

# Chen-Yang Shen

## 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.

87  
papers

7,712  
citations

37  
h-index

87  
g-index

89  
ext. papers

8,787  
ext. citations

10.1  
avg, IF

4.43  
L-index

#	Paper	IF	Citations
87	Genome-wide association study identifies novel breast cancer susceptibility loci. <i>Nature</i> , <b>2007</b> , 447, 1087-93	50.4	1957
86	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , <b>2013</b> , 45, 353-61, 361e1-2	36.3	813
85	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , <b>2017</b> , 551, 92-94	50.4	643
84	Carbamazepine-induced toxic effects and HLA-B*1502 screening in Taiwan. <i>New England Journal of Medicine</i> , <b>2011</b> , 364, 1126-33	59.2	511
83	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , <b>2015</b> , 47, 373-80	36.3	406
82	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , <b>2013</b> , 45, 392-8, 398e1-2	36.3	327
81	Mechanisms of inactivation of E-cadherin in breast carcinoma: modification of the two-hit hypothesis of tumor suppressor gene. <i>Oncogene</i> , <b>2001</b> , 20, 3814-23	9.2	191
80	MicroRNA-30a inhibits cell migration and invasion by downregulating vimentin expression and is a potential prognostic marker in breast cancer. <i>Breast Cancer Research and Treatment</i> , <b>2012</b> , 134, 1081-93	4.4	173
79	Use of HLA-B*58:01 genotyping to prevent allopurinol induced severe cutaneous adverse reactions in Taiwan: national prospective cohort study. <i>BMJ, The</i> , <b>2015</b> , 351, h4848	5.9	115
78	Breast cancer risk associated with genotypic polymorphism of the nonhomologous end-joining genes: a multigenic study on cancer susceptibility. <i>Cancer Research</i> , <b>2003</b> , 63, 2440-6	10.1	111
77	Genome-wide association analysis in East Asians identifies breast cancer susceptibility loci at 1q32.1, 5q14.3 and 15q26.1. <i>Nature Genetics</i> , <b>2014</b> , 46, 886-90	36.3	110
76	Population structure of Han Chinese in the modern Taiwanese population based on 10,000 participants in the Taiwan Biobank project. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 5321-5331	5.6	109
75	Breast cancer risk associated with genotype polymorphism of the catechol estrogen-metabolizing genes: a multigenic study on cancer susceptibility. <i>International Journal of Cancer</i> , <b>2005</b> , 113, 345-53	7.5	105
74	FGFR2 variants and breast cancer risk: fine-scale mapping using African American studies and analysis of chromatin conformation. <i>Human Molecular Genetics</i> , <b>2009</b> , 18, 1692-703	5.6	100
73	Breast cancer risk and the DNA double-strand break end-joining capacity of nonhomologous end-joining genes are affected by BRCA1. <i>Cancer Research</i> , <b>2004</b> , 64, 5013-9	10.1	96
72	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , <b>2014</b> , 4, 4999	17.4	87
71	Ataxia telangiectasia mutated and checkpoint kinase 2 regulate BRCA1 to promote the fidelity of DNA end-joining. <i>Cancer Research</i> , <b>2006</b> , 66, 1391-400	10.1	85

70	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> , <b>2016</b> , 53, 298-309	5.8	83
69	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> , <b>2013</b> , 93, 1046-60	11	80
68	Chk2-dependent phosphorylation of XRCC1 in the DNA damage response promotes base excision repair. <i>EMBO Journal</i> , <b>2008</b> , 27, 3140-50	13	78
67	Burden of total and cause-specific mortality related to tobacco smoking among adults aged $\geq 15$ years in Asia: a pooled analysis of 21 cohorts. <i>PLoS Medicine</i> , <b>2014</b> , 11, e1001631	11.6	76
66	Breast cancer risk is associated with the genes encoding the DNA double-strand break repair Mre11/Rad50/Nbs1 complex. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2007</b> , 16, 2024-32	4	71
65	Breast cancer risk associated with genotypic polymorphism of the mitosis-regulating gene Aurora-A/STK15/BTAK. <i>International Journal of Cancer</i> , <b>2005</b> , 115, 276-83	7.5	60
64	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> , <b>2015</b> , 96, 5-20	11	59
63	DNA double-strand break repair capacity and risk of breast cancer. <i>Carcinogenesis</i> , <b>2007</b> , 28, 1726-30	4.6	52
62	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 6096-111	5.6	48
61	Foxo3a-mediated overexpression of microRNA-622 suppresses tumor metastasis by repressing hypoxia-inducible factor-1 in ERK-responsive lung cancer. <i>Oncotarget</i> , <b>2015</b> , 6, 44222-38	3.3	45
60	The role of BRCA1 in non-homologous end-joining. <i>Cancer Letters</i> , <b>2006</b> , 240, 1-8	9.9	44
59	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. <i>American Journal of Human Genetics</i> , <b>2016</b> , 99, 903-911	11	43
58	A novel estrogen receptor-microRNA 190a-PAR-1-pathway regulates breast cancer progression, a finding initially suggested by genome-wide analysis of loci associated with lymph-node metastasis. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 355-67	5.6	42
57	Genetic variants of BLM interact with RAD51 to increase breast cancer susceptibility. <i>Carcinogenesis</i> , <b>2009</b> , 30, 43-9	4.6	41
56	Increased expression of SRp40 affecting CD44 splicing is associated with the clinical outcome of lymph node metastasis in human breast cancer. <i>Clinica Chimica Acta</i> , <b>2007</b> , 384, 69-74	6.2	41
55	Allelic loss of the BRCA1 and BRCA2 genes and other regions on 17q and 13q in breast cancer among women from Taiwan (area of low incidence but early onset). <i>International Journal of Cancer</i> , <b>1998</b> , 79, 580-7	7.5	40
54	Polymorphism of cytosolic serine hydroxymethyltransferase, estrogen and breast cancer risk among Chinese women in Taiwan. <i>Breast Cancer Research and Treatment</i> , <b>2008</b> , 111, 145-55	4.4	40
53	The clinical implications of MMP-11 and CK-20 expression in human breast cancer. <i>Clinica Chimica Acta</i> , <b>2010</b> , 411, 234-41	6.2	39

52	Association between N-acetyltransferase 2 (NAT2) genetic polymorphism and development of breast cancer in post-menopausal Chinese women in Taiwan, an area of great increase in breast cancer incidence. <i>International Journal of Cancer</i> , <b>1999</b> , 82, 175-9	7.5	39
51	MicroRNA-30a increases tight junction protein expression to suppress the epithelial-mesenchymal transition and metastasis by targeting Slug in breast cancer. <i>Oncotarget</i> , <b>2016</b> , 7, 16462-78	3.3	38
50	Unique features of breast cancer in Asian women--breast cancer in Taiwan as an example. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , <b>2010</b> , 118, 300-3	5.1	37
49	Synergistic effects of polymorphisms in DNA repair genes and endogenous estrogen exposure on female breast cancer risk. <i>Annals of Surgical Oncology</i> , <b>2010</b> , 17, 760-71	3.1	37
48	Genetic variation in the premature aging gene WRN: a case-control study on breast cancer susceptibility. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2007</b> , 16, 263-9	4	37
47	Genetic susceptibility to the development and progression of breast cancer associated with polymorphism of cell cycle and ubiquitin ligase genes. <i>Carcinogenesis</i> , <b>2009</b> , 30, 1562-70	4.6	36
46	Aberrant expression of cell-cycle regulator cyclin D1 in breast cancer is related to chromosomal genomic instability. <i>Genes Chromosomes and Cancer</i> , <b>2002</b> , 34, 276-84	5	34
45	Increased Cellular Levels of MicroRNA-9 and MicroRNA-221 Correlate with Cancer Stemness and Predict Poor Outcome in Human Breast Cancer. <i>Cellular Physiology and Biochemistry</i> , <b>2018</b> , 48, 2205-2218 <sup>9</sup>	3.9	31
44	High-resolution 19p13.2-13.3 allelotyping of breast carcinomas demonstrates frequent loss of heterozygosity. <i>Genes Chromosomes and Cancer</i> , <b>2004</b> , 41, 250-6	5	31
43	Prognostic significance of cyclin D1, E-catenin, and MTA1 in patients with invasive ductal carcinoma of the breast. <i>Annals of Surgical Oncology</i> , <b>2012</b> , 19, 4129-39	3.1	28
42	Genetic variation in the genome-wide predicted estrogen response element-related sequences is associated with breast cancer development. <i>Breast Cancer Research</i> , <b>2011</b> , 13, R13	8.3	28
41	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. <i>American Journal of Human Genetics</i> , <b>2015</b> , 97, 22-34	11	26
40	Diverse associations between ESR1 polymorphism and breast cancer development and progression. <i>Clinical Cancer Research</i> , <b>2010</b> , 16, 3473-84	12.9	26
39	The Effect of MicroRNA-124 Overexpression on Anti-Tumor Drug Sensitivity. <i>PLoS ONE</i> , <b>2015</b> , 10, e0128472	3.72	26
38	Initiation of the ATM-Chk2 DNA damage response through the base excision repair pathway. <i>Carcinogenesis</i> , <b>2015</b> , 36, 832-40	4.6	23
37	B-Myb Induces APOBEC3B Expression Leading to Somatic Mutation in Multiple Cancers. <i>Scientific Reports</i> , <b>2017</b> , 7, 44089	4.9	22
36	Novel patterns of p53 abnormality in breast cancer from Taiwan: experience from a low-incidence area. <i>British Journal of Cancer</i> , <b>1997</b> , 75, 746-51	8.7	21
35	Breast cancer risk associated with genotypic polymorphism of the genes involved in the estrogen-receptor-signaling pathway: a multigenic study on cancer susceptibility. <i>Journal of Biomedical Science</i> , <b>2006</b> , 13, 419-32	13.3	21

34	Breast cancer risk associated with genotypic polymorphism of the mitotic checkpoint genes: a multigenic study on cancer susceptibility. <i>Carcinogenesis</i> , <b>2007</b> , 28, 1079-86	4.6	21
33	FGFR2 regulates Mre11 expression and double-strand break repair via the MEK-ERK-POU1F1 pathway in breast tumorigenesis. <i>Human Molecular Genetics</i> , <b>2015</b> , 24, 3506-17	5.6	18
32	Fine-scale mapping of the 4q24 locus identifies two independent loci associated with breast cancer risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2015</b> , 24, 1680-91	4	17
31	Hide-then-hitTo explain the importance of genotypic polymorphism of DNA repair genes in determining susceptibility to cancer. <i>Journal of Molecular Cell Biology</i> , <b>2011</b> , 3, 59-65	6.3	15
30	Expression of estrogen receptor-alpha and Ki67 in relation to pathological and molecular features in early-onset infiltrating ductal carcinoma. <i>Journal of Biomedical Science</i> , <b>2004</b> , 11, 911-9	13.3	15
29	Hantavirus infection in Taiwan: the experience of a geographically unique area. <i>Journal of Medical Virology</i> , <b>2000</b> , 60, 237-47	19.7	14
28	Clinical Relevance of Liver Kinase B1(LKB1) Protein and Gene Expression in Breast Cancer. <i>Scientific Reports</i> , <b>2016</b> , 6, 21374	4.9	13
27	The human NANOS3 gene contributes to lung tumour invasion by inducing epithelial-mesenchymal transition. <i>Journal of Pathology</i> , <b>2015</b> , 237, 25-37	9.4	13
26	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. <i>Nature Communications</i> , <b>2014</b> , 5, 4051	17.4	13
25	Fanconi anemia genes in lung adenocarcinoma- a pathway-wide study on cancer susceptibility. <i>Journal of Biomedical Science</i> , <b>2016</b> , 23, 23	13.3	12
24	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. <i>Breast Cancer Research</i> , <b>2014</b> , 16, R51	8.3	12
23	A functional variant near XCL1 gene improves breast cancer survival via promoting cancer immunity. <i>International Journal of Cancer</i> , <b>2020</b> , 146, 2182-2193	7.5	12
22	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. <i>American Journal of Human Genetics</i> , <b>2020</b> , 107, 837-848	11	12
21	Protein deficiency after gastric bypass: The role of common limb length in revision surgery. <i>Surgery for Obesity and Related Diseases</i> , <b>2019</b> , 15, 441-446	3	11
20	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> , <b>2019</b> , 48, 203-211	8.8	9
19	A high-resolution HLA imputation system for the Taiwanese population: a study of the Taiwan Biobank. <i>Pharmacogenomics Journal</i> , <b>2020</b> , 20, 695-704	3.5	8
18	High Prevalence of the BIM Deletion Polymorphism in Young Female Breast Cancer in an East Asian Country. <i>PLoS ONE</i> , <b>2015</b> , 10, e0124908	3.7	8
17	Functional variants at the 21q22.3 locus involved in breast cancer progression identified by screening of genome-wide estrogen response elements. <i>Breast Cancer Research</i> , <b>2014</b> , 16, 455	8.3	5

16	Laser capture microdissection in carcinoma analysis. <i>Methods in Enzymology</i> , <b>2002</b> , 356, 137-44	1.7	4
15	The Causal Relationship of Circulating Triglyceride and Glycated Hemoglobin: A Mendelian Randomization Study. <i>Journal of Clinical Endocrinology and Metabolism</i> , <b>2020</b> , 105,	5.6	4
14	Blood multiomics reveal insights into population clusters with low prevalence of diabetes, dyslipidemia and hypertension. <i>PLoS ONE</i> , <b>2020</b> , 15, e0229922	3.7	3
13	Detecting Genetic Ancestry and Adaptation in the Taiwanese Han People. <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 4149-4165	8.3	3
12	Rare variants discovery by extensive whole-genome sequencing of the Han Chinese population in Taiwan: Applications to cardiovascular medicine. <i>Journal of Advanced Research</i> , <b>2021</b> , 30, 147-158	13	3
11	Humoral immune responses and cytomegalovirus excretion in children with asymptomatic infection. <i>Journal of Medical Virology</i> , <b>1994</b> , 44, 37-42	19.7	2
10	Taiwan Biobank: a rich biomedical research database of the Taiwanese population		2
9	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> , <b>2021</b> , 108, 1190-1203	11	1
8	Genome-wide association study identifies genetic risk loci for adiposity in a Taiwanese population.. <i>PLoS Genetics</i> , <b>2022</b> , 18, e1009952	6	0
7	A common variant in 11q23.3 associated with hyperlipidemia is mediated by the binding and regulation of GATA4.. <i>Npj Genomic Medicine</i> , <b>2022</b> , 7, 4	6.2	0
6	Body mass index and type 2 diabetes and breast cancer survival: a Mendelian randomization study. <i>American Journal of Cancer Research</i> , <b>2021</b> , 11, 3921-3934	4.4	
5	Blood multiomics reveal insights into population clusters with low prevalence of diabetes, dyslipidemia and hypertension <b>2020</b> , 15, e0229922		
4	Blood multiomics reveal insights into population clusters with low prevalence of diabetes, dyslipidemia and hypertension <b>2020</b> , 15, e0229922		
3	Blood multiomics reveal insights into population clusters with low prevalence of diabetes, dyslipidemia and hypertension <b>2020</b> , 15, e0229922		
2	Blood multiomics reveal insights into population clusters with low prevalence of diabetes, dyslipidemia and hypertension <b>2020</b> , 15, e0229922		
1	Relevance of the MHC region for breast cancer susceptibility in Asians.. <i>Breast Cancer</i> , <b>2022</b> , 1	3.4	