

Jianjun Liu

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

300
papers

28,812
citations

80
h-index

166
g-index

309
ext. papers

34,117
ext. citations

11.8
avg. IF

5.16
L-index

#	Paper	IF	Citations
300	Variant landscape of the RYR1 gene based on whole genome sequencing of the Singaporean population.. <i>Scientific Reports</i> , 2022 , 12, 5429	4.9	
299	Mapping genomic loci implicates genes and synaptic biology in schizophrenia.. <i>Nature</i> , 2022 ,	50.4	35
298	Multiple environmental exposures and obesity in eastern China: An individual exposure evaluation model.. <i>Chemosphere</i> , 2022 , 134316	8.4	0
297	A polygenic risk score for nasopharyngeal carcinoma shows potential for risk stratification and personalized screening.. <i>Nature Communications</i> , 2022 , 13, 1966	17.4	0
296	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. <i>Nature Genetics</i> , 2022 ,	36.3	7
295	Genetic associations with healthy ageing among Chinese adults 2022 , 8,		
294	Improving polygenic prediction in ancestrally diverse populations.. <i>Nature Genetics</i> , 2022 , 54, 573-580	36.3	5
293	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022 , 5,	6.7	1
292	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. <i>Molecular Psychiatry</i> , 2021 , 26, 2111-2125	15.1	3
291	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021 ,	50.4	24
290	Identification of Three Novel Susceptibility Loci for Inflammatory Bowel Disease in Koreans in an Extended Genome-Wide Association Study. <i>Journal of Crohns and Colitis</i> , 2021 , 15, 1898-1907	1.5	0
289	Observed Extreme AirSea Heat Flux Variations during Three Tropical Cyclones in the Tropical Southeastern Indian Ocean. <i>Journal of Climate</i> , 2021 , 34, 3683-3705	4.4	0
288	Low frequency variants associated with leukocyte telomere length in the Singapore Chinese population. <i>Communications Biology</i> , 2021 , 4, 519	6.7	2
287	The trans-ancestral genomic architecture of glycemc traits. <i>Nature Genetics</i> , 2021 , 53, 840-860	36.3	44
286	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. <i>Nature Communications</i> , 2021 , 12, 3505	17.4	5
285	The association of genetically determined serum glycine with cardiovascular risk in East Asians. <i>Nutrition, Metabolism and Cardiovascular Diseases</i> , 2021 , 31, 1840-1844	4.5	0
284	Using off-target data from whole-exome sequencing to improve genotyping accuracy, association analysis and polygenic risk prediction. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	3

283	Midlife Leukocyte Telomere Length as an Indicator for Handgrip Strength in Late Life. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2021 , 76, 172-175	6.4	1
282	Discovery of Novel Genetic Risk Loci for Acute Central Serous Chorioretinopathy and Genetic Pleiotropic Effect With Age-Related Macular Degeneration. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 696885	5.7	1
281	A comprehensive risk score for effective risk stratification and screening of nasopharyngeal carcinoma. <i>Nature Communications</i> , 2021 , 12, 5189	17.4	5
280	HLA Class-II-Restricted CD8 T Cells Contribute to the Promiscuous Immune Response in Dapsone-Hypersensitive Patients. <i>Journal of Investigative Dermatology</i> , 2021 , 141, 2412-2425.e2	4.3	4
279	Identification of type 2 diabetes loci in 433,540 East Asian individuals. <i>Nature</i> , 2020 , 582, 240-245	50.4	89
278	Expression Quantitative Trait Loci (eQTL) Mapping in Korean Patients With Crohn's Disease and Identification of Potential Causal Genes Through Integration With Disease Associations. <i>Frontiers in Genetics</i> , 2020 , 11, 486	4.5	4
277	Germline Polymorphisms and Length of Survival of Nasopharyngeal Carcinoma: An Exome-Wide Association Study in Multiple Cohorts. <i>Advanced Science</i> , 2020 , 7, 1903727	13.6	4
276	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. <i>Diabetes Research and Clinical Practice</i> , 2020 , 161, 107992	7.4	1
275	Association of variants with hemoglobin A1c and impact on diabetes diagnosis in East Asian individuals. <i>BMJ Open Diabetes Research and Care</i> , 2020 , 8,	4.5	7
274	Validation study of HLA-B*13:01 as a biomarker of dapson hypersensitivity syndrome in leprosy patients in Indonesia. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0008746	4.8	5
273	Genetic liability in individuals at ultra-high risk of psychosis: A comparison study of 9 psychiatric traits. <i>PLoS ONE</i> , 2020 , 15, e0243104	3.7	1
272	Interaction between a haptoglobin genetic variant and coronary artery disease (CAD) risk factors on CAD severity in Singaporean Chinese population. <i>Molecular Genetics & Genomic Medicine</i> , 2020 , 8, e1450	2.3	1
271	Effect of plasma polyunsaturated fatty acid levels on leukocyte telomere lengths in the Singaporean Chinese population. <i>Nutrition Journal</i> , 2020 , 19, 119	4.3	3
270	Genome-Wide Association for HbA1c in Malay Identified Deletion on SLC4A1 that Influences HbA1c Independent of Glycemia. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020 , 105,	5.6	4
269	ITPKB and ZNF184 are associated with Parkinson's disease risk in East Asians. <i>Neurobiology of Aging</i> , 2020 , 86, 201.e15-201.e17	5.6	2
268	Analysis of 47 Non-MHC Ankylosing Spondylitis Susceptibility Loci Regarding Associated Variants across Whites and Han Chinese. <i>Journal of Rheumatology</i> , 2020 , 47, 674-681	4.1	1
267	Tuberculosis infection and lung adenocarcinoma: Mendelian randomization and pathway analysis of genome-wide association study data from never-smoking Asian women. <i>Genomics</i> , 2020 , 112, 1223-1232	4.3	8
266	Identification of Risk Loci for Parkinson Disease in Asians and Comparison of Risk Between Asians and Europeans: A Genome-Wide Association Study. <i>JAMA Neurology</i> , 2020 , 77, 746-754	17.2	84

265	Validation study of HLA-B*13:01 as a biomarker of dapson hypersensitivity syndrome in leprosy patients in Indonesia 2020 , 14, e0008746		
264	Validation study of HLA-B*13:01 as a biomarker of dapson hypersensitivity syndrome in leprosy patients in Indonesia 2020 , 14, e0008746		
263	Validation study of HLA-B*13:01 as a biomarker of dapson hypersensitivity syndrome in leprosy patients in Indonesia 2020 , 14, e0008746		
262	Validation study of HLA-B*13:01 as a biomarker of dapson hypersensitivity syndrome in leprosy patients in Indonesia 2020 , 14, e0008746		
261	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019 , 10, 4130	17.4	43
260	Association of Birth Weight With Type 2 Diabetes and Glycemic Traits: A Mendelian Randomization Study. <i>JAMA Network Open</i> , 2019 , 2, e1910915	10.4	14
259	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019 , 188, 1033-1054	3.8	39
258	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019 , 10, 376	17.4	41
257	Genome sequencing analysis identifies Epstein-Barr virus subtypes associated with high risk of nasopharyngeal carcinoma. <i>Nature Genetics</i> , 2019 , 51, 1131-1136	36.3	70
256	Loci for human leukocyte telomere length in the Singaporean Chinese population and trans-ethnic genetic studies. <i>Nature Communications</i> , 2019 , 10, 2491	17.4	29
255	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019 , 51, 957-972	36.3	217
254	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019 , 570, 71-76	50.4	129
253	Association of TRAP1 with infliximab-induced mucosal healing in Crohn's disease. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2019 , 34, 2118-2125	4	1
252	Evaluation of Prospective HLA-B*13:01 Screening to Prevent Dapsone Hypersensitivity Syndrome in Patients With Leprosy. <i>JAMA Dermatology</i> , 2019 , 155, 666-672	5.1	29
251	Dapsone- and nitroso dapsone-specific activation of T cells from hypersensitive patients expressing the risk allele HLA-B*13:01. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2019 , 74, 1533-1548	9.3	19
250	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. <i>Human Molecular Genetics</i> , 2019 , 28, 2615-2633	5.6	14
249	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019 , 51, 636-648	36.3	59
248	Large-Scale Whole-Genome Sequencing of Three Diverse Asian Populations in Singapore. <i>Cell</i> , 2019 , 179, 736-749.e15	56.2	51

247	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019 , 10, 4957	17.4	40
246	Comparative genetic architectures of schizophrenia in East Asian and European populations. <i>Nature Genetics</i> , 2019 , 51, 1670-1678	36.3	185
245	Evaluation of novel Parkinson disease candidate genes in the Chinese population. <i>Neurobiology of Aging</i> , 2019 , 74, 235.e1-235.e4	5.6	5
244	Disruption of LRRK2 in Zebrafish leads to hyperactivity and weakened antibacterial response. <i>Biochemical and Biophysical Research Communications</i> , 2018 , 497, 1104-1109	3.4	11
243	Association of the novel susceptible locus rs9266150 with clinical features of psoriasis vulgaris in the Chinese Han population. <i>Experimental Dermatology</i> , 2018 , 27, 748-753	4	1
242	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018 , 102, 375-400	11	59
241	Novel Susceptibility Loci for Moyamoya Disease Revealed by a Genome-Wide Association Study. <i>Stroke</i> , 2018 , 49, 11-18	6.7	31
240	A Genome-Wide Association Study of Diabetic Kidney Disease in Subjects With Type 2 Diabetes. <i>Diabetes</i> , 2018 , 67, 1414-1427	0.9	71
239	ImmunoChip Meta-Analysis of Inflammatory Bowel Disease Identifies Three Novel Loci and Four Novel Associations in Previously Reported Loci. <i>Journal of Crohns and Colitis</i> , 2018 , 12, 730-741	1.5	16
238	Array-based sequencing of filaggrin gene for comprehensive detection of disease-associated variants. <i>Journal of Allergy and Clinical Immunology</i> , 2018 , 141, 814-816	11.5	26
237	ENPP1 Mutation Causes Recessive Cole Disease by Altering Melanogenesis. <i>Journal of Investigative Dermatology</i> , 2018 , 138, 291-300	4.3	11
236	Exome Sequencing and Rare Variant Analysis Reveals Multiple Filaggrin Mutations in Bangladeshi Families with Atopic Eczema and Additional Risk Genes. <i>Journal of Investigative Dermatology</i> , 2018 , 138, 2674-2677	4.3	19
235	Gene-diet interaction effects on BMI levels in the Singapore Chinese population. <i>Nutrition Journal</i> , 2018 , 17, 31	4.3	7
234	An Intergenic Variant rs9268877 Between HLA-DRA and HLA-DRB Contributes to the Clinical Course and Long-term Outcome of Ulcerative Colitis. <i>Journal of Crohns and Colitis</i> , 2018 , 12, 1113-1121	1.5	10
233	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018 , 13, e0198166	3.7	31
232	Meta-analysis of three genome-wide association studies identifies two loci that predict survival and treatment outcome in breast cancer. <i>Oncotarget</i> , 2018 , 9, 4249-4257	3.3	8
231	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. <i>Nature Communications</i> , 2018 , 9, 5052	17.4	29
230	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases: A Mendelian Randomization Study. <i>JAMA Oncology</i> , 2017 , 3, 636-651	13.4	236

229	Genome-wide analyses of non-syndromic cleft lip with palate identify 14 novel loci and genetic heterogeneity. <i>Nature Communications</i> , 2017 , 8, 14364	17.4	131
228	Association analyses of East Asian individuals and trans-ancestry analyses with European individuals reveal new loci associated with cholesterol and triglyceride levels. <i>Human Molecular Genetics</i> , 2017 , 26, 1770-1784	5.6	90
227	Possible Interaction Between Cigarette Smoking and HLA-DRB1 Variation in the Risk of Follicular Lymphoma. <i>American Journal of Epidemiology</i> , 2017 , 185, 681-687	3.8	7
226	Arterial stiffness is an independent predictor for albuminuria progression among Asians with type 2 diabetes-A prospective cohort study. <i>Journal of Diabetes and Its Complications</i> , 2017 , 31, 933-938	3.2	15
225	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017 , 66, 2019-2032	0.9	29
224	Genome-Wide Association Study Meta-Analysis of Long-Term Average Blood Pressure in East Asians. <i>Circulation: Cardiovascular Genetics</i> , 2017 , 10, e001527		20
223	Integration of expression quantitative trait loci and pleiotropy identifies a novel psoriasis susceptibility gene, PTPN1. <i>Journal of Gene Medicine</i> , 2017 , 19, e2939	3.5	3
222	Exome chip meta-analysis identifies novel loci and East Asian-specific coding variants that contribute to lipid levels and coronary artery disease. <i>Nature Genetics</i> , 2017 , 49, 1722-1730	36.3	83
221	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. <i>PLoS Medicine</i> , 2017 , 14, e1002383	11.6	223
220	Estimation of kinship coefficient in structured and admixed populations using sparse sequencing data. <i>PLoS Genetics</i> , 2017 , 13, e1007021	6	13
219	Genome-Wide Analysis of Protein-Coding Variants in Leprosy. <i>Journal of Investigative Dermatology</i> , 2017 , 137, 2544-2551	4.3	26
218	Association Analysis of the MHC in Lupus Nephritis. <i>Journal of the American Society of Nephrology: JASN</i> , 2017 , 28, 3383-3394	12.7	13
217	Genetic association of telomere length with hepatocellular carcinoma risk: A Mendelian randomization analysis. <i>Cancer Epidemiology</i> , 2017 , 50, 39-45	2.8	10
216	Germline variation in ADAMTSL1 is associated with prognosis following breast cancer treatment in young women. <i>Nature Communications</i> , 2017 , 8, 1632	17.4	13
215	Utility of genetic and non-genetic risk factors in predicting coronary heart disease in Singaporean Chinese. <i>European Journal of Preventive Cardiology</i> , 2017 , 24, 153-160	3.9	9
214	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017 , 4, 170179	8.2	22
213	Genome-wide association study identifies a missense variant at APOA5 for coronary artery disease in Multi-Ethnic Cohorts from Southeast Asia. <i>Scientific Reports</i> , 2017 , 7, 17921	4.9	14
212	TP53-based interaction analysis identifies cis-eQTL variants for TP53BP2, FBXO28, and FAM53A that associate with survival and treatment outcome in breast cancer. <i>Oncotarget</i> , 2017 , 8, 18381-18398	3.3	7

211	Genome-wide association study of Parkinson's disease in East Asians. <i>Human Molecular Genetics</i> , 2017 , 26, 226-232	5.6	75
210	Association between GWAS-identified lung adenocarcinoma susceptibility loci and EGFR mutations in never-smoking Asian women, and comparison with findings from Western populations. <i>Human Molecular Genetics</i> , 2017 , 26, 454-465	5.6	40
209	Evaluation of transethnic fine mapping with population-specific and cosmopolitan imputation reference panels in diverse Asian populations. <i>European Journal of Human Genetics</i> , 2016 , 24, 592-9	5.3	4
208	Association study confirms two susceptibility loci for breast cancer in Chinese Han women. <i>Breast Cancer Research and Treatment</i> , 2016 , 159, 433-42	4.4	3
207	Identification of Loci at 1q21 and 16q23 That Affect Susceptibility to Inflammatory Bowel Disease in Koreans. <i>Gastroenterology</i> , 2016 , 151, 1096-1099.e4	13.3	22
206	Interaction Between Peroxisome Proliferator Activated Receptor α and Epithelial Membrane Protein 2 Polymorphisms Influences HDL-C Levels in the Chinese Population. <i>Annals of Human Genetics</i> , 2016 , 80, 282-93	2.2	
205	Low Hfe defensin gene copy number increases the risk for IgA nephropathy and renal dysfunction. <i>Science Translational Medicine</i> , 2016 , 8, 345ra88	17.5	21
204	An extended genome-wide association study identifies novel susceptibility loci for nasopharyngeal carcinoma. <i>Human Molecular Genetics</i> , 2016 , 25, 3626-3634	5.6	27
203	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. <i>Nature Communications</i> , 2016 , 7, 11843	17.4	59
202	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016 , 7, 11375	17.4	64
201	Fine-mapping analysis revealed complex pleiotropic effect and tissue-specific regulatory mechanism of TNFSF15 in primary biliary cholangitis, Crohn's disease and leprosy. <i>Scientific Reports</i> , 2016 , 6, 31429	4.9	9
200	Linking a genome-wide association study signal to a LRRK2 coding variant in Parkinson's disease. <i>Movement Disorders</i> , 2016 , 31, 484-7	7	8
199	Preparation and catalytic performance of a novel highly dispersed bifunctional catalyst Pt@Fe-MCM-41. <i>RSC Advances</i> , 2016 , 6, 13461-13468	3.7	8
198	Meta-analysis of genome-wide association studies identifies multiple lung cancer susceptibility loci in never-smoking Asian women. <i>Human Molecular Genetics</i> , 2016 , 25, 620-9	5.6	32
197	Functional variants of 17q12-21 are associated with allergic asthma but not allergic rhinitis. <i>Journal of Allergy and Clinical Immunology</i> , 2016 , 137, 758-66.e3	11.5	24
196	Fine mapping the MHC region identified four independent variants modifying susceptibility to chronic hepatitis B in Han Chinese. <i>Human Molecular Genetics</i> , 2016 , 25, 1225-32	5.6	24
195	Common susceptibility variants are shared between schizophrenia and psoriasis in the Han Chinese population. <i>Journal of Psychiatry and Neuroscience</i> , 2016 , 41, 413-421	4.5	10
194	Identification of Ten Additional Susceptibility Loci for Ulcerative Colitis Through ImmunoChip Analysis in Koreans. <i>Inflammatory Bowel Diseases</i> , 2016 , 22, 13-9	4.5	30

193	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016 , 536, 41-47	50.4	704
192	Patient survival and tumor characteristics associated with CHEK2:p.I157T - findings from the Breast Cancer Association Consortium. <i>Breast Cancer Research</i> , 2016 , 18, 98	8.3	26
191	A large-scale genome-wide association and meta-analysis identified four novel susceptibility loci for leprosy. <i>Nature Communications</i> , 2016 , 7, 13760	17.4	37
190	The HLA Alleles B*0801 and DRB1*0301 Are Associated with Dermatitis Herpetiformis in a Chinese Population. <i>Journal of Investigative Dermatology</i> , 2016 , 136, 530-532	4.3	3
189	Deep sequencing of the MHC region in the Chinese population contributes to studies of complex disease. <i>Nature Genetics</i> , 2016 , 48, 740-6	36.3	129
188	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. <i>Cancer Research</i> , 2016 , 76, 5103-14	10.1	66
187	Genetic risk of extranodal natural killer T-cell lymphoma: a genome-wide association study. <i>Lancet Oncology</i> , 2016 , 17, 1240-7	21.7	58
186	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , 2015 , 47, 373-80	36.3	406
185	Synthesis, characterization and catalytic performance of well-ordered mesoporous Ni-MCM-41 with high nickel content. <i>Microporous and Mesoporous Materials</i> , 2015 , 208, 181-187	5.3	37
184	Improving power for robust trans-ethnic meta-analysis of rare and low-frequency variants with a partitioning approach. <i>European Journal of Human Genetics</i> , 2015 , 23, 238-44	5.3	2
183	Interaction effects between Paraoxonase 1 variants and cigarette smoking on risk of coronary heart disease in a Singaporean Chinese population. <i>Atherosclerosis</i> , 2015 , 240, 40-5	3.1	14
182	Candidate locus analysis of the TERT-CLPTM1L cancer risk region on chromosome 5p15 identifies multiple independent variants associated with endometrial cancer risk. <i>Human Genetics</i> , 2015 , 134, 231-45	6.3	30
181	ImmunoChip analysis identification of 6 additional susceptibility loci for Crohn's disease in Koreans. <i>Inflammatory Bowel Diseases</i> , 2015 , 21, 1-7	4.5	43
180	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. <i>Nature Genetics</i> , 2015 , 47, 1282-1293	36.3	223
179	Genome-wide analysis of the genetic regulation of gene expression in human neutrophils. <i>Nature Communications</i> , 2015 , 6, 7971	17.4	21
178	Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. <i>Human Molecular Genetics</i> , 2015 , 24, 1791-800	5.6	71
177	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. <i>Human Molecular Genetics</i> , 2015 , 24, 285-98	5.6	35
176	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. <i>Human Molecular Genetics</i> , 2015 , 24, 1478-92	5.6	46

175	A genome-wide association study of n-3 and n-6 plasma fatty acids in a Singaporean Chinese population. <i>Genes and Nutrition</i> , 2015 , 10, 53	4.3	35
174	A polymorphism in the base excision repair gene PARP2 is associated with differential prognosis by chemotherapy among postmenopausal breast cancer patients. <i>BMC Cancer</i> , 2015 , 15, 978	4.8	6
173	Genetic variants associated with longer telomere length are associated with increased lung cancer risk among never-smoking women in Asia: a report from the female lung cancer consortium in Asia. <i>International Journal of Cancer</i> , 2015 , 137, 311-9	7.5	55
172	Analysis of Heritability and Shared Heritability Based on Genome-Wide Association Studies for Thirteen Cancer Types. <i>Journal of the National Cancer Institute</i> , 2015 , 107, djv279	9.7	107
171	Genetics of Type 2 Diabetes and Clinical Utility. <i>Genes</i> , 2015 , 6, 372-84	4.2	26
170	Prediction of breast cancer risk based on profiling with common genetic variants. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	324
169	Genome-wide meta-analysis identifies multiple novel associations and ethnic heterogeneity of psoriasis susceptibility. <i>Nature Communications</i> , 2015 , 6, 6916	17.4	115
168	Characterization of large structural genetic mosaicism in human autosomes. <i>American Journal of Human Genetics</i> , 2015 , 96, 487-97	11	77
167	Polymorphism at 19q13.41 Predicts Breast Cancer Survival Specifically after Endocrine Therapy. <i>Clinical Cancer Research</i> , 2015 , 21, 4086-4096	12.9	10
166	A common variant near TGFBR3 is associated with primary open angle glaucoma. <i>Human Molecular Genetics</i> , 2015 , 24, 3880-92	5.6	84
165	Genome-wide association meta-analysis identifies novel variants associated with fasting plasma glucose in East Asians. <i>Diabetes</i> , 2015 , 64, 291-8	0.9	43
164	Genetic variants of inducible costimulator are associated with allergic asthma susceptibility. <i>Journal of Allergy and Clinical Immunology</i> , 2015 , 135, 556-8	11.5	3
163	New loci and coding variants confer risk for age-related macular degeneration in East Asians. <i>Nature Communications</i> , 2015 , 6, 6063	17.4	118
162	A functional brain-derived neurotrophic factor (BDNF) gene variant increases the risk of moderate-to-severe allergic rhinitis. <i>Journal of Allergy and Clinical Immunology</i> , 2015 , 135, 1486-93.e8	11.5	19
161	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015 , 24, 2966-84	5.6	36
160	Discovery of six new susceptibility loci and analysis of pleiotropic effects in leprosy. <i>Nature Genetics</i> , 2015 , 47, 267-71	36.3	86
159	The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients. <i>Oncotarget</i> , 2015 , 6, 7390-407	3.3	14
158	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. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014 , 23, 658-69	4	63

157	Genome-wide association study identifies 25 known breast cancer susceptibility loci as risk factors for triple-negative breast cancer. <i>Carcinogenesis</i> , 2014 , 35, 1012-9	4.6	121
156	A large-scale screen for coding variants predisposing to psoriasis. <i>Nature Genetics</i> , 2014 , 46, 45-50	36.3	148
155	Genome-wide association study identifies five susceptibility loci for follicular lymphoma outside the HLA region. <i>American Journal of Human Genetics</i> , 2014 , 95, 462-71	11	74
154	Gene-age interactions in blood pressure regulation: a large-scale investigation with the CHARGE, Global BPgen, and ICBP Consortia. <i>American Journal of Human Genetics</i> , 2014 , 95, 24-38	11	80
153	A common missense variant in NUDT15 confers susceptibility to thiopurine-induced leukopenia. <i>Nature Genetics</i> , 2014 , 46, 1017-20	36.3	321
152	Genome-wide association study of Crohn's disease in Koreans revealed three new susceptibility loci and common attributes of genetic susceptibility across ethnic populations. <i>Gut</i> , 2014 , 63, 80-7	19.2	130
151	Synthesis and properties of acrylonitrile-methyl itaconate copolymers as spun carbon fiber precursors. <i>Fibers and Polymers</i> , 2014 , 15, 1583-1588	2	4
150	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014 , 4, 4999	17.4	87
149	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. <i>Human Molecular Genetics</i> , 2014 , 23, 6034-46	5.6	11
148	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. <i>Breast Cancer Research</i> , 2014 , 16, R51	8.3	12
147	A genome wide meta-analysis study for identification of common variation associated with breast cancer prognosis. <i>PLoS ONE</i> , 2014 , 9, e101488	3.7	24
146	MicroRNA related polymorphisms and breast cancer risk. <i>PLoS ONE</i> , 2014 , 9, e109973	3.7	37
145	A comprehensive association analysis confirms ZMIZ1 to be a susceptibility gene for vitiligo in Chinese population. <i>Journal of Medical Genetics</i> , 2014 , 51, 345-53	5.8	15
144	Multiple nonglycemic genomic loci are newly associated with blood level of glycated hemoglobin in East Asians. <i>Diabetes</i> , 2014 , 63, 2551-62	0.9	46
143	Analysis of non-synonymous-coding variants of Parkinson's disease-related pathogenic and susceptibility genes in East Asian populations. <i>Human Molecular Genetics</i> , 2014 , 23, 3891-7	5.6	26
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125	Germline variation in TP53 regulatory network genes associates with breast cancer survival and treatment outcome. <i>International Journal of Cancer</i> , 2013 , 132, 2044-55	7.5	9
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122	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013 , 45, 353-61, 361e1-2	36.3	813

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120	Genome-wide association analyses in Han Chinese identify two new susceptibility loci for amyotrophic lateral sclerosis. <i>Nature Genetics</i> , 2013 , 45, 697-700	36.3	52
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7	The Trans-Ancestral Genomic Architecture of Glycaemic Traits		1
6	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes		1
5	Trans-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation		10
4	Rare coding variants in 35 genes associate with circulating lipid levels in a multi-ancestry analysis of 170,000 exomes		2
3	Genetic discovery and translational decision support from exome sequencing of 20,791 type 2 diabetes cases and 24,440 controls from five ancestries		2
2	Large-scale whole-genome sequencing of three diverse Asian populations in Singapore		3
1	Identification of type 2 diabetes loci in 433,540 East Asian individuals		4