

Jirong Long

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.

114 papers	6,159 citations	41 h-index	77 g-index
122 ext. papers	8,035 ext. citations	9.4 avg, IF	4.29 L-index

#	Paper	IF	Citations
114	Cis-regulation of antisense noncoding RNA at the JAZF1 locus in type 2 diabetes.. <i>Journal of Gene Medicine</i> , 2022 , e3407	3.5	0
113	Association Between Long-Term Regular Exercise and Gut Microbiota Among Middle-Aged and Older Urban Chinese.. <i>International Journal of Sport Nutrition and Exercise Metabolism</i> , 2022 , 1-9	4.4	0
112	Associations of genetic susceptibility to 16 cancers with risk of breast cancer overall and by intrinsic subtypes.. <i>Human Genetics and Genomics Advances</i> , 2022 , 3, 100077	0.8	1
111	UACA locus is associated with breast cancer chemoresistance and survival.. <i>Npj Breast Cancer</i> , 2022 , 8, 39	7.8	1
110	Incorporating Polygenic Risk Scores and Nongenetic Risk Factors for Breast Cancer Risk Prediction Among Asian Women.. <i>JAMA Network Open</i> , 2022 , 5, e2149030	10.4	2
109	2SFucosyllactose Ameliorates Chemotherapy-Induced Intestinal Mucositis by Protecting Intestinal Epithelial Cells Against Apoptosis. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2021 ,	7.9	5
108	The oral microbiome in relation to pancreatic cancer risk in African Americans. <i>British Journal of Cancer</i> , 2021 ,	8.7	2
107	Incorporating European GWAS findings improve polygenic risk prediction accuracy of breast cancer among East Asians. <i>Genetic Epidemiology</i> , 2021 , 45, 471-484	2.6	2
106	Functional Genomic Analyses of the 21q22.3 Locus Identifying Functional Variants and Candidate Gene for Breast Cancer Risk. <i>Cancers</i> , 2021 , 13,	6.6	1
105	Associations between Genetically Predicted Circulating Protein Concentrations and Endometrial Cancer Risk. <i>Cancers</i> , 2021 , 13,	6.6	3
104	Legume Consumption and Gut Microbiome in Elderly Chinese Men and Women. <i>Journal of Nutrition</i> , 2021 , 151, 2399-2408	4.1	1
103	Association between ALDH2 and ADH1B Polymorphisms and the Risk for Colorectal Cancer in Koreans. <i>Cancer Research and Treatment</i> , 2021 , 53, 754-762	5.2	4
102	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. <i>American Journal of Human Genetics</i> , 2021 , 108, 1190-1203	11	1
101	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. <i>International Journal of Cancer</i> , 2021 , 148, 307-319	7.5	13
100	Identifying Novel Susceptibility Genes for Colorectal Cancer Risk From a Transcriptome-Wide Association Study of 125,478 Subjects. <i>Gastroenterology</i> , 2021 , 160, 1164-1178.e6	13.3	15
99	Multi-omics analysis to identify susceptibility genes for colorectal cancer. <i>Human Molecular Genetics</i> , 2021 , 30, 321-330	5.6	2
98	Discovery of structural deletions in breast cancer predisposition genes using whole genome sequencing data from > 2000 women of African-ancestry. <i>Human Genetics</i> , 2021 , 140, 1449-1457	6.3	1

97	Association of oral microbiota with lung cancer risk in a low-income population in the Southeastern USA. <i>Cancer Causes and Control</i> , 2021 , 32, 1423-1432	2.8	2
96	Novel strategy for disease risk prediction incorporating predicted gene expression and DNA methylation data: a multi-phased study of prostate cancer. <i>Cancer Communications</i> , 2021 ,	9.4	1
95	Integrating Genome and Methylome Data to Identify Candidate DNA Methylation Biomarkers for Pancreatic Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021 , 30, 2079-2087	4	0
94	Polygenic risk scores for prediction of breast cancer risk in Asian populations.. <i>Genetics in Medicine</i> , 2021 ,	8.1	2
93	Identification of novel breast cancer susceptibility loci in meta-analyses conducted among Asian and European descendants. <i>Nature Communications</i> , 2020 , 11, 1217	17.4	16
92	Evaluating polygenic risk scores in assessing risk of nine solid and hematologic cancers in European descendants. <i>International Journal of Cancer</i> , 2020 , 147, 3416-3423	7.5	5
91	Genome-wide meta-analysis associates GPSM1 with type 2 diabetes, a plausible gene involved in skeletal muscle function. <i>Journal of Human Genetics</i> , 2020 , 65, 411-420	4.3	3
90	Transcriptome-wide association study of breast cancer risk by estrogen-receptor status. <i>Genetic Epidemiology</i> , 2020 , 44, 442-468	2.6	9
89	Associations between Genetically Predicted Blood Protein Biomarkers and Pancreatic Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020 , 29, 1501-1508	4	9
88	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020 , 52, 56-73	36.3	56
87	Identification of Novel Loci and New Risk Variant in Known Loci for Colorectal Cancer Risk in East Asians. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020 , 29, 477-486	4	4
86	Discovery of rare coding variants in OGDHL and BRCA2 in relation to breast cancer risk in Chinese women. <i>International Journal of Cancer</i> , 2020 , 146, 2175-2181	7.5	5
85	An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. <i>Nature Communications</i> , 2020 , 11, 3905	17.4	12
84	Mendelian Randomization Analysis of n-6 Polyunsaturated Fatty Acid Levels and Pancreatic Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020 , 29, 2735-2739	4	2
83	From tobacco smoking to cancer mutational signature: a mediation analysis strategy to explore the role of epigenetic changes. <i>BMC Cancer</i> , 2020 , 20, 880	4.8	6
82	Genetically Predicted Levels of DNA Methylation Biomarkers and Breast Cancer Risk: Data From 228 951 Women of European Descent. <i>Journal of the National Cancer Institute</i> , 2020 , 112, 295-304	9.7	18
81	Evaluation of associations between genetically predicted circulating protein biomarkers and breast cancer risk. <i>International Journal of Cancer</i> , 2020 , 146, 2130-2138	7.5	9
80	Evaluation of pathogenetic mutations in breast cancer predisposition genes in population-based studies conducted among Chinese women. <i>Breast Cancer Research and Treatment</i> , 2020 , 181, 465-473	4.4	7

79	Evaluating the Utility of Polygenic Risk Scores in Identifying High-Risk Individuals for Eight Common Cancers. <i>JNCI Cancer Spectrum</i> , 2020 , 4, pkaa021	4.6	27
78	Re-evaluating genetic variants identified in candidate gene studies of breast cancer risk using data from nearly 280,000 women of Asian and European ancestry. <i>EBioMedicine</i> , 2019 , 48, 203-211	8.8	9
77	Oral microbiome and obesity in a large study of low-income and African-American populations. <i>Journal of Oral Microbiology</i> , 2019 , 11, 1650597	6.3	24
76	Two truncating variants in FANCC and breast cancer risk. <i>Scientific Reports</i> , 2019 , 9, 12524	4.9	2
75	Integrative genomic analyses of APOBEC-mutational signature, expression and germline deletion of APOBEC3 genes, and immunogenicity in multiple cancer types. <i>BMC Medical Genomics</i> , 2019 , 12, 131	3.7	23
74	Cigarette smoking and oral microbiota in low-income and African-American populations. <i>Journal of Epidemiology and Community Health</i> , 2019 , 73, 1108-1115	5.1	16
73	Discovery of a Pathogenic Variant rs139379666 (p. P2974L) in for Breast Cancer Risk in Chinese Populations. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019 , 28, 1308-1315	4	2
72	Identification of Novel Susceptibility Loci and Genes for Prostate Cancer Risk: A Transcriptome-Wide Association Study in Over 140,000 European Descendants. <i>Cancer Research</i> , 2019 , 79, 3192-3204	10.1	23
71	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019 , 10, 1741	17.4	47
70	Transcriptome-Wide Association Study Identifies Susceptibility Loci and Genes for Age at Natural Menopause. <i>Reproductive Sciences</i> , 2019 , 26, 496-502	3	4
69	Identifying Putative Susceptibility Genes and Evaluating Their Associations with Somatic Mutations in Human Cancers. <i>American Journal of Human Genetics</i> , 2019 , 105, 477-492	11	12
68	Large-Scale Genome-Wide Association Study of East Asians Identifies Loci Associated With Risk for Colorectal Cancer. <i>Gastroenterology</i> , 2019 , 156, 1455-1466	13.3	55
67	Racial Differences in the Oral Microbiome: Data from Low-Income Populations of African Ancestry and European Ancestry. <i>MSystems</i> , 2019 , 4,	7.6	15
66	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019 , 104, 21-34	11	363
65	Association of oral health with lung cancer risk in a low-income population of African Americans and European Americans in the Southeastern United States. <i>Lung Cancer</i> , 2019 , 127, 90-95	5.9	10
64	Prospective study of oral microbiome and colorectal cancer risk in low-income and African American populations. <i>International Journal of Cancer</i> , 2019 , 144, 2381-2389	7.5	43
63	Genetic Data from Nearly 63,000 Women of European Descent Predicts DNA Methylation Biomarkers and Epithelial Ovarian Cancer Risk. <i>Cancer Research</i> , 2019 , 79, 505-517	10.1	28
62	Exome Sequencing Identifies Genetic Variants Associated with Circulating Lipid Levels in Mexican Americans: The Insulin Resistance Atherosclerosis Family Study (IRASFS). <i>Scientific Reports</i> , 2018 , 8, 56034	4.9	5

61	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
60	A Comprehensive cis-eQTL Analysis Revealed Target Genes in Breast Cancer Susceptibility Loci Identified in Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2018 , 102, 890-903	11	42
59	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. <i>Cancer Research</i> , 2018 , 78, 5419-5430	10.1	32
58	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , 2018 , 9, 3166	17.4	70
57	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. <i>Nature Genetics</i> , 2018 , 50, 968-978	36.3	101
56	Genetic Evidence for the Association between Schizophrenia and Breast Cancer. <i>Journal of Psychiatry and Brain Science</i> , 2018 , 3,	1.7	6
55	Genetic variation in SLC7A2 interacts with calcium and magnesium intakes in modulating the risk of colorectal polyps. <i>Journal of Nutritional Biochemistry</i> , 2017 , 47, 35-40	6.3	4
54	Evaluating genetic variants associated with breast cancer risk in high and moderate-penetrance genes in Asians. <i>Carcinogenesis</i> , 2017 , 38, 511-518	4.6	20
53	Interactions between calcium intake and polymorphisms in genes essential for calcium reabsorption and risk of colorectal neoplasia in a two-phase study. <i>Molecular Carcinogenesis</i> , 2017 , 56, 2258-2266	5	5
52	Evaluation of genetic variants in association with colorectal cancer risk and survival in Asians. <i>International Journal of Cancer</i> , 2017 , 141, 1130-1139	7.5	15
51	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
50	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
49	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017 , 551, 92-94	50.4	643
48	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017 , 49, 1767-1778	36.3	186
47	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. <i>Gynecologic Oncology</i> , 2016 , 141, 386-401	4.9	15
46	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. <i>Human Molecular Genetics</i> , 2016 , 25, 3863-3876	5.6	24
45	Genome-wide association studies in East Asians identify new loci for waist-hip ratio and waist circumference. <i>Scientific Reports</i> , 2016 , 6, 17958	4.9	48
44	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016 , 7, 11375	17.4	64

43	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016 , 7, 12675	17.4	53
42	Genome-wide association study in East Asians identifies two novel breast cancer susceptibility loci. <i>Human Molecular Genetics</i> , 2016 , 25, 3361-3371	5.6	22
41	Genome-wide association studies in the Japanese population identify seven novel loci for type 2 diabetes. <i>Nature Communications</i> , 2016 , 7, 10531	17.4	99
40	No evidence that protein truncating variants in BRIP1 are associated with breast cancer risk: implications for gene panel testing. <i>Journal of Medical Genetics</i> , 2016 , 53, 298-309	5.8	83
39	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. <i>Nature Genetics</i> , 2016 , 48, 374-86	36.3	93
38	Identification of Susceptibility Loci and Genes for Colorectal Cancer Risk. <i>Gastroenterology</i> , 2016 , 150, 1633-1645	13.3	64
37	Evaluation of potential regulatory function of breast cancer risk locus at 6q25.1. <i>Carcinogenesis</i> , 2016 , 37, 163-168	4.6	11
36	The Circadian Rhythm Gene Arntl2 Is a Metastasis Susceptibility Gene for Estrogen Receptor-Negative Breast Cancer. <i>PLoS Genetics</i> , 2016 , 12, e1006267	6	30
35	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. <i>International Journal of Cancer</i> , 2016 , 139, 1303-1317	7.5	26
34	Calcium/magnesium intake ratio, but not magnesium intake, interacts with genetic polymorphism in relation to colorectal neoplasia in a two-phase study. <i>Molecular Carcinogenesis</i> , 2016 , 55, 1449-57	5	7
33	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. <i>Breast Cancer Research</i> , 2016 , 18, 64	8.3	25
32	Prediction of breast cancer risk based on common genetic variants in women of East Asian ancestry. <i>Breast Cancer Research</i> , 2016 , 18, 124	8.3	34
31	Genomic Characterization of Esophageal Squamous Cell Carcinoma Reveals Critical Genes Underlying Tumorigenesis and Poor Prognosis. <i>American Journal of Human Genetics</i> , 2016 , 98, 709-27	11	95
30	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. <i>Cancer Causes and Control</i> , 2016 , 27, 679-93	2.8	15
29	Association between genetic risk score for telomere length and risk of breast cancer. <i>Cancer Causes and Control</i> , 2016 , 27, 1219-28	2.8	14
28	Age at menarche and age at natural menopause in East Asian women: a genome-wide association study. <i>Age</i> , 2016 , 38, 513-523		30
27	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
26	Whole-exome sequencing identifies OR2W3 mutation as a cause of autosomal dominant retinitis pigmentosa. <i>Scientific Reports</i> , 2015 , 5, 9236	4.9	20

25	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	74
24	Fine-scale mapping of the 4q24 locus identifies two independent loci associated with breast cancer risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 1680-91	4	17
23	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
22	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
21	Whole-Exome Sequencing Identifies Novel Somatic Mutations in Chinese Breast Cancer Patients. <i>Journal of Molecular and Genetic Medicine: an International Journal of Biomedical Research</i> , 2015 , 9,	2.5	15
20	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
19	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015 , 24, 2966-84	5.6	36
18	Fine-scale mapping of the 5q11.2 breast cancer locus reveals at least three independent risk variants regulating MAP3K1. <i>American Journal of Human Genetics</i> , 2015 , 96, 5-20	11	59
17	Large-scale genetic study in East Asians identifies six new loci associated with colorectal cancer risk. <i>Nature Genetics</i> , 2014 , 46, 533-42	36.3	175
16	Genome-wide association analysis in East Asians identifies breast cancer susceptibility loci at 1q32.1, 5q14.3 and 15q26.1. <i>Nature Genetics</i> , 2014 , 46, 886-90	36.3	110
15	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014 , 4, 4999	17.4	87
14	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
13	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
12	Meta-analysis of genome-wide association studies in East Asian-ancestry populations identifies four new loci for body mass index. <i>Human Molecular Genetics</i> , 2014 , 23, 5492-504	5.6	141
11	Meta-analysis of genome-wide association studies in African Americans provides insights into the genetic architecture of type 2 diabetes. <i>PLoS Genetics</i> , 2014 , 10, e1004517	6	151
10	FTO genetic variants, dietary intake and body mass index: insights from 177,330 individuals. <i>Human Molecular Genetics</i> , 2014 , 23, 6961-72	5.6	120
9	Improved variant calling accuracy by merging replicates in whole-exome sequencing studies. <i>BioMed Research International</i> , 2014 , 2014, 319534	3	9
8	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

7	A common deletion in the APOBEC3 genes and breast cancer risk. <i>Journal of the National Cancer Institute</i> , 2013 , 105, 573-9	9.7	109
6	Evaluating genome-wide association study-identified breast cancer risk variants in African-American women. <i>PLoS ONE</i> , 2013 , 8, e58350	3.7	58
5	Exome sequencing generates high quality data in non-target regions. <i>BMC Genomics</i> , 2012 , 13, 194	4.5	95
4	Genome-wide association study in east Asians identifies novel susceptibility loci for breast cancer. <i>PLoS Genetics</i> , 2012 , 8, e1002532	6	118
3	Identification of a functional genetic variant at 16q12.1 for breast cancer risk: results from the Asia Breast Cancer Consortium. <i>PLoS Genetics</i> , 2010 , 6, e1001002	6	93
2	Evaluation of breast cancer susceptibility loci in Chinese women. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010 , 19, 2357-65	4	87
1	Genome-wide association study identifies a new breast cancer susceptibility locus at 6q25.1. <i>Nature Genetics</i> , 2009 , 41, 324-8	36.3	434