

Jianjun Liu

List of Publications by Year in descending order

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Version: 2024-02-01

299
papers

38,591
citations

3726

89
h-index

3402

183
g-index

309
all docs

309
docs citations

309
times ranked

49119
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948. | 9.4 | 2,634 |
| 2 | Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. <i>Nature</i> , 2011, 476, 214-219. | 13.7 | 2,400 |
| 3 | Genome-wide association study identifies novel breast cancer susceptibility loci. <i>Nature</i> , 2007, 447, 1087-1093. | 13.7 | 2,165 |
| 4 | Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838. | 13.7 | 1,789 |
| 5 | A Global Map of p53 Transcription-Factor Binding Sites in the Human Genome. <i>Cell</i> , 2006, 124, 207-219. | 13.5 | 1,060 |
| 6 | Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013, 45, 353-361. | 9.4 | 960 |
| 7 | The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47. | 13.7 | 952 |
| 8 | Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022, 604, 502-508. | 13.7 | 929 |
| 9 | 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, 250-263. | 3.0 | 596 |
| 10 | A common coding variant in CASP8 is associated with breast cancer risk. <i>Nature Genetics</i> , 2007, 39, 352-358. | 9.4 | 591 |
| 11 | Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013, 45, 501-512. | 9.4 | 578 |
| 12 | A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972. | 9.4 | 549 |
| 13 | Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , 2015, 47, 373-380. | 9.4 | 513 |
| 14 | 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, 371-384. | 9.4 | 493 |
| 15 | Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2011, 43, 984-989. | 9.4 | 481 |
| 16 | Comparative genetic architectures of schizophrenia in East Asian and European populations. <i>Nature Genetics</i> , 2019, 51, 1670-1678. | 9.4 | 440 |
| 17 | A common missense variant in NUDT15 confers susceptibility to thiopurine-induced leukopenia. <i>Nature Genetics</i> , 2014, 46, 1017-1020. | 9.4 | 438 |
| 18 | Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. <i>Nature Genetics</i> , 2009, 41, 585-590. | 9.4 | 434 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. <i>Journal of the National Cancer Institute</i> , 2015, 107, . | 3.0 | 428 |
| 20 | Genome Scan Meta-Analysis of Schizophrenia and Bipolar Disorder, Part III: Bipolar Disorder. <i>American Journal of Human Genetics</i> , 2003, 73, 49-62. | 2.6 | 400 |
| 21 | Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. <i>JAMA Oncology</i> , 2017, 3, 636. | 3.4 | 376 |
| 22 | A genome-wide association study of nasopharyngeal carcinoma identifies three new susceptibility loci. <i>Nature Genetics</i> , 2010, 42, 599-603. | 9.4 | 374 |
| 23 | Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013, 45, 392-398. | 9.4 | 374 |
| 24 | The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679. | 13.7 | 353 |
| 25 | 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. | 3.9 | 341 |
| 26 | The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860. | 9.4 | 341 |
| 27 | Genetic Structure of the Han Chinese Population Revealed by Genome-wide SNP Variation. <i>American Journal of Human Genetics</i> , 2009, 85, 775-785. | 2.6 | 316 |
| 28 | Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. <i>PLoS Genetics</i> , 2008, 4, e1000054. | 1.5 | 315 |
| 29 | Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. <i>Nature Genetics</i> , 2012, 44, 260-268. | 9.4 | 303 |
| 30 | 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. | 9.4 | 294 |
| 31 | A Genomewide Screen for Autism Susceptibility Loci. <i>American Journal of Human Genetics</i> , 2001, 69, 327-340. | 2.6 | 287 |
| 32 | Genome-wide association analysis identifies new lung cancer susceptibility loci in never-smoking women in Asia. <i>Nature Genetics</i> , 2012, 44, 1330-1335. | 9.4 | 286 |
| 33 | Identification of type 2 diabetes loci in 433,540 East Asian individuals. <i>Nature</i> , 2020, 582, 240-245. | 13.7 | 282 |
| 34 | A common variant at the TERT-CLPTM1L locus is associated with estrogen receptor-negative breast cancer. <i>Nature Genetics</i> , 2011, 43, 1210-1214. | 9.4 | 279 |
| 35 | Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. <i>Nature Genetics</i> , 2013, 45, 155-163. | 9.4 | 269 |
| 36 | Genome-wide association analysis identifies three new breast cancer susceptibility loci. <i>Nature Genetics</i> , 2012, 44, 312-318. | 9.4 | 256 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 37 | Meta-analysis identifies multiple loci associated with kidney function-related traits in east Asian populations. <i>Nature Genetics</i> , 2012, 44, 904-909. | 9.4 | 254 |
| 38 | 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. | 2.6 | 253 |
| 39 | Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. <i>Nature Genetics</i> , 2022, 54, 560-572. | 9.4 | 250 |
| 40 | Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019, 570, 71-76. | 13.7 | 248 |
| 41 | A Genomewide Screen of 345 Families for Autism-Susceptibility Loci. <i>American Journal of Human Genetics</i> , 2003, 73, 886-897. | 2.6 | 247 |
| 42 | 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, 582-595. | 2.6 | 218 |
| 43 | 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, 1129-1145. | 1.2 | 209 |
| 44 | Improving polygenic prediction in ancestrally diverse populations. <i>Nature Genetics</i> , 2022, 54, 573-580. | 9.4 | 209 |
| 45 | Genome-wide analyses of non-syndromic cleft lip with palate identify 14 novel loci and genetic heterogeneity. <i>Nature Communications</i> , 2017, 8, 14364. | 5.8 | 207 |
| 46 | 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. | 2.6 | 201 |
| 47 | Genome-wide association analyses identify three new susceptibility loci for primary angle closure glaucoma. <i>Nature Genetics</i> , 2012, 44, 1142-1146. | 9.4 | 196 |
| 48 | Deep sequencing of the MHC region in the Chinese population contributes to studies of complex disease. <i>Nature Genetics</i> , 2016, 48, 740-746. | 9.4 | 188 |
| 49 | A large-scale screen for coding variants predisposing to psoriasis. <i>Nature Genetics</i> , 2014, 46, 45-50. | 9.4 | 183 |
| 50 | Genetic Architecture of a Morphological Shape Difference Between Two <i>Drosophila</i> Species. <i>Genetics</i> , 2000, 154, 299-310. | 1.2 | 180 |
| 51 | CWAS 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. | 1.5 | 177 |
| 52 | Identification of Risk Loci for Parkinson Disease in Asians and Comparison of Risk Between Asians and Europeans. <i>JAMA Neurology</i> , 2020, 77, 746. | 4.5 | 170 |
| 53 | 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, 5373-5384. | 1.4 | 168 |
| 54 | <i>CHEK2</i> *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, 4308-4316. | 0.8 | 162 |

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|----|--|-----|-----------|
| 55 | Identification of two new loci at IL23R and RAB32 that influence susceptibility to leprosy. <i>Nature Genetics</i> , 2011, 43, 1247-1251. | 9.4 | 159 |
| 56 | 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, 80-87. | 6.1 | 157 |
| 57 | Genome-wide meta-analysis identifies multiple novel associations and ethnic heterogeneity of psoriasis susceptibility. <i>Nature Communications</i> , 2015, 6, 6916. | 5.8 | 154 |
| 58 | Genome-wide association study of follicular lymphoma identifies a risk locus at 6p21.32. <i>Nature Genetics</i> , 2010, 42, 661-664. | 9.4 | 152 |
| 59 | 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, 3289-3303. | 1.4 | 152 |
| 60 | 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. | 3.0 | 152 |
| 61 | New loci and coding variants confer risk for age-related macular degeneration in East Asians. <i>Nature Communications</i> , 2015, 6, 6063. | 5.8 | 147 |
| 62 | Genome-wide association study identifies 25 known breast cancer susceptibility loci as risk factors for triple-negative breast cancer. <i>Carcinogenesis</i> , 2014, 35, 1012-1019. | 1.3 | 145 |
| 63 | Genome-wide association study identifies a common variant associated with risk of endometrial cancer. <i>Nature Genetics</i> , 2011, 43, 451-454. | 9.4 | 141 |
| 64 | A genome-wide association study in Han Chinese identifies new susceptibility loci for ankylosing spondylitis. <i>Nature Genetics</i> , 2012, 44, 73-77. | 9.4 | 140 |
| 65 | New loci associated with chronic hepatitis B virus infection in Han Chinese. <i>Nature Genetics</i> , 2013, 45, 1499-1503. | 9.4 | 140 |
| 66 | Evidence of Gene-Environment Interactions between Common Breast Cancer Susceptibility Loci and Established Environmental Risk Factors. <i>PLoS Genetics</i> , 2013, 9, e1003284. | 1.5 | 136 |
| 67 | A Genome-Wide Association Study of Diabetic Kidney Disease in Subjects With Type 2 Diabetes. <i>Diabetes</i> , 2018, 67, 1414-1427. | 0.3 | 136 |
| 68 | 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. | 1.4 | 135 |
| 69 | Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019, 10, 4130. | 5.8 | 133 |
| 70 | Genome sequencing analysis identifies Epstein-Barr virus subtypes associated with high risk of nasopharyngeal carcinoma. <i>Nature Genetics</i> , 2019, 51, 1131-1136. | 9.4 | 133 |
| 71 | Transferability of Type 2 Diabetes Implicated Loci in Multi-Ethnic Cohorts from Southeast Asia. <i>PLoS Genetics</i> , 2011, 7, e1001363. | 1.5 | 131 |
| 72 | 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. | 9.4 | 129 |

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|----|---|------|-----------|
| 73 | Large-Scale Whole-Genome Sequencing of Three Diverse Asian Populations in Singapore. <i>Cell</i> , 2019, 179, 736-749.e15. | 13.5 | 126 |
| 74 | 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. | 2.6 | 123 |
| 75 | 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. | 1.5 | 114 |
| 76 | 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. | 9.4 | 112 |
| 77 | Common variants in ZNF365 are associated with both mammographic density and breast cancer risk. <i>Nature Genetics</i> , 2011, 43, 185-187. | 9.4 | 109 |
| 78 | Common Breast Cancer Susceptibility Loci Are Associated with Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2011, 71, 6240-6249. | 0.4 | 109 |
| 79 | 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. | 2.6 | 109 |
| 80 | Breast cancer risk prediction and individualised screening based on common genetic variation and breast density measurement. <i>Breast Cancer Research</i> , 2012, 14, R25. | 2.2 | 108 |
| 81 | Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014, 5, 4999. | 5.8 | 105 |
| 82 | A common variant near TGFBR3 is associated with primary open angle glaucoma. <i>Human Molecular Genetics</i> , 2015, 24, 3880-3892. | 1.4 | 105 |
| 83 | Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. <i>Human Molecular Genetics</i> , 2015, 24, 1791-1800. | 1.4 | 105 |
| 84 | 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, 210-217. | 2.6 | 104 |
| 85 | Discovery of six new susceptibility loci and analysis of pleiotropic effects in leprosy. <i>Nature Genetics</i> , 2015, 47, 267-271. | 9.4 | 103 |
| 86 | Common Breast Cancer Susceptibility Variants in <i>LSP1</i> and <i>RAD51L1</i> Are Associated with Mammographic Density Measures that Predict Breast Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 1156-1166. | 1.1 | 101 |
| 87 | Characterization of Large Structural Genetic Mosaicism in Human Autosomes. <i>American Journal of Human Genetics</i> , 2015, 96, 487-497. | 2.6 | 101 |
| 88 | Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. <i>Cancer Research</i> , 2016, 76, 5103-5114. | 0.4 | 100 |
| 89 | 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, 1012-1018. | 3.0 | 99 |
| 90 | 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, 1046-1060. | 2.6 | 98 |

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|-----|---|-----|-----------|
| 91 | QUANTITATIVE GENETIC ANALYSIS OF DIVERGENCE IN MALE SECONDARY SEXUAL TRAITS BETWEEN <i>DROSOPHILA SIMULANS</i> AND <i>DROSOPHILA MAURITIANA</i> . <i>Evolution; International Journal of Organic Evolution</i> , 1997, 51, 816-832. | 1.1 | 97 |
| 92 | Genome-wide Association Study Identifies Five Susceptibility Loci for Follicular Lymphoma outside the HLA Region. <i>American Journal of Human Genetics</i> , 2014, 95, 462-471. | 2.6 | 96 |
| 93 | Genome-wide association study of Parkinson's disease in East Asians. <i>Human Molecular Genetics</i> , 2017, 26, ddw379. | 1.4 | 94 |
| 94 | 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. | 1.1 | 94 |
| 95 | CWAS 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. | 1.5 | 93 |
| 96 | Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375. | 5.8 | 93 |
| 97 | Genomewide Linkage Analysis of Celiac Disease in Finnish Families. <i>American Journal of Human Genetics</i> , 2002, 70, 51-59. | 2.6 | 90 |
| 98 | A combined analysis of genome-wide association studies in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2011, 126, 717-727. | 1.1 | 90 |
| 99 | 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, 6616-6633. | 1.4 | 90 |
| 100 | Association of TNFSF15 With Crohn's Disease in Koreans. <i>American Journal of Gastroenterology</i> , 2008, 103, 1437-1442. | 0.2 | 86 |
| 101 | Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. <i>Nature Communications</i> , 2016, 7, 11843. | 5.8 | 86 |
| 102 | Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019, 188, 1033-1054. | 1.6 | 85 |
| 103 | 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, 356-368. | 1.3 | 84 |
| 104 | Association of ESR1 gene tagging SNPs with breast cancer risk. <i>Human Molecular Genetics</i> , 2009, 18, 1131-1139. | 1.4 | 84 |
| 105 | Genetic risk of extranodal natural killer T-cell lymphoma: a genome-wide association study. <i>Lancet Oncology</i> , The, 2016, 17, 1240-1247. | 5.1 | 84 |
| 106 | Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957. | 5.8 | 84 |
| 107 | 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. | 2.2 | 82 |
| 108 | The role of genetic breast cancer susceptibility variants as prognostic factors. <i>Human Molecular Genetics</i> , 2012, 21, 3926-3939. | 1.4 | 80 |

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|-----|---|-----|-----------|
| 109 | A Genome-wide Association Study of Early-Onset Breast Cancer Identifies <i>PCSK9</i> 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, 658-669. | 1.1 | 77 |
| 110 | Genome-Wide Association Study for Atopy and Allergic Rhinitis in a Singapore Chinese Population. <i>PLoS ONE</i> , 2011, 6, e19719. | 1.1 | 77 |
| 111 | Genome-Wide Association Study of Ulcerative Colitis in Koreans Suggests Extensive Overlapping of Genetic Susceptibility With Caucasians. <i>Inflammatory Bowel Diseases</i> , 2013, 19, 954-966. | 0.9 | 76 |
| 112 | Interethnic analyses of blood pressure loci in populations of East Asian and European descent. <i>Nature Communications</i> , 2018, 9, 5052. | 5.8 | 75 |
| 113 | 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, 935-941. | 2.6 | 74 |
| 114 | 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, 311-319. | 2.3 | 72 |
| 115 | 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, 339-348. | 1.2 | 72 |
| 116 | Identification of four novel variants that influence central corneal thickness in multi-ethnic Asian populations. <i>Human Molecular Genetics</i> , 2012, 21, 437-445. | 1.4 | 69 |
| 117 | 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, 1108-1119. | 1.4 | 68 |
| 118 | The Genetic Structure of the Swedish Population. <i>PLoS ONE</i> , 2011, 6, e22547. | 1.1 | 67 |
| 119 | Genome-wide association analyses in Han Chinese identify two new susceptibility loci for amyotrophic lateral sclerosis. <i>Nature Genetics</i> , 2013, 45, 697-700. | 9.4 | 67 |
| 120 | Novel Susceptibility Loci for Moyamoya Disease Revealed by a Genome-Wide Association Study. <i>Stroke</i> , 2018, 49, 11-18. | 1.0 | 66 |
| 121 | Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376. | 5.8 | 64 |
| 122 | Loci for human leukocyte telomere length in the Singaporean Chinese population and trans-ethnic genetic studies. <i>Nature Communications</i> , 2019, 10, 2491. | 5.8 | 64 |
| 123 | Comparing methods for performing trans-ethnic meta-analysis of genome-wide association studies. <i>Human Molecular Genetics</i> , 2013, 22, 2303-2311. | 1.4 | 63 |
| 124 | Multiple Nonglycemic Genomic Loci Are Newly Associated With Blood Level of Glycated Hemoglobin in East Asians. <i>Diabetes</i> , 2014, 63, 2551-2562. | 0.3 | 61 |
| 125 | Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. <i>American Journal of Human Genetics</i> , 2013, 93, 236-248. | 2.6 | 60 |
| 126 | ImmunoChIP Analysis Identification of 6 Additional Susceptibility Loci for Crohn's Disease in Koreans. <i>Inflammatory Bowel Diseases</i> , 2015, 21, 1-7. | 0.9 | 60 |

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|-----|---|-----|-----------|
| 127 | Genome-Wide Association Meta-analysis Identifies Novel Variants Associated With Fasting Plasma Glucose in East Asians. <i>Diabetes</i> , 2015, 64, 291-298. | 0.3 | 59 |
| 128 | Mutational dynamics of the SARS coronavirus in cell culture and human populations isolated in 2003. <i>BMC Infectious Diseases</i> , 2004, 4, 32. | 1.3 | 58 |
| 129 | Five Polymorphisms and Breast Cancer Risk: Results from the Breast Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009, 18, 1610-1616. | 1.1 | 57 |
| 130 | A large-scale genome-wide association and meta-analysis identified four novel susceptibility loci for leprosy. <i>Nature Communications</i> , 2016, 7, 13760. | 5.8 | 54 |
| 131 | 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. | 1.2 | 53 |
| 132 | Evaluation of Prospective HLA-B*13:01 Screening to Prevent Dapsone Hypersensitivity Syndrome in Patients With Leprosy. <i>JAMA Dermatology</i> , 2019, 155, 666. | 2.0 | 52 |
| 133 | Association of variants in FRAP1 and PDGFRA with corneal curvature in Asian populations from Singapore. <i>Human Molecular Genetics</i> , 2011, 20, 3693-3698. | 1.4 | 51 |
| 134 | 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. | 1.1 | 51 |
| 135 | Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. <i>Human Molecular Genetics</i> , 2015, 24, 1478-1492. | 1.4 | 50 |
| 136 | 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> , 2016, 26, ddw414. | 1.4 | 50 |
| 137 | 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, 620-629. | 1.4 | 50 |
| 138 | MicroRNA Related Polymorphisms and Breast Cancer Risk. <i>PLoS ONE</i> , 2014, 9, e109973. | 1.1 | 49 |
| 139 | Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. <i>Nature Communications</i> , 2021, 12, 3505. | 5.8 | 49 |
| 140 | A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017, 66, 2019-2032. | 0.3 | 47 |
| 141 | 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, 189-194. | 2.4 | 43 |
| 142 | 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, 804-807. | 9.4 | 43 |
| 143 | Natural positive selection and north-south genetic diversity in East Asia. <i>European Journal of Human Genetics</i> , 2012, 20, 102-110. | 1.4 | 42 |
| 144 | Identification of Inherited Genetic Variations Influencing Prognosis in Early-Onset Breast Cancer. <i>Cancer Research</i> , 2013, 73, 1883-1891. | 0.4 | 42 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
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| 293 | 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. | 1.4 | 1 |
| 294 | Variant landscape of the RYR1 gene based on whole genome sequencing of the Singaporean population. <i>Scientific Reports</i> , 2022, 12, 5429. | 1.6 | 1 |
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