ZoltÃ¡n Kutalik

List of Publications by Year in descending order

153 papers	36,405 citations	13099 68 h-index	7160 153 g-index
186 all docs	186 docs citations	186 times ranked	44106 citing authors

#	Article	IF	Citations
1	The genetic etiology of periodic limb movement in sleep. Sleep, 2023, 46, .	1.1	4
2	From pharmacogenetics to pharmaco-omics: Milestones and future directions. Human Genetics and Genomics Advances, 2022, 3, 100100.	1.7	14
3	The individual and global impact of copy-number variants on complex human traits. American Journal of Human Genetics, 2022, 109, 647-668.	6.2	31
4	Using genetic variation to disentangle the complex relationship between food intake and health outcomes. PLoS Genetics, 2022, 18, e1010162.	3.5	12
5	Polynomial Mendelian randomization reveals non-linear causal effects for obesity-related traits. Human Genetics and Genomics Advances, 2022, 3, 100124.	1.7	11
6	Possible association of 16p11.2 copy number variation with altered lymphocyte and neutrophil counts. Npj Genomic Medicine, 2022, 7, .	3.8	3
7	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	12.0	79
8	Causal Inference Methods to Integrate Omics and Complex Traits. Cold Spring Harbor Perspectives in Medicine, 2021, 11, a040493.	6.2	9
9	Obesity and atypical depression symptoms: findings from Mendelian randomization in two European cohorts. Translational Psychiatry, 2021, 11, 96.	4.8	31
10	Gene regulation contributes to explain the impact of early life socioeconomic disadvantage on adult inflammatory levels in two cohort studies. Scientific Reports, 2021, 11, 3100.	3.3	15
11	Triangulating evidence from longitudinal and Mendelian randomization studies of metabolomic biomarkers for type 2 diabetes. Scientific Reports, 2021, 11, 6197.	3.3	18
12	HSD17B7 gene in selfâ€renewal and oncogenicity of keratinocytes from Black versus White populations. EMBO Molecular Medicine, 2021, 13, e14133.	6.9	8
13	Composite trait Mendelian randomization reveals distinct metabolic and lifestyle consequences of differences in body shape. Communications Biology, 2021, 4, 1064.	4.4	13
14	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.	21.4	590
15	Differentially expressed genes reflect disease-induced rather than disease-causing changes in the transcriptome. Nature Communications, 2021, 12, 5647.	12.8	61
16	Mendelian randomization to assess causality between uromodulin, blood pressure and chronic kidney disease. Kidney International, 2021, 100, 1282-1291.	5.2	20
17	Untargeted Metabolome- and Transcriptome-Wide Association Study Suggests Causal Genes Modulating Metabolite Concentrations in Urine. Journal of Proteome Research, 2021, 20, 5103-5114.	3.7	6
18	Probabilistic inference of the genetic architecture underlying functional enrichment of complex traits. Nature Communications, 2021, 12, 6972.	12.8	14

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19	Simultaneous estimation of bi-directional causal effects and heritable confounding from GWAS summary statistics. Nature Communications, 2021, 12, 7274.	12.8	32
20	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. Biological Psychiatry, 2020, 87, 419-430.	1.3	27
21	Using instrumental variables to estimate the attributable fraction. Statistical Methods in Medical Research, 2020, 29, 2063-2073.	1.5	1
22	FADS3 is a Î”14Z sphingoid base desaturase that contributes to gender differences in the human plasma sphingolipidome. Journal of Biological Chemistry, 2020, 295, 1889-1897.	3.4	64
23	Weight Loss Directly Influences Intermediate-Term Remission of Diabetes Mellitus After Bariatric Surgery: A Retrospective Case-Control Study. Obesity Surgery, 2020, 30, 1332-1338.	2.1	3
24	Genetic comorbidity between major depression and cardioâ€•metabolic traits, stratified by age at onset of major depression. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2020, 183, 309-330.	1.7	33
25	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.6	26
26	Commentary on: â€œThe contribution of tissue-specific BMI-associated gene sets to cardiometabolic disease risk: a Mendelian randomization studyâ€• International Journal of Epidemiology, 2020, 49, 1257-1258.	1.9	4
27	bGWAS: an R package to perform Bayesian genome wide association studies. Bioinformatics, 2020, 36, 4374-4376.	4.1	10
28	Quantification of the overall contribution of gene-environment interaction for obesity-related traits. Nature Communications, 2020, 11, 1385.	12.8	31
29	Influence of Genetic Ancestry on Human Serum Proteome. American Journal of Human Genetics, 2020, 106, 303-314.	6.2	19
30	Genome-wide gene-environment analyses of major depressive disorder and reported lifetime traumatic experiences in UK Biobank. Molecular Psychiatry, 2020, 25, 1430-1446.	7.9	116
31	Heterogeneity in Obesity: Genetic Basis and Metabolic Consequences. Current Diabetes Reports, 2020, 20, 1.	4.2	25
32	Genetic immune and inflammatory markers associated with diabetes in solid organ transplant recipients. American Journal of Transplantation, 2019, 19, 238-246.	4.7	5
33	Mendelian randomization integrating GWAS and eQTL data reveals genetic determinants of complex and clinical traits. Nature Communications, 2019, 10, 3300.	12.8	193
34	A frequent variant in the Japanese population determines quasi-Mendelian inheritance of rare retinal ciliopathy. Nature Communications, 2019, 10, 2884.	12.8	21
35	Genome-wide Association Study of Change in Fasting Glucose over time in 13,807 non-diabetic European Ancestry Individuals. Scientific Reports, 2019, 9, 9439.	3.3	5
36	Cross-species functional modules link proteostasis to human normal aging. PLoS Computational Biology, 2019, 15, e1007162.	3.2	11

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37	Disentangling the genetics of lean mass. American Journal of Clinical Nutrition, 2019, 109, 276-287.	4.7	38
38	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
39	The Human-Specific BOLA2 Duplication Modifies Iron Homeostasis and Anemia Predisposition in Chromosome 16p11.2 Autism Individuals. American Journal of Human Genetics, 2019, 105, 947-958.	6.2	30
40	Assessment of network module identification across complex diseases. Nature Methods, 2019, 16, 843-852.	19.0	213
41	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	6.2	21
42	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	21.4	402
43	Dysregulation of a long noncoding RNA reduces leptin leading to a leptin-responsive form of obesity. Nature Medicine, 2019, 25, 507-516.	30.7	79
44	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
45	Mendelian randomisation analyses find pulmonary factors mediate the effect of height on coronary artery disease. Communications Biology, 2019, 2, 119.	4.4	35
46	Genetic studies of accelerometer-based sleep measures yield new insights into human sleep behaviour. Nature Communications, 2019, 10, 1585.	12.8	189
47	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
48	Early life socioeconomic position and adult systemic inflammation: the role of gene regulation. European Journal of Public Health, 2019, 29, .	0.3	0
49	A Five-Decision Testing Procedure to Infer the Value of a Unidimensional Parameter. American Statistician, 2019, 73, 321-326.	1.6	0
50	Genetic and clinic predictors of new onset diabetes mellitus after transplantation. Pharmacogenomics Journal, 2019, 19, 53-64.	2.0	9
51	Genomics of 1 million parent lifespans implicates novel pathways and common diseases and distinguishes survival chances. ELife, 2019, 8, .	6.0	170
52	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681.	21.4	2,224
53	The protocadherin 17 gene affects cognition, personality, amygdala structure and function, synapse development and risk of major mood disorders. Molecular Psychiatry, 2018, 23, 400-412.	7.9	60
54	Multiethnic Meta-Analysis Identifies RAI1 as a Possible Obstructive Sleep Apneaâ€“related Quantitative Trait Locus in Men. American Journal of Respiratory Cell and Molecular Biology, 2018, 58, 391-401.	2.9	65

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55	Large-scale whole-exome sequencing association studies identify rare functional variants influencing serum urate levels. Nature Communications, 2018, 9, 4228.	12.8	43
56	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	6.2	326
57	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
58	A joint view on genetic variants for adiposity differentiates subtypes with distinct metabolic implications. Nature Communications, 2018, 9, 1946.	12.8	33
59	Evaluation and application of summary statistic imputation to discover new height-associated loci. PLoS Genetics, 2018, 14, e1007371.	3.5	43
60	Addendum: A joint view on genetic variants for adiposity differentiates subtypes with distinct metabolic implications. Nature Communications, 2018, 9, 2861.	12.8	16
61	Copy Number Variation. Methods in Molecular Biology, 2018, 1793, 231-258.	0.9	31
62	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
63	An Integrated Systems Genetics and Omics Toolkit to Probe Gene Function. Cell Systems, 2018, 6, 90-102.e4.	6.2	47
64	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
65	Quantifying the extent to which index event biases influence large genetic association studies. Human Molecular Genetics, 2017, 26, ddw433.	2.9	40
66	CRTC2 polymorphism as a risk factor for the incidence of metabolic syndrome in patients with solid organ transplantation. Pharmacogenomics Journal, 2017, 17, 69-75.	2.0	11
67	Genome-wide Association for Major Depression Through Age at Onset Stratification: Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. Biological Psychiatry, 2017, 81, 325-335.	1.3	175
68	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
69	cis -Acting Complex-Trait-Associated lincRNA Expression Correlates with Modulation of Chromosomal Architecture. Cell Reports, 2017, 18, 2280-2288.	6.4	67
70	A systematic review and metaâ€analysis of <scp>HCV</scp> clearance. Liver International, 2017, 37, 1431-1445.	3.9	37
71	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426
72	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169

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73	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	3.3	98
74	Geneâ€“obesogenic environment interactions in the UK Biobank study. International Journal of Epidemiology, 2017, 46, dyw337.	1.9	159
75	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. Biological Psychiatry, 2017, 82, 322-329.	1.3	84
76	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	12.8	64
77	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. Nature Communications, 2017, 8, 910.	12.8	118
78	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	2.7	123
79	Bayesian association scan reveals loci associated with human lifespan and linked biomarkers. Nature Communications, 2017, 8, 15842.	12.8	64
80	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	12.8	147
81	Common variants at 2q11.2, 8q21.3, and 11q13.2 are associated with major mood disorders. Translational Psychiatry, 2017, 7, 1273.	4.8	9
82	Impact of CD14 Polymorphisms on Anti-Apolipoprotein A-1 IgG-Related Coronary Artery Disease Prediction in the General Population. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 2342-2349.	2.4	27
83	Across-cohort QC analyses of GWAS summary statistics from complex traits. European Journal of Human Genetics, 2017, 25, 137-146.	2.8	18
84	Anti-Apolipoprotein A-1 IgG Predict All-Cause Mortality and Are Associated with Fc Receptor-Like 3 Polymorphisms. Frontiers in Immunology, 2017, 8, 437.	4.8	30
85	Risk prediction of developing venous thrombosis in combined oral contraceptive users. PLoS ONE, 2017, 12, e0182041.	2.5	31
86	Genome-Wide Association between Transcription Factor Expression and Chromatin Accessibility Reveals Regulators of Chromatin Accessibility. PLoS Computational Biology, 2017, 13, e1005311.	3.2	23
87	C-reactive protein upregulates the whole blood expression of CD59 - an integrative analysis. PLoS Computational Biology, 2017, 13, e1005766.	3.2	44
88	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
89	Approaches to detect genetic effects that differ between two strata in genome-wide meta-analyses: Recommendations based on a systematic evaluation. PLoS ONE, 2017, 12, e0181038.	2.5	27
90	New quality measure for SNP array based CNV detection. Bioinformatics, 2016, 32, 3298-3305.	4.1	36

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91	Association of genetic risk scores with body mass index in Swiss psychiatric cohorts. Pharmacogenetics and Genomics, 2016, 26, 208-217.	1.5	3
92	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
93	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	27.8	406
94	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
95	ORMDL3 expression levels have no influence on the activity of serine palmitoyltransferase. FASEB Journal, 2016, 30, 4289-4300.	0.5	27
96	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
97	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	7.1	110
98	Prevalence and determinants of periodic limb movements in the general population. Annals of Neurology, 2016, 79, 464-474.	5.3	112
99	Meta-analysis of genome-wide association studies of anxiety disorders. Molecular Psychiatry, 2016, 21, 1391-1399.	7.9	373
100	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. Diabetes, 2016, 65, 803-817.	0.6	131
101	Impact of a cis-associated gene expression SNP on chromosome 20q11.22 on bipolar disorder susceptibility, hippocampal structure and cognitive performance. British Journal of Psychiatry, 2016, 208, 128-137.	2.8	11
102	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	12.8	153
103	Tissue-specific regulatory circuits reveal variable modular perturbations across complex diseases. Nature Methods, 2016, 13, 366-370.	19.0	306
104	Fast and Rigorous Computation of Gene and Pathway Scores from SNP-Based Summary Statistics. PLoS Computational Biology, 2016, 12, e1004714.	3.2	330
105	Weighted Genetic Risk Scores and Prediction of Weight Gain in Solid Organ Transplant Populations. PLoS ONE, 2016, 11, e0164443.	2.5	7
106	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	3.5	331
107	Copy Number Variations and Cognitive Phenotypes in Unselected Populations. JAMA - Journal of the American Medical Association, 2015, 313, 2044.	7.4	143
108	A genetic risk score combining 32 SNPs is associated with body mass index and improves obesity prediction in people with major depressive disorder. BMC Medicine, 2015, 13, 86.	5.5	56

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109	Quantifying Genomic Privacy via Inference Attack with High-Order SNV Correlations. , 2015, , .		19
110	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
111	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
112	The 16p11.2 locus modulates brain structures common to autism, schizophrenia and obesity. Molecular Psychiatry, 2015, 20, 140-147.	7.9	160
113	EasyStrata: evaluation and visualization of stratified genome-wide association meta-analysis data. Bioinformatics, 2015, 31, 259-261.	4.1	71
114	Genome-wide association study of kidney function decline in individuals of European descent. Kidney International, 2015, 87, 1017-1029.	5.2	113
115	Impact of common risk factors of fibrosis progression in chronic hepatitis C. Gut, 2015, 64, 1605-1615.	12.1	85
116	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	7.9	235
117	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	2.5	64
118	Influence of MCHR2 and MCHR2-AS1 Genetic Polymorphisms on Body Mass Index in Psychiatric Patients and In Population-Based Subjects with Present or Past Atypical Depression. PLoS ONE, 2015, 10, e0139155.	2.5	16
119	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. PLoS Genetics, 2014, 10, e1004508.	3.5	80
120	Genome-Wide Association Study of Metabolic Traits Reveals Novel Gene-Metabolite-Disease Links. PLoS Genetics, 2014, 10, e1004132.	3.5	86
121	Reduced IFNÎ»4 activity is associated with improved HCV clearance and reduced expression of interferon-stimulated genes. Nature Communications, 2014, 5, 5699.	12.8	117
122	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	12.8	192
123	Common Variants in UMOD Associate with Urinary Uromodulin Levels. Journal of the American Society of Nephrology: JASN, 2014, 25, 1869-1882.	6.1	85
124	Gene-Age Interactions in Blood Pressure Regulation: A Large-Scale Investigation with the CHARGE, Global BPgen, and ICBP Consortia. American Journal of Human Genetics, 2014, 95, 24-38.	6.2	109
125	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
126	Multilayered Genetic and Omics Dissection of Mitochondrial Activity in a Mouse Reference Population. Cell, 2014, 158, 1415-1430.	28.9	222

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127	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
128	Quality control and conduct of genome-wide association meta-analyses. Nature Protocols, 2014, 9, 1192-1212.	12.0	398
129	DQB1 Locus Alone Explains Most of the Risk and Protection in Narcolepsy with Cataplexy in Europe. Sleep, 2014, 37, 19-25.	1.1	164
130	Influence ofCRTC1Polymorphisms on Body Mass Index and Fat Mass in Psychiatric Patients and the General Adult Population. JAMA Psychiatry, 2013, 70, 1011.	11.0	42
131	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
132	A mega-analysis of genome-wide association studies for major depressive disorder. Molecular Psychiatry, 2013, 18, 497-511.	7.9	1,002
133	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	3.5	371
134	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. Nature Genetics, 2013, 45, 76-82.	21.4	293
135	The Growing Importance of CNVs: New Insights for Detection and Clinical Interpretation. Frontiers in Genetics, 2013, 4, 92.	2.3	49
136	A 600â€…kb deletion syndrome at 16p11.2 leads to energy imbalance and neuropsychiatric disorders. Journal of Medical Genetics, 2012, 49, 660-668.	3.2	251
137	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	27.8	383
138	Genome-Wide Association Study Identifies Variants Associated With Progression of Liver Fibrosis From HCV Infection. Gastroenterology, 2012, 143, 1244-1252.e12.	1.3	142
139	Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. Nature, 2011, 478, 97-102.	27.8	394
140	Sensitivity of Genome-Wide-Association Signals to Phenotyping Strategy: The PROP-TAS2R38 Taste Association as a Benchmark. PLoS ONE, 2011, 6, e27745.	2.5	41
141	Genome-wide association study identifies two loci strongly affecting transferrin glycosylation. Human Molecular Genetics, 2011, 20, 3710-3717.	2.9	31
142	Novel method to estimate the phenotypic variation explained by genome-wide association studies reveals large fraction of the missing heritability. Genetic Epidemiology, 2011, 35, 341-349.	1.3	23
143	Methods for testing association between uncertain genotypes and quantitative traits. Biostatistics, 2011, 12, 1-17.	1.5	35
144	Physical Activity Attenuates the Influence of FTO Variants on Obesity Risk: A Meta-Analysis of 218,166 Adults and 19,268 Children. PLoS Medicine, 2011, 8, e1001116.	8.4	446

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145	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
146	Genome-wide association study identifies new HLA class II haplotypes strongly protective against narcolepsy. Nature Genetics, 2010, 42, 786-789.	21.4	170
147	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	21.4	836
148	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	21.4	2,634
149	Genetic Variation in IL28B Is Associated With Chronic Hepatitis C and Treatment Failure: A Genome-Wide Association Study. Gastroenterology, 2010, 138, 1338-1345.e7.	1.3	1,056
150	Genes mirror geography within Europe. Nature, 2008, 456, 98-101.	27.8	1,287
151	A modular approach for integrative analysis of large-scale gene-expression and drug-response data. Nature Biotechnology, 2008, 26, 531-539.	17.5	111
152	Estimating parameters for generalized mass action models using constraint propagation. Mathematical Biosciences, 2007, 208, 607-620.	1.9	47
153	S-system parameter estimation for noisy metabolic profiles using Newton-flow analysis. IET Systems Biology, 2007, 1, 174-180.	1.5	48