

LDlink: a web-based application for exploring population
linking correlated alleles of possible functional variants

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Citation Report

#	ARTICLE	IF	CITATIONS
1	A Genome-Wide Scan Identifies Variants in <i>NFIB</i> Associated with Metastasis in Patients with Osteosarcoma. <i>Cancer Discovery</i> , 2015, 5, 920-931.	7.7	88
2	Meta-Analysis of Tourette Syndrome and Attention Deficit Hyperactivity Disorder Provides Support for a Shared Genetic Basis. <i>Frontiers in Neuroscience</i> , 2016, 10, 340.	1.4	26
3	Targeted Re-Sequencing Approach of Candidate Genes Implicates Rare Potentially Functional Variants in Tourette Syndrome Etiology. <i>Frontiers in Neuroscience</i> , 2016, 10, 428.	1.4	29
4	Variant Discovery and Fine Mapping of Genetic Loci Associated with Blood Pressure Traits in Hispanics and African Americans. <i>PLoS ONE</i> , 2016, 11, e0164132.	1.1	24
5	Analysis of Haplotype Sequences. , 0, , .		8
6	Immunometabolic Pathways in BCG-Induced Trained Immunity. <i>Cell Reports</i> , 2016, 17, 2562-2571.	2.9	467
7	Mosaic loss of chromosome Y is associated with common variation near <i>TCL1A</i> . <i>Nature Genetics</i> , 2016, 48, 563-568.	9.4	134
8	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. <i>American Journal of Human Genetics</i> , 2016, 99, 636-646.	2.6	67
9	Assessing the role of insulin-like growth factors and binding proteins in prostate cancer using Mendelian randomization: Genetic variants as instruments for circulating levels. <i>International Journal of Cancer</i> , 2016, 139, 1520-1533.	2.3	26
10	Polymorphisms in <i>SLCO1B1</i> and <i>UGT1A1</i> are associated with sorafenib-induced toxicity. <i>Pharmacogenomics</i> , 2016, 17, 1483-1490.	0.6	26
11	Functional characterization of the 12p12.1 renal cancer-susceptibility locus implicates <i>BHLHE41</i> . <i>Nature Communications</i> , 2016, 7, 12098.	5.8	30
12	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. <i>Cancer Discovery</i> , 2016, 6, 1052-1067.	7.7	157
13	Genome-wide association analyses identify new susceptibility loci for oral cavity and pharyngeal cancer. <i>Nature Genetics</i> , 2016, 48, 1544-1550.	9.4	164
14	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). <i>Scientific Reports</i> , 2016, 6, 32512.	1.6	19
15	Ancient DNA reveals selection acting on genes associated with hypoxia response in pre-Columbian Peruvian Highlanders in the last 8500 years. <i>Scientific Reports</i> , 2016, 6, 23485.	1.6	26
16	Genomics and CSF analyses implicate thyroid hormone in hippocampal sclerosis of aging. <i>Acta Neuropathologica</i> , 2016, 132, 841-858.	3.9	28
17	A Common Variant at the 14q32 Endometrial Cancer Risk Locus Activates <i>AKT1</i> through <i>YY1</i> Binding. <i>American Journal of Human Genetics</i> , 2016, 98, 1159-1169.	2.6	32
18	Genome-wide association study using family-based cohorts identifies the <i>WLS</i> and <i>CCDC170/ESR1</i> loci as associated with bone mineral density. <i>BMC Genomics</i> , 2016, 17, 136.	1.2	44

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19	Enhancer scanning to locate regulatory regions in genomic loci. <i>Nature Protocols</i> , 2016, 11, 46-60.	5.5	14
20	Analysis of genetics and DNA methylation in osteoarthritis: What have we learnt about the disease?. <i>Seminars in Cell and Developmental Biology</i> , 2017, 62, 57-66.	2.3	75
21	The influence of genetic susceptibility and calcium plus vitamin D supplementation on fracture risk. <i>American Journal of Clinical Nutrition</i> , 2017, 105, 970-979.	2.2	15
22	Novel Genetic Variants in Carboxylesterase 1 Predict Severe Early-Onset Capecitabine-Related Toxicity. <i>Clinical Pharmacology and Therapeutics</i> , 2017, 102, 796-804.	2.3	30
23	Immune-Array Analysis in Sporadic Inclusion Body Myositis Reveals HLA-DRB1 Amino Acid Heterogeneity Across the Myositis Spectrum. <i>Arthritis and Rheumatology</i> , 2017, 69, 1090-1099.	2.9	41
24	Decreased calcium pump expression in human erythrocytes is connected to a minor haplotype in the ATP2B4 gene. <i>Cell Calcium</i> , 2017, 65, 73-79.	1.1	29
25	Worldwide Distribution of Cytochrome P450 Alleles: A Meta-Analysis of Population-scale Sequencing Projects. <i>Clinical Pharmacology and Therapeutics</i> , 2017, 102, 688-700.	2.3	430
26	3'-UTR SNP rs2229611 in G6PC1 affects mRNA stability, expression and Glycogen Storage Disease type-1a risk. <i>Clinica Chimica Acta</i> , 2017, 471, 46-54.	0.5	15
27	GWAS identifies population-specific new regulatory variants in FUT6 associated with plasma B12 concentrations in Indians. <i>Human Molecular Genetics</i> , 2017, 26, 2551-2564.	1.4	30
28	The impact of common dopamine D2 receptor gene polymorphisms on D2/3 receptor availability: C957T as a key determinant in putamen and ventral striatum. <i>Translational Psychiatry</i> , 2017, 7, e1091-e1091.	2.4	35
29	Gene-Hormone Therapy Interaction and Fracture Risk in Postmenopausal Women. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2017, 102, 1908-1916.	1.8	5
30	Genome-wide association study meta-analysis for quantitative ultrasound parameters of bone identifies five novel loci for broadband ultrasound attenuation. <i>Human Molecular Genetics</i> , 2017, 26, 2791-2802.	1.4	32
31	Genome-Wide Association Study to Identify Susceptibility Loci That Modify Radiation-Related Risk for Breast Cancer After Childhood Cancer. <i>Journal of the National Cancer Institute</i> , 2017, 109, .	3.0	66
32	Germline Genetic Variants and Lung Cancer Survival in African Americans. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 1288-1295.	1.1	7
33	Genome-wide association study identifies multiple risk loci for renal cell carcinoma. <i>Nature Communications</i> , 2017, 8, 15724.	5.8	106
34	A methylome-wide mQTL analysis reveals associations of methylation sites with GAD1 and HDAC3 SNPs and a general psychiatric risk score. <i>Translational Psychiatry</i> , 2017, 7, e1002-e1002.	2.4	29
35	Complement receptor 1 gene polymorphisms are associated with cardiovascular risk. <i>Atherosclerosis</i> , 2017, 257, 16-21.	0.4	22
36	An eQTL variant of ZXDC is associated with IFN- γ production following Mycobacterium tuberculosis antigen-specific stimulation. <i>Scientific Reports</i> , 2017, 7, 12800.	1.6	5

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37	<i>IKZF1</i> Gene in Childhood B-cell Precursor Acute Lymphoblastic Leukemia: Interplay between Genetic Susceptibility and Somatic Abnormalities. <i>Cancer Prevention Research</i> , 2017, 10, 738-744.	0.7	11
38	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. <i>Nature Communications</i> , 2017, 8, 910.	5.8	118
39	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475,000 Individuals. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	48
40	Genome-wide association study identifies the SERPINB gene cluster as a susceptibility locus for food allergy. <i>Nature Communications</i> , 2017, 8, 1056.	5.8	75
41	Oxytocin Receptor Polymorphisms are Differentially Associated with Social Abilities across Neurodevelopmental Disorders. <i>Scientific Reports</i> , 2017, 7, 11618.	1.6	36
42	Holocene Selection for Variants Associated With General Cognitive Ability: Comparing Ancient and Modern Genomes. <i>Twin Research and Human Genetics</i> , 2017, 20, 271-280.	0.3	22
43	Association of microRNA-125a and microRNA-499a polymorphisms in chronic periodontitis in a sample south Indian population: A hospital-based genetic association study. <i>Gene</i> , 2017, 631, 10-15.	1.0	10
44	Single nucleotide polymorphism in the COL11A2 gene associated with lowered heat pain sensitivity in knee osteoarthritis. <i>Molecular Pain</i> , 2017, 13, 174480691772425.	1.0	11
45	Identification of a functionally significant tri-allelic genotype in the Tyrosinase gene (TYR) causing hypomorphic oculocutaneous albinism (OCA1B). <i>Scientific Reports</i> , 2017, 7, 4415.	1.6	47
46	Neutralizing Antibody Responses to Viral Infections Are Linked to the Non-classical MHC Class II Gene H2-Ob. <i>Immunity</i> , 2017, 47, 310-322.e7.	6.6	42
47	Genetic Variants Related to Longer Telomere Length are Associated with Increased Risk of Renal Cell Carcinoma. <i>European Urology</i> , 2017, 72, 747-754.	0.9	39
48	Clinical Evidence Supports a Protective Role for CXCL5 in Coronary Artery Disease. <i>American Journal of Pathology</i> , 2017, 187, 2895-2911.	1.9	50
49	A Type 2 Diabetes-Associated Functional Regulatory Variant in a Pancreatic Islet Enhancer at the <i>ADCY5</i> Locus. <i>Diabetes</i> , 2017, 66, 2521-2530.	0.3	54
50	Pharmacogenetic testing through the direct-to-consumer genetic testing company 23andMe. <i>BMC Medical Genomics</i> , 2017, 10, 47.	0.7	25
51	Genotypes of SLC22A4 and SLC22A5 regulatory loci are predictive of the response of chronic myeloid leukemia patients to imatinib treatment. <i>Journal of Experimental and Clinical Cancer Research</i> , 2017, 36, 55.	3.5	17
52	Assocplots: a Python package for static and interactive visualization of multiple-group GWAS results. <i>Bioinformatics</i> , 2017, 33, 432-434.	1.8	19
53	Chronic Periodontitis Genome-wide Association Study in the Hispanic Community Health Study / Study of Latinos. <i>Journal of Dental Research</i> , 2017, 96, 64-72.	2.5	52
54	Gene polymorphisms of desaturase enzymes of polyunsaturated fatty acid metabolism and adiponutrin and the increased risk of nonalcoholic fatty liver disease. <i>Meta Gene</i> , 2017, 11, 152-156.	0.3	7

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55	Whole genome analysis on the genetic backgrounds associated with the secondary failure to etanercept in patients with rheumatoid arthritis. <i>Modern Rheumatology</i> , 2017, 27, 271-277.	0.9	2
57	Ataxia Telangiectasia-Mutated (ATM) Polymorphisms and Risk of Lung Cancer in a Chinese Population. <i>Frontiers in Public Health</i> , 2017, 5, 102.	1.3	4
58	Recent Advances in Experimental Whole Genome Haplotyping Methods. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1944.	1.8	12
59	Mediterranean Diet Adherence and Genetic Background Roles within a Web-Based Nutritional Intervention: The Food4Me Study. <i>Nutrients</i> , 2017, 9, 1107.	1.7	25
60	SNP Variants in Major Histocompatibility Complex Are Associated with Sarcoidosis Susceptibility—A Joint Analysis in Four European Populations. <i>Frontiers in Immunology</i> , 2017, 8, 422.	2.2	31
61	A CREB1 Gene Polymorphism (rs2253206) Is Associated with Prospective Memory in a Healthy Cohort. <i>Frontiers in Behavioral Neuroscience</i> , 2017, 11, 86.	1.0	7
62	<i>FOXP3</i> Allelic Variants and Haplotype Structures Are Associated with Aggressive Breast Cancer Subtypes. <i>Disease Markers</i> , 2017, 2017, 1-8.	0.6	12
63	Association of IFIH1 and pro-inflammatory mediators: Potential new clues in SLE-associated pathogenesis. <i>PLoS ONE</i> , 2017, 12, e0171193.	1.1	11
64	Shared genetic risk between migraine and coronary artery disease: A genome-wide analysis of common variants. <i>PLoS ONE</i> , 2017, 12, e0185663.	1.1	44
65	Identification and characterization of a FOXA2-regulated transcriptional enhancer at a type 2 diabetes intronic locus that controls GCKR expression in liver cells. <i>Genome Medicine</i> , 2017, 9, 63.	3.6	21
66	Genomic variants in the FTO gene are associated with sporadic amyotrophic lateral sclerosis in Greek patients. <i>Human Genomics</i> , 2017, 11, 30.	1.4	21
67	Whole transcriptome analysis of human erythropoietic cells during ontogenesis suggests a role of VEGFA gene as modulator of fetal hemoglobin and pharmacogenomic biomarker of treatment response to hydroxyurea in β^2 -type hemoglobinopathy patients. <i>Human Genomics</i> , 2017, 11, 24.	1.4	11
68	Genome-wide meta-analysis in Japanese populations identifies novel variants at the TMC6—TMC8 and SIX3—SIX2 loci associated with HbA1c. <i>Scientific Reports</i> , 2017, 7, 16147.	1.6	28
69	miRNAs as drivers of TMPRSS2-ERG negative prostate tumors in African American men. <i>Frontiers in Bioscience - Landmark</i> , 2017, 22, 212-229.	3.0	14
70	Effects of Type 1 Diabetes Risk Alleles on Immune Cell Gene Expression. <i>Genes</i> , 2017, 8, 167.	1.0	17
71	Population differentiation in allele frequencies of obesity-associated SNPs. <i>BMC Genomics</i> , 2017, 18, 861.	1.2	40
72	Characterizing key nucleotide polymorphisms of hepatitis C virus-disease associations via mass-spectrometric genotyping. <i>International Journal of Oncology</i> , 2017, 52, 441-452.	1.4	0
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75	Genetic determinants of glycated hemoglobin levels in the Greenlandic Inuit population. European Journal of Human Genetics, 2018, 26, 868-875.	1.4	6
76	Genomic profiling in advanced stage non-small-cell lung cancer patients with platinum-based chemotherapy identifies germline variants with prognostic value in SMYD2. Cancer Treatment and Research Communications, 2018, 15, 21-31.	0.7	9
77	Regionally clustered <i>ABCC8</i> polymorphisms in a prospective cohort predict cerebral oedema and outcome in severe traumatic brain injury. Journal of Neurology, Neurosurgery and Psychiatry, 2018, 89, 1152-1162.	0.9	36
78	Medical relevance of protein-truncating variants across 337,205 individuals in the UK Biobank study. Nature Communications, 2018, 9, 1612.	5.8	95
79	Genome-Wide Associations of Global Electrical Heterogeneity ECG Phenotype: The ARIC (Atherosclerosis Risk in Communities) Study and CHS (Cardiovascular Health Study). Journal of the American Heart Association, 2018, 7, .	1.6	31
80	Mismatch repair single nucleotide polymorphisms and thyroid cancer susceptibility. Oncology Letters, 2018, 15, 6715-6726.	0.8	11
81	<i>CDKN2A/B</i> T2D Genome-Wide Association Study Risk SNPs Impact Locus Gene Expression and Proliferation in Human Islets. Diabetes, 2018, 67, 872-884.	0.3	41
82	LDassoc: an online tool for interactively exploring genome-wide association study results and prioritizing variants for functional investigation. Bioinformatics, 2018, 34, 887-889.	1.8	89
83	Human-Specific Mutations and Positively Selected Sites in MARCO Confer Functional Changes. Molecular Biology and Evolution, 2018, 35, 440-450.	3.5	11
84	PhenoRank: reducing study bias in gene prioritization through simulation. Bioinformatics, 2018, 34, 2087-2095.	1.8	30
85	<i>HER2</i> Ile655Val polymorphism is negatively associated with breast cancer susceptibility. Journal of Clinical Laboratory Analysis, 2018, 32, e22406.	0.9	11
86	Genetic variation of GRIA3 gene is associated with vulnerability to methamphetamine dependence and its associated psychosis. Journal of Psychopharmacology, 2018, 32, 309-315.	2.0	11
87	Transforming growth factor beta 1 (TGF β 1) polymorphisms and haplotype structures have dual roles in breast cancer pathogenesis. Journal of Cancer Research and Clinical Oncology, 2018, 144, 645-655.	1.2	17
88	Effect of genetic variation in <i>UGT1A</i> and <i>ABCB1</i> on moxifloxacin pharmacokinetics in South African patients with tuberculosis. Pharmacogenomics, 2018, 19, 17-29.	0.6	16
89	Genome-wide meta-analyses identifies novel taxane-induced peripheral neuropathy-associated loci. Pharmacogenetics and Genomics, 2018, 28, 49-55.	0.7	26
90	Candidate gene analysis in the São Paulo Epidemiologic Sleep Study (EPISONO) shows an association of variant in PDE4D and sleepiness. Sleep Medicine, 2018, 47, 106-112.	0.8	7
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92	Effect of ABCB1 C3435T Polymorphism on Pharmacokinetics of Antipsychotics and Antidepressants. <i>Basic and Clinical Pharmacology and Toxicology</i> , 2018, 123, 474-485.	1.2	51
93	Genetics in multiple sclerosis: Updates in the era of big data. <i>Clinical and Experimental Neuroimmunology</i> , 2018, 9, 19-24.	0.5	3
94	Thyroid Stimulating Hormone and Bone Mineral Density: Evidence From a Two-Sample Mendelian Randomization Study and a Candidate Gene Association Study. <i>Journal of Bone and Mineral Research</i> , 2018, 33, 1318-1325.	3.1	25
95	A genome-wide association study on photic sneeze syndrome in a Japanese population. <i>Journal of Human Genetics</i> , 2018, 63, 765-768.	1.1	3
96	Genome Wide Association Study Identifies the <i>HMGC2</i> Locus to be Associated With Chlorothalidone Induced Glucose Increase in Hypertensive Patients. <i>Journal of the American Heart Association</i> , 2018, 7, .	1.6	13
97	The highly pleiotropic gene <i>SLC39A8</i> as an opportunity to gain insight into the molecular pathogenesis of schizophrenia. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2018, 177, 274-283.	1.1	52
98	Interleukin 7 receptor alpha Thr244Ile genetic polymorphism is associated with susceptibility and prognostic markers in breast cancer subgroups. <i>Cytokine</i> , 2018, 103, 121-126.	1.4	17
99	Novel genetic loci associated HLA-B*08:01 positive myasthenia gravis. <i>Journal of Autoimmunity</i> , 2018, 88, 43-49.	3.0	20
100	Cumulative evidence for relationships between multiple variants in the <i>VT11A</i> and <i>TCF7L2</i> genes and cancer incidence. <i>International Journal of Cancer</i> , 2018, 142, 498-513.	2.3	15
101	Genome-wide association studies of albuminuria: towards genetic stratification in diabetes?. <i>Journal of Nephrology</i> , 2018, 31, 475-487.	0.9	13
102	A hypermorphic antioxidant response element is associated with increased MS4A6A expression and Alzheimer's disease. <i>Redox Biology</i> , 2018, 14, 686-693.	3.9	21
103	Longitudinal Analysis of Genetic Susceptibility and BMI Throughout Adult Life. <i>Diabetes</i> , 2018, 67, 248-255.	0.3	38
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105	Identification of Pleiotropic Cancer Susceptibility Variants from Genome-Wide Association Studies Reveals Functional Characteristics. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 75-85.	1.1	25
106	A germ-line deletion of APOBEC3B does not contribute to subtype-specific childhood acute lymphoblastic leukemia etiology. <i>Haematologica</i> , 2018, 103, e29-e31.	1.7	1
107	Identification of CDC42BPG as a novel susceptibility locus for hyperuricemia in a Japanese population. <i>Molecular Genetics and Genomics</i> , 2018, 293, 371-379.	1.0	12
108	The SETDB2 locus: evidence for a genetic link between handedness and atopic disease. <i>Heredity</i> , 2018, 120, 77-82.	1.2	8
109	Leveraging Human Genetics to Guide Cancer Drug Development. <i>JCO Clinical Cancer Informatics</i> , 2018, 2, 1-11.	1.0	3

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110	Novel disease syndromes unveiled by integrative multiscale network analysis of diseases sharing molecular effectors and comorbidities. <i>BMC Medical Genomics</i> , 2018, 11, 112.	0.7	8
111	Evaluation of the Association Between Genetic Variants in Circadian Rhythm Genes and Posttraumatic Stress Symptoms Identifies a Potential Functional Allele in the Transcription Factor TEF. <i>Frontiers in Psychiatry</i> , 2018, 9, 597.	1.3	9
112	AFLP-AFLP in silico-NGS approach reveals polymorphisms in repetitive elements in the malignant genome. <i>PLoS ONE</i> , 2018, 13, e0206620.	1.1	0
113	Parkinson-Associated SNCA Enhancer Variants Revealed by Open Chromatin in Mouse Dopamine Neurons. <i>American Journal of Human Genetics</i> , 2018, 103, 874-892.	2.6	30
114	Six NSCL/P Loci Show Associations With Normal-Range Craniofacial Variation. <i>Frontiers in Genetics</i> , 2018, 9, 502.	1.1	20
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116	Six novel susceptibility loci for coronary artery disease and cerebral infarction identified by longitudinal exome-wide association studies in a Japanese population. <i>Biomedical Reports</i> , 2018, 9, 123-134.	0.9	8
117	Chromatin interactions and expression quantitative trait loci reveal genetic drivers of multimorbidities. <i>Nature Communications</i> , 2018, 9, 5198.	5.8	64
118	Genome-epigenome interactions associated with Myalgic Encephalomyelitis/Chronic Fatigue Syndrome. <i>Epigenetics</i> , 2018, 13, 1174-1190.	1.3	28
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122	Defining the molecular signatures of Achilles tendinopathy and anterior cruciate ligament ruptures: A whole-exome sequencing approach. <i>PLoS ONE</i> , 2018, 13, e0205860.	1.1	16
123	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018, 362, .	6.0	781
124	Genome-wide association study of primary open-angle glaucoma in continental and admixed African populations. <i>Human Genetics</i> , 2018, 137, 847-862.	1.8	40
125	Plasticity-related gene 3 (<i>LPPR1</i>) and age at diagnosis of Parkinson disease. <i>Neurology: Genetics</i> , 2018, 4, e271.	0.9	12
126	Applying polygenic risk scoring for psychiatric disorders to a large family with bipolar disorder and major depressive disorder. <i>Communications Biology</i> , 2018, 1, 163.	2.0	17
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129	Association of Genetically Enhanced Lipoprotein Lipase-Mediated Lipolysis and Low-Density Lipoprotein Cholesterol-Lowering Alleles With Risk of Coronary Disease and Type 2 Diabetes. <i>JAMA Cardiology</i> , 2018, 3, 957.	3.0	55
130	Missing single nucleotide polymorphisms in Genetic Risk Scores: A simulation study. <i>PLoS ONE</i> , 2018, 13, e0200630.	1.1	7
131	Cumulative evidence for relationships between multiple variants in 8q24 and colorectal cancer incidence. <i>Medicine (United States)</i> , 2018, 97, e11990.	0.4	2
132	Variants of PEAR1 Are Associated With Outcome in Patients With ACS and Stable CAD Undergoing PCI. <i>Frontiers in Pharmacology</i> , 2018, 9, 490.	1.6	17
133	Exploring the Role of Fallopian Ciliated Cells in the Pathogenesis of High-Grade Serous Ovarian Cancer. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2512.	1.8	30
134	GWAS on family history of Alzheimer's disease. <i>Translational Psychiatry</i> , 2018, 8, 99.	2.4	406
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137	<i>BMI1</i> enhancer polymorphism underlies chromosome 10p12.31 association with childhood acute lymphoblastic leukemia. <i>International Journal of Cancer</i> , 2018, 143, 2647-2658.	2.3	23
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139	Identification of five novel genetic loci related to facial morphology by genome-wide association studies. <i>BMC Genomics</i> , 2018, 19, 481.	1.2	54
140	Adiponectin and coronary artery disease risk: A bi-directional Mendelian randomization study. <i>International Journal of Cardiology</i> , 2018, 268, 222-226.	0.8	24
141	Investigating the shared genetics of non-syndromic cleft lip/palate and facial morphology. <i>PLoS Genetics</i> , 2018, 14, e1007501.	1.5	44
142	Integrative Analysis Identifies Genetic Variants Associated With Autoimmune Diseases Affecting Putative MicroRNA Binding Sites. <i>Frontiers in Genetics</i> , 2018, 9, 139.	1.1	15
143	P450 Pharmacogenetics in Indigenous North American Populations. <i>Journal of Personalized Medicine</i> , 2018, 8, 9.	1.1	22
144	Identification and functional analysis of glycemic trait loci in the China Health and Nutrition Survey. <i>PLoS Genetics</i> , 2018, 14, e1007275.	1.5	30
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146	Association of EGLN1 genetic polymorphisms with SpO2 responses to acute hypobaric hypoxia in a Japanese cohort. <i>Journal of Physiological Anthropology</i> , 2018, 37, 9.	1.0	15
147	Sex-specific glioma genome-wide association study identifies new risk locus at 3p21.31 in females, and finds sex-differences in risk at 8q24.21. <i>Scientific Reports</i> , 2018, 8, 7352.	1.6	56
148	Epigenetic supersimilarity of monozygotic twin pairs. <i>Genome Biology</i> , 2018, 19, 2.	3.8	89
149	Genome-wide association study identifies multiple new loci associated with Ewing sarcoma susceptibility. <i>Nature Communications</i> , 2018, 9, 3184.	5.8	50
150	Global genetic diversity of human apolipoproteins and effects on cardiovascular disease risk. <i>Journal of Lipid Research</i> , 2018, 59, 1987-2000.	2.0	19
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