Jianjun Liu

List of Publications by Year in descending order

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299 papers	38,591 citations	4345 89 h-index	3941 183 g-index
309 all docs	309 docs citations	309 times ranked	53736 citing authors

#	Article	IF	Citations
1	Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	2.6	24
2	Variant landscape of the RYR1 gene based on whole genome sequencing of the Singaporean population. Scientific Reports, 2022, 12, 5429.	1.6	1
3	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
4	Multiple environmental exposures and obesity in eastern China: An individual exposure evaluation model. Chemosphere, 2022, 298, 134316.	4.2	11
5	A polygenic risk score for nasopharyngeal carcinoma shows potential for risk stratification and personalized screening. Nature Communications, 2022, 13, 1966.	5.8	19
6	Interaction between cigarette smoking and genetic polymorphisms on the associations with age of natural menopause and reproductive lifespan: the Singapore Chinese Health Study. Human Reproduction, 2022, 37, 1351-1359.	0.4	3
7	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250
8	Genetic associations with healthy ageing among Chinese adults. , 2022, 8, .		1
9	Identification of shared loci associated with both Crohnâ€™s disease and leprosy in East Asians. Human Molecular Genetics, 2022, 31, 3934-3944.	1.4	5
10	Improving polygenic prediction in ancestrally diverse populations. Nature Genetics, 2022, 54, 573-580.	9.4	209
11	Shortened Telomere Length in Sputum Cells of Bronchiectasis Patients is Associated with Dysfunctional Inflammatory Pathways. Lung, 2022, 200, 401-407.	1.4	3
12	Outdoor air pollution enhanced the association between indoor air pollution exposure and hypertension in rural areas of eastern China. Environmental Science and Pollution Research, 2022, 29, 74909-74920.	2.7	4
13	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	2.0	17
14	Using off-target data from whole-exome sequencing to improve genotyping accuracy, association analysis and polygenic risk prediction. Briefings in Bioinformatics, 2021, 22, .	3.2	8
15	Midlife Leukocyte Telomere Length as an Indicator for Handgrip Strength in Late Life. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2021, 76, 172-175.	1.7	4
16	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. Human Genetics and Genomics Advances, 2021, 2, 100013.	1.0	2
17	Identification of Three Novel Susceptibility Loci for Inflammatory Bowel Disease in Koreans in an Extended Genome-Wide Association Study. Journal of Crohn's and Colitis, 2021, 15, 1898-1907.	0.6	13
18	Observed Extreme Airâ€"Sea Heat Flux Variations during Three Tropical Cyclones in the Tropical Southeastern Indian Ocean. Journal of Climate, 2021, 34, 3683-3705.	1.2	12

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19	Low frequency variants associated with leukocyte telomere length in the Singapore Chinese population. Communications Biology, 2021, 4, 519.	2.0	15
20	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
21	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. Nature Communications, 2021, 12, 3505.	5.8	49
22	The association of genetically determined serum glycine with cardiovascular risk in East Asians. Nutrition, Metabolism and Cardiovascular Diseases, 2021, 31, 1840-1844.	1.1	4
23	Discovery of Novel Genetic Risk Loci for Acute Central Serous Chorioretinopathy and Genetic Pleiotropic Effect With Age-Related Macular Degeneration. Frontiers in Cell and Developmental Biology, 2021, 9, 696885.	1.8	2
24	A comprehensive risk score for effective risk stratification and screening of nasopharyngeal carcinoma. Nature Communications, 2021, 12, 5189.	5.8	24
25	HLA Class-IIâ€'Restricted CD8+ T Cells Contribute to the Promiscuous Immune Response in Dapsone-Hypersensitive Patients. Journal of Investigative Dermatology, 2021, 141, 2412-2425.e2.	0.3	12
26	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
27	ITPKB and ZNF184 are associated with Parkinson's disease risk in East Asians. Neurobiology of Aging, 2020, 86, 201.e15-201.e17.	1.5	4
28	Analysis of 47 Non-MHC Ankylosing Spondylitis Susceptibility Loci Regarding Associated Variants across Whites and Han Chinese. Journal of Rheumatology, 2020, 47, 674-681.	1.0	4
29	Tuberculosis infection and lung adenocarcinoma: Mendelian randomization and pathway analysis of genome-wide association study data from never-smoking Asian women. Genomics, 2020, 112, 1223-1232.	1.3	15
30	Interaction between a haptoglobin genetic variant and coronary artery disease (CAD) risk factors on CAD severity in Singaporean Chinese population. Molecular Genetics & Genomic Medicine, 2020, 8, e1450.	0.6	3
31	Effect of plasma polyunsaturated fatty acid levels on leukocyte telomere lengths in the Singaporean Chinese population. Nutrition Journal, 2020, 19, 119.	1.5	16
32	Genome-Wide Association for HbA1c in Malay Identified Deletion on SLC4A1 that Influences HbA1c Independent of Glycemia. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 3854-3864.	1.8	9
33	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	4.1	17
34	Identification of type 2 diabetes loci in 433,540 East Asian individuals. Nature, 2020, 582, 240-245.	13.7	282
35	Expression Quantitative Trait Loci (eQTL) Mapping in Korean Patients With Crohnâ€™s Disease and Identification of Potential Causal Genes Through Integration With Disease Associations. Frontiers in Genetics, 2020, 11, 486.	1.1	15
36	Germline Polymorphisms and Length of Survival of Nasopharyngeal Carcinoma: An Exomeâ€Wide Association Study in Multiple Cohorts. Advanced Science, 2020, 7, 1903727.	5.6	12

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37	Plasma osteoprotegerin as a biomarker of poor glycaemic control that predicts progression of albuminuria in type 2 diabetes mellitus: A 3-year longitudinal cohort study. Diabetes Research and Clinical Practice, 2020, 161, 107992.	1.1	5
38	Association of G6PD variants with hemoglobin A1c and impact on diabetes diagnosis in East Asian individuals. BMJ Open Diabetes Research and Care, 2020, 8, e001091.	1.2	12
39	Identification of Risk Loci for Parkinson Disease in Asians and Comparison of Risk Between Asians and Europeans. JAMA Neurology, 2020, 77, 746.	4.5	170
40	Validation study of HLA-B*13:01 as a biomarker of dapsone hypersensitivity syndrome in leprosy patients in Indonesia. PLoS Neglected Tropical Diseases, 2020, 14, e0008746.	1.3	17
41	Genetic liability in individuals at ultra-high risk of psychosis: A comparison study of 9 psychiatric traits. PLoS ONE, 2020, 15, e0243104.	1.1	3
42	Title is missing!. , 2020, 14, e0008746.		0
43	Title is missing!. , 2020, 14, e0008746.		0
44	Title is missing!. , 2020, 14, e0008746.		0
45	Title is missing!. , 2020, 14, e0008746.		0
46	Large-Scale Whole-Genome Sequencing of Three Diverse Asian Populations in Singapore. Cell, 2019, 179, 736-749.e15.	13.5	126
47	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
48	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	5.8	133
49	Association of Birth Weight With Type 2 Diabetes and Glycemic Traits. JAMA Network Open, 2019, 2, e1910915.	2.8	41
50	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	1.6	85
51	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	5.8	64
52	Genome sequencing analysis identifies Epsteinâ€“Barr virus subtypes associated with high risk of nasopharyngeal carcinoma. Nature Genetics, 2019, 51, 1131-1136.	9.4	133
53	Loci for human leukocyte telomere length in the Singaporean Chinese population and trans-ethnic genetic studies. Nature Communications, 2019, 10, 2491.	5.8	64
54	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549

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55	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	13.7	248
56	Association of TRAP1 with infliximabâ€induced mucosal healing in Crohn's disease. Journal of Gastroenterology and Hepatology (Australia), 2019, 34, 2118-2125.	1.4	6
57	Evaluation of ProspectiveHLA-B*13:01Screening to Prevent Dapsone Hypersensitivity Syndrome in Patients With Leprosy. JAMA Dermatology, 2019, 155, 666.	2.0	52
58	Dapsoneâ€and nitroso dapsoneâ€specific activation of T cells from hypersensitive patients expressing the risk allele HLAâ€B*13:01. Allergy: European Journal of Allergy and Clinical Immunology, 2019, 74, 1533-1548.	2.7	37
59	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.	1.4	31
60	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	9.4	112
61	Comparative genetic architectures of schizophrenia in East Asian and European populations. Nature Genetics, 2019, 51, 1670-1678.	9.4	440
62	Evaluation of novel Parkinson's disease candidate genes in the Chinese population. Neurobiology of Aging, 2019, 74, 235.e1-235.e4.	1.5	7
63	Disruption of LRRK2 in Zebrafish leads to hyperactivity and weakened antibacterial response. Biochemical and Biophysical Research Communications, 2018, 497, 1104-1109.	1.0	15
64	Association of the novel susceptible locus rs9266150 with clinical features of psoriasis vulgaris in the Chinese Han population. Experimental Dermatology, 2018, 27, 748-753.	1.4	1
65	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.	2.6	123
66	Novel Susceptibility Loci for Moyamoya Disease Revealed by a Genome-Wide Association Study. Stroke, 2018, 49, 11-18.	1.0	66
67	A Genome-Wide Association Study of Diabetic Kidney Disease in Subjects With Type 2 Diabetes. Diabetes, 2018, 67, 1414-1427.	0.3	136
68	Immunochip Meta-Analysis of Inflammatory Bowel Disease Identifies Three Novel Loci and Four Novel Associations in Previously Reported Loci. Journal of Crohn's and Colitis, 2018, 12, 730-741.	0.6	38
69	Array-based sequencing of filaggrin gene for comprehensive detection of disease-associated variants. Journal of Allergy and Clinical Immunology, 2018, 141, 814-816.	1.5	36
70	ENPP1 Mutation Causes Recessive Cole Disease by Altering Melanogenesis. Journal of Investigative Dermatology, 2018, 138, 291-300.	0.3	23
71	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. Nature Communications, 2018, 9, 5052.	5.8	75
72	Exome Sequencing and Rare Variant Analysis RevealsÂMultiple Filaggrin Mutations in BangladeshiÂFamilies with Atopic Eczema andÂAdditional Risk Genes. Journal of Investigative Dermatology, 2018, 138, 2674-2677.	0.3	37

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73	Gene-diet interaction effects on BMI levels in the Singapore Chinese population. Nutrition Journal, 2018, 17, 31.	1.5	11
74	An Intergenic Variant rs9268877 Between HLA-DRA and HLA-DRB Contributes to the Clinical Course and Long-term Outcome of Ulcerative Colitis. Journal of Crohn's and Colitis, 2018, 12, 1113-1121.	0.6	12
75	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	1.1	94
76	Meta-analysis of three genome-wide association studies identifies two loci that predict survival and treatment outcome in breast cancer. Oncotarget, 2018, 9, 4249-4257.	0.8	8
77	Genome-wide association study of Parkinsonâ€™s disease in East Asians. Human Molecular Genetics, 2017, 26, ddw379.	1.4	94
78	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	3.4	376
79	Genome-wide analyses of non-syndromic cleft lip with palate identify 14 novel loci and genetic heterogeneity. Nature Communications, 2017, 8, 14364.	5.8	207
80	Association analyses of East Asian individuals and trans-ancestry analyses with European individuals reveal new loci associated with cholesterol and triglyceride levels. Human Molecular Genetics, 2017, 26, 1770-1784.	1.4	135
81	Possible Interaction Between Cigarette Smoking and HLA-DRB1 Variation in the Risk of Follicular Lymphoma. American Journal of Epidemiology, 2017, 185, 681-687.	1.6	10
82	Arterial stiffness is an independent predictor for albuminuria progression among Asians with type 2 diabetesâ€”A prospective cohort study. Journal of Diabetes and Its Complications, 2017, 31, 933-938.	1.2	20
83	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.3	47
84	Genome-Wide Association Study Meta-Analysis of Long-Term Average Blood Pressure in East Asians. Circulation: Cardiovascular Genetics, 2017, 10, e001527.	5.1	26
85	Integration of expression quantitative trait loci and pleiotropy identifies a novel psoriasis susceptibility gene, PTPN1. Journal of Gene Medicine, 2017, 19, e2939.	1.4	5
86	Exome chip meta-analysis identifies novel loci and East Asianâ€“specific coding variants that contribute to lipid levels and coronary artery disease. Nature Genetics, 2017, 49, 1722-1730.	9.4	129
87	Genome-Wide Analysis of Protein-Coding Variants in Leprosy. Journal of Investigative Dermatology, 2017, 137, 2544-2551.	0.3	37
88	Association Analysis of the MHC in Lupus Nephritis. Journal of the American Society of Nephrology: JASN, 2017, 28, 3383-3394.	3.0	21
89	Genetic association of telomere length with hepatocellular carcinoma risk: A Mendelian randomization analysis. Cancer Epidemiology, 2017, 50, 39-45.	0.8	14
90	Germline variation in ADAMTSL1 is associated with prognosis following breast cancer treatment in young women. Nature Communications, 2017, 8, 1632.	5.8	18

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91	Utility of genetic and non-genetic risk factors in predicting coronary heart disease in Singaporean Chinese. European Journal of Preventive Cardiology, 2017, 24, 153-160.	0.8	11
92	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
93	Genome-wide association study identifies a missense variant at APOA5 for coronary artery disease in Multi-Ethnic Cohorts from Southeast Asia. Scientific Reports, 2017, 7, 17921.	1.6	28
94	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. PLoS Medicine, 2017, 14, e1002383.	3.9	341
95	Estimation of kinship coefficient in structured and admixed populations using sparse sequencing data. PLoS Genetics, 2017, 13, e1007021.	1.5	27
96	TP53-based interaction analysis identifies cis-eQTL variants for TP53BP2, FBXO28, and FAM53A that associate with survival and treatment outcome in breast cancer. Oncotarget, 2017, 8, 18381-18398.	0.8	14
97	Common susceptibility variants are shared between schizophrenia and psoriasis in the Han Chinese population. Journal of Psychiatry and Neuroscience, 2016, 41, 413-421.	1.4	19
98	Identification of Ten Additional Susceptibility Loci for Ulcerative Colitis Through Immunochip Analysis in Koreans. Inflammatory Bowel Diseases, 2016, 22, 13-19.	0.9	40
99	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
100	Patient survival and tumor characteristics associated with CHEK2:p.I157T â€“ findings from the Breast Cancer Association Consortium. Breast Cancer Research, 2016, 18, 98.	2.2	39
101	Association between GWAS-identified lung adenocarcinoma susceptibility loci andEGFRmutations in never-smoking Asian women, and comparison with findings from Western populations. Human Molecular Genetics, 2016, 26, ddw414.	1.4	50
102	A large-scale genome-wide association and meta-analysis identified four novel susceptibility loci for leprosy. Nature Communications, 2016, 7, 13760.	5.8	54
103	The HLA Alleles B*0801 and DRB1*0301 Are Associated with Dermatitis Herpetiformis in a Chinese Population. Journal of Investigative Dermatology, 2016, 136, 530-532.	0.3	7
104	Deep sequencing of the MHC region in the Chinese population contributes to studies of complex disease. Nature Genetics, 2016, 48, 740-746.	9.4	188
105	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. Cancer Research, 2016, 76, 5103-5114.	0.4	100
106	Genetic risk of extranodal natural killer T-cell lymphoma: a genome-wide association study. Lancet Oncology, The, 2016, 17, 1240-1247.	5.1	84
107	Association study confirms two susceptibility loci for breast cancer in Chinese Han women. Breast Cancer Research and Treatment, 2016, 159, 433-442.	1.1	5
108	Identification of Loci at 1q21 and 16q23 That Affect Susceptibility to Inflammatory Bowel Disease in Koreans. Gastroenterology, 2016, 151, 1096-1099.e4.	0.6	30

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109	Interaction Between Peroxisome Proliferator Activated Receptor Î´ and Epithelial Membrane Protein 2 Polymorphisms Influences HDLâ€€ Levels in the Chinese Population. Annals of Human Genetics, 2016, 80, 282-293.	0.3	1
110	Low Î±-defensin gene copy number increases the risk for IgA nephropathy and renal dysfunction. Science Translational Medicine, 2016, 8, 345ra88.	5.8	35
111	An extended genome-wide association study identifies novel susceptibility loci for nasopharyngeal carcinoma. Human Molecular Genetics, 2016, 25, 3626-3634.	1.4	42
112	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	5.8	86
113	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
114	Fine-mapping analysis revealed complex pleiotropic effect and tissue-specific regulatory mechanism of TNFSF15 in primary biliary cholangitis, Crohnâ€™s disease and leprosy. Scientific Reports, 2016, 6, 31429.	1.6	15
115	Linking a genomeâ€wide association study signal to a LRRK2 coding variant in Parkinson's disease. Movement Disorders, 2016, 31, 484-487.	2.2	8
116	Preparation and catalytic performance of a novelÂhighly dispersed bifunctional catalyst Pt@Fe-MCM-41. RSC Advances, 2016, 6, 13461-13468.	1.7	11
117	Meta-analysis of genome-wide association studies identifies multiple lung cancer susceptibility loci in never-smoking Asian women. Human Molecular Genetics, 2016, 25, 620-629.	1.4	50
118	Functional variants of 17q12-21 are associated with allergic asthma but not allergic rhinitis. Journal of Allergy and Clinical Immunology, 2016, 137, 758-766.e3.	1.5	34
119	Fine mapping the MHC region identified four independent variants modifying susceptibility to chronic hepatitis B in Han Chinese. Human Molecular Genetics, 2016, 25, 1225-1232.	1.4	33
120	Evaluation of transethnic fine mapping with population-specific and cosmopolitan imputation reference panels in diverse Asian populations. European Journal of Human Genetics, 2016, 24, 592-599.	1.4	4
121	A genome-wide association study of n-3 and n-6 plasma fatty acids in a Singaporean Chinese population. Genes and Nutrition, 2015, 10, 53.	1.2	53
122	A polymorphism in the base excision repair gene PARP2 is associated with differential prognosis by chemotherapy among postmenopausal breast cancer patients. BMC Cancer, 2015, 15, 978.	1.1	6
123	<scp>G</scp>enetic variants associated with longer telomere length are associated with increased lung cancer risk among neverâ€smoking women in Asia: a report from the female lung cancer consortium in Asia. International Journal of Cancer, 2015, 137, 311-319.	2.3	72
124	Analysis of Heritability and Shared Heritability Based on Genome-Wide Association Studies for Thirteen Cancer Types. Journal of the National Cancer Institute, 2015, 107, djv279.	3.0	152
125	Genetics of Type 2 Diabetes and Clinical Utility. Genes, 2015, 6, 372-384.	1.0	34
126	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428

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127	Genome-wide meta-analysis identifies multiple novel associations and ethnic heterogeneity of psoriasis susceptibility. Nature Communications, 2015, 6, 6916.	5.8	154
128	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	2.6	101
129	Polymorphism at 19q13.41 Predicts Breast Cancer Survival Specifically after Endocrine Therapy. Clinical Cancer Research, 2015, 21, 4086-4096.	3.2	12
130	A common variant near TGFBR3 is associated with primary open angle glaucoma. Human Molecular Genetics, 2015, 24, 3880-3892.	1.4	105
131	Genome-Wide Association Meta-analysis Identifies Novel Variants Associated With Fasting Plasma Glucose in East Asians. Diabetes, 2015, 64, 291-298.	0.3	59
132	Genetic variants of inducible costimulator are associated with allergic asthma susceptibility. Journal of Allergy and Clinical Immunology, 2015, 135, 556-558.e13.	1.5	4
133	New loci and coding variants confer risk for age-related macular degeneration in East Asians. Nature Communications, 2015, 6, 6063.	5.8	147
134	A functional brain-derived neurotrophic factor (BDNF) gene variant increases the risk of moderate-to-severe allergic rhinitis. Journal of Allergy and Clinical Immunology, 2015, 135, 1486-1493.e8.	1.5	24
135	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
136	Discovery of six new susceptibility loci and analysis of pleiotropic effects in leprosy. Nature Genetics, 2015, 47, 267-271.	9.4	103
137	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	9.4	513
138	Synthesis, characterization and catalytic performance of well-ordered mesoporous Ni-MCM-41 with high nickel content. Microporous and Mesoporous Materials, 2015, 208, 181-187.	2.2	38
139	Improving power for robust trans-ethnic meta-analysis of rare and low-frequency variants with a partitioning approach. European Journal of Human Genetics, 2015, 23, 238-244.	1.4	3
140	Interaction effects between Paraoxonase 1 variants and cigarette smoking on risk of coronary heart disease in a Singaporean Chinese population. Atherosclerosis, 2015, 240, 40-45.	0.4	17
141	Candidate locus analysis of the TERTâ€“CLPTM1L cancer risk region on chromosome 5p15 identifies multiple independent variants associated with endometrial cancer risk. Human Genetics, 2015, 134, 231-245.	1.8	34
142	Immunochip Analysis Identification of 6 Additional Susceptibility Loci for CrohnÊ¼s Disease in Koreans. Inflammatory Bowel Diseases, 2015, 21, 1-7.	0.9	60
143	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.	9.4	294
144	Genome-wide analysis of the genetic regulation of gene expression in human neutrophils. Nature Communications, 2015, 6, 7971.	5.8	23

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145	Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. Human Molecular Genetics, 2015, 24, 1791-1800.	1.4	105
146	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. Human Molecular Genetics, 2015, 24, 285-298.	1.4	38
147	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. Human Molecular Genetics, 2015, 24, 1478-1492.	1.4	50
148	The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients. Oncotarget, 2015, 6, 7390-7407.	0.8	15
149	A Genome Wide Meta-Analysis Study for Identification of Common Variation Associated with Breast Cancer Prognosis. PLoS ONE, 2014, 9, e101488.	1.1	42
150	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	1.1	49
151	A comprehensive association analysis confirmsZMIZ1to be a susceptibility gene for vitiligo in Chinese population. Journal of Medical Genetics, 2014, 51, 345-353.	1.5	21
152	Multiple Nonglycemic Genomic Loci Are Newly Associated With Blood Level of Glycated Hemoglobin in East Asians. Diabetes, 2014, 63, 2551-2562.	0.3	61
153	Analysis of non-synonymous-coding variants of Parkinson's disease-related pathogenic and susceptibility genes in East Asian populations. Human Molecular Genetics, 2014, 23, 3891-3897.	1.4	28
154	A meta-analysis of genome-wide association studies for adiponectin levels in East Asians identifies a novel locus near WDR11-FGFR2. Human Molecular Genetics, 2014, 23, 1108-1119.	1.4	68
155	iCall: a genotype-calling algorithm for rare, low-frequency and common variants on the Illumina exome array. Bioinformatics, 2014, 30, 1714-1720.	1.8	2
156	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. Nature Communications, 2014, 5, 4051.	5.8	16
157	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. Human Molecular Genetics, 2014, 23, 6616-6633.	1.4	90
158	A comprehensive evaluation of the role of genetic variation in follicular lymphoma survival. BMC Medical Genetics, 2014, 15, 113.	2.1	17
159	Breast cancer risk assessment using genetic variants and risk factors in a Singapore Chinese population. Breast Cancer Research, 2014, 16, R64.	2.2	30
160	A Genome-wide Association Study of Early-Onset Breast Cancer Identifies PFKM as a Novel Breast Cancer Gene and Supports a Common Genetic Spectrum for Breast Cancer at Any Age. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 658-669.	1.1	77
161	Genome-wide association study identifies 25 known breast cancer susceptibility loci as risk factors for triple-negative breast cancer. Carcinogenesis, 2014, 35, 1012-1019.	1.3	145
162	A large-scale screen for coding variants predisposing to psoriasis. Nature Genetics, 2014, 46, 45-50.	9.4	183

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163	Genome-wide Association Study Identifies Five Susceptibility Loci for Follicular Lymphoma outside the HLA Region. American Journal of Human Genetics, 2014, 95, 462-471.	2.6	96
164	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.	2.6	109
165	A common missense variant in NUDT15 confers susceptibility to thiopurine-induced leukopenia. Nature Genetics, 2014, 46, 1017-1020.	9.4	438
166	Genome-wide association study of Crohn's disease in Koreans revealed three new susceptibility loci and common attributes of genetic susceptibility across ethnic populations. Gut, 2014, 63, 80-87.	6.1	157
167	Synthesis and properties of acrylonitrile-methyl itaconate copolymers as spun carbon fiber precursors. Fibers and Polymers, 2014, 15, 1583-1588.	1.1	4
168	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
169	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	1.4	12
170	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. Breast Cancer Research, 2014, 16, R51.	2.2	14
171	Genome-Wide Linkage, Exome Sequencing and Functional Analyses Identify ABCB6 as the Pathogenic Gene of Dyschromatosis Universalis Hereditaria. PLoS ONE, 2014, 9, e87250.	1.1	28
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173	Analysis of POFUT1 Gene Mutation in a Chinese Family with Dowling-Degos Disease. PLoS ONE, 2014, 9, e104496.	1.1	8
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