

Jianjun Liu

List of Publications by Citations

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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	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010 , 42, 937-48	36.3	2267
299	Genome-wide association study identifies novel breast cancer susceptibility loci. <i>Nature</i> , 2007 , 447, 1087-93	50.4	1957
298	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. <i>Nature</i> , 2011 , 476, 214-9	50.4	1948
297	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010 , 467, 832-8	50.4	1514
296	A global map of p53 transcription-factor binding sites in the human genome. <i>Cell</i> , 2006 , 124, 207-19	56.2	958
295	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
294	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016 , 536, 41-47	50.4	704
293	A common coding variant in CASP8 is associated with breast cancer risk. <i>Nature Genetics</i> , 2007 , 39, 352-8	36.3	557
292	Associations of breast cancer risk factors with tumor subtypes: a pooled analysis from the Breast Cancer Association Consortium studies. <i>Journal of the National Cancer Institute</i> , 2011 , 103, 250-63	9.7	513
291	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013 , 45, 501-12	36.3	437
290	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. <i>Nature Genetics</i> , 2013 , 45, 371-84, 384e1-2	36.3	422
289	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
288	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2011 , 43, 984-9	36.3	406
287	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. <i>Nature Genetics</i> , 2009 , 41, 585-90	36.3	393
286	Genome scan meta-analysis of schizophrenia and bipolar disorder, part III: Bipolar disorder. <i>American Journal of Human Genetics</i> , 2003 , 73, 49-62	11	353
285	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013 , 45, 392-8, 398e1-2	36.3	327
284	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

283	A common missense variant in NUDT15 confers susceptibility to thiopurine-induced leukopenia. <i>Nature Genetics</i> , 2014 , 46, 1017-20	36.3	321
282	A genome-wide association study of nasopharyngeal carcinoma identifies three new susceptibility loci. <i>Nature Genetics</i> , 2010 , 42, 599-603	36.3	306
281	Heterogeneity of breast cancer associations with five susceptibility loci by clinical and pathological characteristics. <i>PLoS Genetics</i> , 2008 , 4, e1000054	6	280
280	A genomewide screen for autism susceptibility loci. <i>American Journal of Human Genetics</i> , 2001 , 69, 327-401	40.1	267
279	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptor-negative breast cancer. <i>Nature Genetics</i> , 2011 , 43, 1210-4	36.3	253
278	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. <i>Nature Genetics</i> , 2012 , 44, 260-8	36.3	243
277	Genetic structure of the Han Chinese population revealed by genome-wide SNP variation. <i>American Journal of Human Genetics</i> , 2009 , 85, 775-85	11	241
276	Genome-wide association analysis identifies new lung cancer susceptibility loci in never-smoking women in Asia. <i>Nature Genetics</i> , 2012 , 44, 1330-5	36.3	237
275	Genome-wide association analysis identifies three new breast cancer susceptibility loci. <i>Nature Genetics</i> , 2012 , 44, 312-8	36.3	237
274	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
273	A genomewide screen of 345 families for autism-susceptibility loci. <i>American Journal of Human Genetics</i> , 2003 , 73, 886-97	11	224
272	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
271	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
270	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. <i>Nature Genetics</i> , 2013 , 45, 155-63	36.3	222
269	Evidence for a language quantitative trait locus on chromosome 7q in multiplex autism families. <i>American Journal of Human Genetics</i> , 2002 , 70, 60-71	11	222
268	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
267	Meta-analysis identifies multiple loci associated with kidney function-related traits in east Asian populations. <i>Nature Genetics</i> , 2012 , 44, 904-9	36.3	201
266	Combined analysis from eleven linkage studies of bipolar disorder provides strong evidence of susceptibility loci on chromosomes 6q and 8q. <i>American Journal of Human Genetics</i> , 2005 , 77, 582-95	11	192

265	Comparative genetic architectures of schizophrenia in East Asian and European populations. <i>Nature Genetics</i> , 2019 , 51, 1670-1678	36.3	185
264	Functional variants at the 11q13 risk locus for breast cancer regulate cyclin D1 expression through long-range enhancers. <i>American Journal of Human Genetics</i> , 2013 , 92, 489-503	11	167
263	Genome-wide association analyses identify three new susceptibility loci for primary angle closure glaucoma. <i>Nature Genetics</i> , 2012 , 44, 1142-1146	36.3	160
262	Genetic analysis of a morphological shape difference in the male genitalia of <i>Drosophila simulans</i> and <i>D. mauritiana</i> . <i>Genetics</i> , 1996 , 142, 1129-45	4	159
261	A large-scale screen for coding variants predisposing to psoriasis. <i>Nature Genetics</i> , 2014 , 46, 45-50	36.3	148
260	Genetic architecture of a morphological shape difference between two <i>Drosophila</i> species. <i>Genetics</i> , 2000 , 154, 299-310	4	146
259	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. <i>Human Molecular Genetics</i> , 2012 , 21, 5373-84	5.6	143
258	GWAS identifies novel susceptibility loci on 6p21.32 and 21q21.3 for hepatocellular carcinoma in chronic hepatitis B virus carriers. <i>PLoS Genetics</i> , 2012 , 8, e1002791	6	142
257	Low penetrance breast cancer susceptibility loci are associated with specific breast tumor subtypes: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2011 , 20, 3289-303	5.6	140
256	Genome-wide association study of follicular lymphoma identifies a risk locus at 6p21.32. <i>Nature Genetics</i> , 2010 , 42, 661-4	36.3	137
255	CHEK2*1100delC heterozygosity in women with breast cancer associated with early death, breast cancer-specific death, and increased risk of a second breast cancer. <i>Journal of Clinical Oncology</i> , 2012 , 30, 4308-16	2.2	134
254	Identification of two new loci at IL23R and RAB32 that influence susceptibility to leprosy. <i>Nature Genetics</i> , 2011 , 43, 1247-51	36.3	133
253	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
252	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
251	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019 , 570, 71-76	50.4	129
250	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
249	A genome-wide association study in Han Chinese identifies new susceptibility loci for ankylosing spondylitis. <i>Nature Genetics</i> , 2011 , 44, 73-7	36.3	123
248	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

247	Genome-wide association study identifies a common variant associated with risk of endometrial cancer. <i>Nature Genetics</i> , 2011 , 43, 451-4	36.3	121
246	Transferability of type 2 diabetes implicated loci in multi-ethnic cohorts from Southeast Asia. <i>PLoS Genetics</i> , 2011 , 7, e1001363	6	119
245	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
244	Genome-wide meta-analysis identifies multiple novel associations and ethnic heterogeneity of psoriasis susceptibility. <i>Nature Communications</i> , 2015 , 6, 6916	17.4	115
243	Evidence of gene-environment interactions between common breast cancer susceptibility loci and established environmental risk factors. <i>PLoS Genetics</i> , 2013 , 9, e1003284	6	112
242	New loci associated with chronic hepatitis B virus infection in Han Chinese. <i>Nature Genetics</i> , 2013 , 45, 1499-503	36.3	108
241	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
240	Common breast cancer susceptibility loci are associated with triple-negative breast cancer. <i>Cancer Research</i> , 2011 , 71, 6240-9	10.1	100
239	A comprehensive linkage analysis of chromosome 21q22 supports prior evidence for a putative bipolar affective disorder locus. <i>American Journal of Human Genetics</i> , 1999 , 64, 210-7	11	99
238	Common variants in ZNF365 are associated with both mammographic density and breast cancer risk. <i>Nature Genetics</i> , 2011 , 43, 185-7	36.3	96
237	Deletion of the WD40 domain of LRRK2 in Zebrafish causes Parkinsonism-like loss of neurons and locomotive defect. <i>PLoS Genetics</i> , 2010 , 6, e1000914	6	96
236	Breast cancer risk prediction and individualised screening based on common genetic variation and breast density measurement. <i>Breast Cancer Research</i> , 2012 , 14, R25	8.3	93
235	Common breast cancer susceptibility variants in LSP1 and RAD51L1 are associated with mammographic density measures that predict breast cancer risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012 , 21, 1156-66	4	92
234	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
233	Risk of estrogen receptor-positive and -negative breast cancer and single-nucleotide polymorphism 2q35-rs13387042. <i>Journal of the National Cancer Institute</i> , 2009 , 101, 1012-8	9.7	90
232	Identification of type 2 diabetes loci in 433,540 East Asian individuals. <i>Nature</i> , 2020 , 582, 240-245	50.4	89
231	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014 , 4, 4999	17.4	87
230	Discovery of six new susceptibility loci and analysis of pleiotropic effects in leprosy. <i>Nature Genetics</i> , 2015 , 47, 267-71	36.3	86

229	A combined analysis of genome-wide association studies in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2011 , 126, 717-27	4.4	85
228	A common variant near TGFBR3 is associated with primary open angle glaucoma. <i>Human Molecular Genetics</i> , 2015 , 24, 3880-92	5.6	84
227	GWAS of follicular lymphoma reveals allelic heterogeneity at 6p21.32 and suggests shared genetic susceptibility with diffuse large B-cell lymphoma. <i>PLoS Genetics</i> , 2011 , 7, e1001378	6	84
226	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
225	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
224	QUANTITATIVE GENETIC ANALYSIS OF DIVERGENCE IN MALE SECONDARY SEXUAL TRAITS BETWEEN DROSOPHILA SIMULANS AND DROSOPHILA MAURITIANA. <i>Evolution; International Journal of Organic Evolution</i> , 1997 , 51, 816-832	3.8	81
223	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
222	Fine-scale mapping of the FGFR2 breast cancer risk locus: putative functional variants differentially bind FOXA1 and E2F1. <i>American Journal of Human Genetics</i> , 2013 , 93, 1046-60	11	80
221	Genomewide linkage analysis of celiac disease in Finnish families. <i>American Journal of Human Genetics</i> , 2002 , 70, 51-9	11	80
220	Characterization of large structural genetic mosaicism in human autosomes. <i>American Journal of Human Genetics</i> , 2015 , 96, 487-97	11	77
219	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. <i>Human Molecular Genetics</i> , 2014 , 23, 6616-33	5.6	77
218	Association of ESR1 gene tagging SNPs with breast cancer risk. <i>Human Molecular Genetics</i> , 2009 , 18, 1131-9	5.6	75
217	The role of genetic breast cancer susceptibility variants as prognostic factors. <i>Human Molecular Genetics</i> , 2012 , 21, 3926-39	5.6	75
216	Characterization of the human glutamate receptor subunit 3 gene (GRIA3), a candidate for bipolar disorder and nonspecific X-linked mental retardation. <i>Genomics</i> , 1999 , 62, 356-68	4.3	75
215	Genome-wide association study of Parkinson disease in East Asians. <i>Human Molecular Genetics</i> , 2017 , 26, 226-232	5.6	75
214	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
213	Assessing interactions between the associations of common genetic susceptibility variants, reproductive history and body mass index with breast cancer risk in the breast cancer association consortium: a combined case-control study. <i>Breast Cancer Research</i> , 2010 , 12, R110	8.3	74
212	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

211	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
210	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
209	Association of TNFSF15 with Crohn's disease in Koreans. <i>American Journal of Gastroenterology</i> , 2008 , 103, 1437-42	0.7	69
208	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
207	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016 , 7, 11375	17.4	64
206	A genome-wide association study of early-onset breast cancer identifies PFKFB3 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
205	Genome-wide association study of ulcerative colitis in Koreans suggests extensive overlapping of genetic susceptibility with Caucasians. <i>Inflammatory Bowel Diseases</i> , 2013 , 19, 954-66	4.5	62
204	Identification of four novel variants that influence central corneal thickness in multi-ethnic Asian populations. <i>Human Molecular Genetics</i> , 2012 , 21, 437-45	5.6	61
203	Genome-wide association study for atopy and allergic rhinitis in a Singapore Chinese population. <i>PLoS ONE</i> , 2011 , 6, e19719	3.7	60
202	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
201	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
200	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. <i>Nature Communications</i> , 2016 , 7, 11843	17.4	59
199	Identification of IL18RAP/IL18R1 and IL12B as leprosy risk genes demonstrates shared pathogenesis between inflammation and infectious diseases. <i>American Journal of Human Genetics</i> , 2012 , 91, 935-41	11	58
198	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
197	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
196	An introgression analysis of quantitative trait loci that contribute to a morphological difference between <i>Drosophila simulans</i> and <i>D. mauritiana</i> . <i>Genetics</i> , 1997 , 145, 339-48	4	54
195	A meta-analysis of genome-wide association studies for adiponectin levels in East Asians identifies a novel locus near WDR11-FGFR2. <i>Human Molecular Genetics</i> , 2014 , 23, 1108-19	5.6	53
194	The genetic structure of the Swedish population. <i>PLoS ONE</i> , 2011 , 6, e22547	3.7	53

193	Five polymorphisms and breast cancer risk: results from the Breast Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009 , 18, 1610-6	4	53
192	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
191	Large-Scale Whole-Genome Sequencing of Three Diverse Asian Populations in Singapore. <i>Cell</i> , 2019 , 179, 736-749.e15	56.2	51
190	Meta-analysis of gene-level associations for rare variants based on single-variant statistics. <i>American Journal of Human Genetics</i> , 2013 , 93, 236-48	11	49
189	Comparison of 6q25 breast cancer hits from Asian and European Genome Wide Association Studies in the Breast Cancer Association Consortium (BCAC). <i>PLoS ONE</i> , 2012 , 7, e42380	3.7	49
188	Comparing methods for performing trans-ethnic meta-analysis of genome-wide association studies. <i>Human Molecular Genetics</i> , 2013 , 22, 2303-11	5.6	48
187	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
186	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
185	Association of variants in FRAP1 and PDGFRA with corneal curvature in Asian populations from Singapore. <i>Human Molecular Genetics</i> , 2011 , 20, 3693-8	5.6	46
184	Mutational dynamics of the SARS coronavirus in cell culture and human populations isolated in 2003. <i>BMC Infectious Diseases</i> , 2004 , 4, 32	4	46
183	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021 , 53, 840-860	36.3	44
182	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019 , 10, 4130	17.4	43
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	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
179	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019 , 10, 376	17.4	41
178	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019 , 10, 4957	17.4	40
177	A follow-up linkage study supports evidence for a bipolar affective disorder locus on chromosome 21q22. <i>American Journal of Medical Genetics Part A</i> , 2001 , 105, 189-94		40
176	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

175	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
174	Natural positive selection and north-south genetic diversity in East Asia. <i>European Journal of Human Genetics</i> , 2012 , 20, 102-110	5.3	38
173	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
172	MicroRNA related polymorphisms and breast cancer risk. <i>PLoS ONE</i> , 2014 , 9, e109973	3.7	37
171	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
170	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015 , 24, 2966-84	5.6	36
169	Identification of inherited genetic variations influencing prognosis in early-onset breast cancer. <i>Cancer Research</i> , 2013 , 73, 1883-91	10.1	36
168	Multi-variant pathway association analysis reveals the importance of genetic determinants of estrogen metabolism in breast and endometrial cancer susceptibility. <i>PLoS Genetics</i> , 2010 , 6, e1001012	6	36
167	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
166	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
165	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022 ,	50.4	35
164	11q13 is a susceptibility locus for hormone receptor positive breast cancer. <i>Human Mutation</i> , 2012 , 33, 1123-32	4.7	33
163	Genome-wide meta-analysis of five Asian cohorts identifies PDGFRA as a susceptibility locus for corneal astigmatism. <i>PLoS Genetics</i> , 2011 , 7, e1002402	6	33
162	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
161	A genome-wide association scan on estrogen receptor-negative breast cancer. <i>Breast Cancer Research</i> , 2010 , 12, R93	8.3	32
160	Novel Susceptibility Loci for Moyamoya Disease Revealed by a Genome-Wide Association Study. <i>Stroke</i> , 2018 , 49, 11-18	6.7	31
159	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
158	Genome-wide association study of B cell non-Hodgkin lymphoma identifies 3q27 as a susceptibility locus in the Chinese population. <i>Nature Genetics</i> , 2013 , 45, 804-7	36.3	31

157	Missense variants in ATM in 26,101 breast cancer cases and 29,842 controls. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010 , 19, 2143-51	4	31
156	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
155	ESR1 and EGF genetic variation in relation to breast cancer risk and survival. <i>Breast Cancer Research</i> , 2008 , 10, R15	8.3	30
154	SARS transmission pattern in Singapore reassessed by viral sequence variation analysis. <i>PLoS Medicine</i> , 2005 , 2, e43	11.6	30
153	Linkage disequilibrium mapping of CHEK2: common variation and breast cancer risk. <i>PLoS Medicine</i> , 2006 , 3, e168	11.6	30
152	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
151	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
150	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
149	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
148	Polymorphisms in oxidative stress-related genes and postmenopausal breast cancer risk. <i>International Journal of Cancer</i> , 2011 , 129, 1467-76	7.5	29
147	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. <i>Nature Communications</i> , 2018 , 9, 5052	17.4	29
146	Swedish population substructure revealed by genome-wide single nucleotide polymorphism data. <i>PLoS ONE</i> , 2011 , 6, e16747	3.7	28
145	Identification of a novel percent mammographic density locus at 12q24. <i>Human Molecular Genetics</i> , 2012 , 21, 3299-305	5.6	28
144	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
143	Evidence for an association of HLA-DRB1*15 and DRB1*09 with leprosy and the impact of DRB1*09 on disease onset in a Chinese Han population. <i>BMC Medical Genetics</i> , 2009 , 10, 133	2.1	27
142	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
141	Coding variants at hexa-allelic amino acid 13 of HLA-DRB1 explain independent SNP associations with follicular lymphoma risk. <i>American Journal of Human Genetics</i> , 2013 , 93, 167-72	11	26
140	Genome-Wide Analysis of Protein-Coding Variants in Leprosy. <i>Journal of Investigative Dermatology</i> , 2017 , 137, 2544-2551	4.3	26

139	Genetics of Type 2 Diabetes and Clinical Utility. <i>Genes</i> , 2015 , 6, 372-84	4.2	26
138	Analysis of non-synonymous-coding variants of Parkinson 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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18	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes		1
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4	Validation study of HLA-B*13:01 as a biomarker of dapsone hypersensitivity syndrome in leprosy patients in Indonesia 2020 , 14, e0008746		
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2	Validation study of HLA-B*13:01 as a biomarker of dapsone hypersensitivity syndrome in leprosy patients in Indonesia 2020 , 14, e0008746		
1	Genetic associations with healthy ageing among Chinese adults 2022 , 8,		