagus irregularis and Gigaspora margarita is high and isolate-dependent. *Molecular Ecology*, **2016**, 25, 2816-32	5.7	41
72	Single base resolution analysis of 5-hydroxymethylcytosine in 188 human genes: implications for hepatic gene expression. *Nucleic Acids Research*, **2016**, 44, 6756-69	20.1	14
71	Genome-wide association study identifies 74 loci associated with educational attainment. *Nature*, **2016**, 533, 539-42	50.4	850
70	Whole-genome expression analysis reveals genes associated with treatment response to escitalopram in major depression. *European Neuropsychopharmacology*, **2016**, 26, 1475-1483	1.2	14
69	CDH13 promoter SNPs with pleiotropic effect on cardiometabolic parameters represent methylation QTLs. *Human Genetics*, **2015**, 134, 291-303	6.3	28
68	Cell Specific eQTL Analysis without Sorting Cells. *PLoS Genetics*, **2015**, 11, e1005223	6	81
67	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	50.4	119
66	A meta-analysis of gene expression signatures of blood pressure and hypertension. *PLoS Genetics*, **2015**, 11, e1005035	6	83
65	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. *American Journal of Human Genetics*, **2015**, 97, 576-92	11	649
64	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. *Nature Genetics*, **2015**, 47, 1294-1303	36.3	226
63	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. *Nature Genetics*, **2015**, 47, 1282-1293	36.3	223
62	Genome-wide genetic homogeneity between sexes and populations for human height and body mass index. *Human Molecular Genetics*, **2015**, 24, 7445-9	5.6	49
61	The transcriptional landscape of age in human peripheral blood. *Nature Communications*, **2015**, 6, 8570	17.4	335
60	Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. *Nature Genetics*, **2015**, 47, 1114-20	36.3	522
59	An epidemiological perspective of personalized medicine: the Estonian experience. *Journal of Internal Medicine*, **2015**, 277, 188-200	10.8	18
58	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. *Molecular Psychiatry*, **2015**, 20, 647-656	15.1	167

57	Age-related profiling of DNA methylation in CD8+ T cells reveals changes in immune response and transcriptional regulator genes. *Scientific Reports*, **2015**, 5, 13107	4.9	81
56	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	2.4	
55	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	6	220
54	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25,000 subjects. *Molecular Psychiatry*, **2015**, 20, 735-43	15.1	39
53	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
52	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
51	Dominance genetic variation contributes little to the missing heritability for human complex traits. *American Journal of Human Genetics*, **2015**, 96, 377-85	11	138
50	Cohort Profile: Estonian Biobank of the Estonian Genome Center, University of Tartu. *International Journal of Epidemiology*, **2015**, 44, 1137-47	7.8	175
49	A common 16p11.2 inversion underlies the joint susceptibility to asthma and obesity. *American Journal of Human Genetics*, **2014**, 94, 361-72	11	46
48	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. *Nature Communications*, **2014**, 5, 4926	17.4	121
47	Partitioning heritability of regulatory and cell-type-specific variants across 11 common diseases. *American Journal of Human Genetics*, **2014**, 95, 535-52	11	411
46	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. *Nature*, **2014**, 514, 92-97	50.4	401
45	Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86	36.3	1339
44	Genetic and epigenetic regulation of gene expression in fetal and adult human livers. *BMC Genomics*, **2014**, 15, 860	4.5	90
43	A meta-analysis of genome-wide association studies identifies novel variants associated with osteoarthritis of the hip. *Annals of the Rheumatic Diseases*, **2014**, 73, 2130-6	2.4	95
42	Using RNA sequencing for identifying gene imprinting and random monoallelic expression in human placenta. *Epigenetics*, **2014**, 9, 1397-409	5.7	42
41	Occupational irritants and asthma: an Estonian cross-sectional study of 34,000 adults. *European Respiratory Journal*, **2014**, 44, 647-56	13.6	16
40	CpG sites associated with NRP1, NRXN2 and miR-29b-2 are hypomethylated in monocytes during ageing. *Immunity and Ageing*, **2014**, 11, 1	9.7	21

39	Population distribution and ancestry of the cancer protective MDM2 SNP285 (rs117039649). *Oncotarget*, **2014**, 5, 8223-34	3.3	21
38	Meta-analysis of gene-level associations for rare variants based on single-variant statistics. *American Journal of Human Genetics*, **2013**, 93, 236-48	11	49
37	A missense mutation in DUSP6 is associated with Class III malocclusion. *Journal of Dental Research*, **2013**, 92, 893-8	8.1	35
36	Ontogeny, distribution and potential roles of 5-hydroxymethylcytosine in human liver function. *Genome Biology*, **2013**, 14, R83	18.3	54
35	Systematic identification of trans eQTLs as putative drivers of known disease associations. *Nature Genetics*, **2013**, 45, 1238-1243	36.3	1244
34	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics*, **2013**, 45, 501-12	36.3	437
33	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics*, **2013**, 45, 621-31	36.3	219
32	GWAS of 126,559 individuals identifies genetic variants associated with educational attainment. *Science*, **2013**, 340, 1467-71	33.3	563
31	A genome-wide association study of early menopause and the combined impact of identified variants. *Human Molecular Genetics*, **2013**, 22, 1465-72	5.6	82
30	In-solution hybrid capture of bisulfite-converted DNA for targeted bisulfite sequencing of 174 ADME genes. *Nucleic Acids Research*, **2013**, 41, e72	20.1	38
29	DNA methylation dynamics in the hepatic CYP3A4 gene promoter. *Biochimie*, **2012**, 94, 2338-44	4.6	46
28	Evidence of inbreeding depression on human height. *PLoS Genetics*, **2012**, 8, e1002655	6	62
27	DNA methylation analysis of bone marrow cells at diagnosis of acute lymphoblastic leukemia and at remission. *PLoS ONE*, **2012**, 7, e34513	3.7	33
26	Methylation markers of early-stage non-small cell lung cancer. *PLoS ONE*, **2012**, 7, e39813	3.7	51
25	DNA methylation for subtype classification and prediction of treatment outcome in patients with childhood acute lymphoblastic leukemia. *Blood*, **2010**, 115, 1214-25	2.2	115
24	A novel polymorphism in ABCB1 gene, CYP2B6*6 and sex predict single-dose efavirenz population pharmacokinetics in Ugandans. *British Journal of Clinical Pharmacology*, **2009**, 68, 690-9	3.8	102
23	Allele-specific expression and gene methylation in the control of CYP1A2 mRNA level in human livers. *Pharmacogenomics Journal*, **2009**, 9, 208-17	3.5	47
22	Allele-specific gene expression patterns in primary leukemic cells reveal regulation of gene expression by CpG site methylation. *Genome Research*, **2009**, 19, 1-11	9.7	62

21	Genotyping single nucleotide polymorphisms by multiplex minisequencing using tag-arrays. *Methods in Molecular Biology*, **2009**, 529, 215-29	1.4	2
20	Positional cloning by fast-track SNP-mapping in Drosophila melanogaster. *Nature Protocols*, **2008**, 3, 1751-65	18.8	5
19	Expression of BCR-ABL1 oncogene relative to ABL1 gene changes overtime in chronic myeloid leukemia. *Biochemical and Biophysical Research Communications*, **2008**, 366, 848-51	3.4	4
18	Comprehensive evaluation of the genetic variants of interferon regulatory factor 5 (IRF5) reveals a novel 5 bp length polymorphism as strong risk factor for systemic lupus erythematosus. *Human Molecular Genetics*, **2008**, 17, 872-81	5.6	158
17	Interferon regulatory factor 5 (IRF5) gene variants are associated with multiple sclerosis in three distinct populations. *Journal of Medical Genetics*, **2008**, 45, 362-9	5.8	111
16	An insertion-deletion polymorphism in the interferon regulatory Factor 5 (IRF5) gene confers risk of inflammatory bowel diseases. *Human Molecular Genetics*, **2007**, 16, 3008-16	5.6	144
15	Allelic imbalance in gene expression as a guide to cis-acting regulatory single nucleotide polymorphisms in cancer cells. *Nucleic Acids Research*, **2007**, 35, e34	20.1	53
14	Detection of alternatively spliced transcripts in leukemia cell lines by minisequencing on microarrays. *Clinical Chemistry*, **2006**, 52, 202-11	5.5	11
13	Genome-wide study identifies association between HLA-B*55:01 and penicillin allergy		2
12	Translating genotype data of 44,000 biobank participants into clinical pharmacogenetic recommendations: challenges and solutions		1
11	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depressive disorder		21
10	Genome-wide association study identifies 30 Loci Associated with Bipolar Disorder		28
9	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4
8	Genome-wide association studies identify 137 loci for DNA methylation biomarkers of ageing		8
7	Genomic and phenomic insights from an atlas of genetic effects on DNA methylation		7
6	Genome-wide Screen of Otosclerosis in Population Biobanks: 18 Loci and Shared Heritability with Skeletal Structure		3
5	Unraveling the polygenic architecture of complex traits using blood eQTL metaanalysis		175
4	Human loss-of-function variants suggest that partial LRRK2 inhibition is a safe therapeutic strategy for Parkinson disease		7

List of Publications

3	Genomic analyses for age at menarche identify 389 independent signals and indicate BMI-independent effects of puberty timing on cancer susceptibility	1
2	Loss-of-function of MFGE8 and protection against coronary atherosclerosis	1
1	FinnGen: Unique genetic insights from combining isolated population and national health register data	11