Chen-Yang Shen

List of Publications by Year
in descending order

88 papers	9,493 citations	76326 40 h-index	62596 80 g-index
89 all docs	89 docs citations	89 times ranked	13629 citing authors

#	Article	IF	Citations
1	Genome-wide association study identifies novel breast cancer susceptibility loci. Nature, 2007, 447, 1087-1093.	27.8	2,165
2	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
3	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	21.4	960
4	Carbamazepine-Induced Toxic Effects and HLA-B*1502 Screening in Taiwan. New England Journal of Medicine, 2011, 364, 1126-1133.	27.0	631
5	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	21.4	513
6	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374
7	Mechanisms of inactivation of E-cadherin in breast carcinoma: modification of the two-hit hypothesis of tumor suppressor gene. Oncogene, 2001, 20, 3814-3823.	5.9	206
8	Population structure of Han Chinese in the modern Taiwanese population based on 10,000 participants in the Taiwan Biobank project. Human Molecular Genetics, 2016, 25, ddw346.	2.9	196
9	MicroRNA-30a inhibits cell migration and invasion by downregulating vimentin expression and is a potential prognostic marker in breast cancer. Breast Cancer Research and Treatment, 2012, 134, 1081-1093.	2.5	188
10	Use of HLA-B*58:01 genotyping to prevent allopurinol induced severe cutaneous adverse reactions in Taiwan: national prospective cohort study. BMJ, The, 2015, 351, h4848.	6.0	148
11	Genome-wide association analysis in East Asians identifies breast cancer susceptibility loci at 1q32.1, 5q14.3 and 15q26.1. Nature Genetics, 2014, 46, 886-890.	21.4	135
12	Breast cancer risk associated with genotypic polymorphism of the nonhomologous end-joining genes: a multigenic study on cancer susceptibility. Cancer Research, 2003, 63, 2440-6.	0.9	132
13	Chk2-dependent phosphorylation of XRCC1 in the DNA damage response promotes base excision repair. EMBO Journal, 2008, 27, 3140-3150.	7.8	110
14	FGFR2 variants and breast cancer risk: fine-scale mapping using African American studies and analysis of chromatin conformation. Human Molecular Genetics, 2009, 18, 1692-1703.	2.9	110
15	Breast cancer risk associated with genotype polymorphism of the catechol estrogen-metabolizing genes: A multigenic study on cancer susceptibility. International Journal of Cancer, 2005, 113, 345-353.	5.1	109
16	Breast Cancer Risk and the DNA Double-Strand Break End-Joining Capacity of Nonhomologous End-Joining Genes Are Affected by BRCA1. Cancer Research, 2004, 64, 5013-5019.	0.9	108
17	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	12.8	105
18	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. American Journal of Human Genetics, 2013, 93, 1046-1060.	6.2	98

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19	Burden of Total and Cause-Specific Mortality Related to Tobacco Smoking among Adults Aged â‰¥45 Years in Asia: A Pooled Analysis of 21 Cohorts. PLoS Medicine, 2014, 11, e1001631.	8.4	98
20	Ataxia Telangiectasia Mutated and Checkpoint Kinase 2 Regulate BRCA1 to Promote the Fidelity of DNA End-Joining. Cancer Research, 2006, 66, 1391-1400.	0.9	97
21	No evidence that protein truncating variants inBRIP1are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	3.2	94
22	Breast Cancer Risk Is Associated with the Genes Encoding the DNA Double-Strand Break Repair Mre11/Rad50/Nbs1 Complex. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 2024-2032.	2.5	86
23	Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating MAP3K1. American Journal of Human Genetics, 2015, 96, 5-20.	6.2	76
24	DNA double-strand break repair capacity and risk of breast cancer. Carcinogenesis, 2007, 28, 1726-1730.	2.8	65
25	Breast cancer risk associated with genotypic polymorphism of the mitosis-regulating geneAurora-A/STK15/BTAK. International Journal of Cancer, 2005, 115, 276-283.	5.1	64
26	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. American Journal of Human Genetics, 2016, 99, 903-911.	6.2	59
27	Foxo3a-mediated overexpression of microRNA-622 suppresses tumor metastasis by repressing hypoxia-inducible factor-1Î± in erk-responsive lung cancer. Oncotarget, 2015, 6, 44222-44238.	1.8	54
28	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	2.9	53
29	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. Human Molecular Genetics, 2014, 23, 355-367.	2.9	52
30	The role of BRCA1 in non-homologous end-joining. Cancer Letters, 2006, 240, 1-8.	7.2	50
31	MicroRNA-30a increases tight junction protein expression to suppress the epithelial-mesenchymal transition and metastasis by targeting Slug in breast cancer. Oncotarget, 2016, 7, 16462-16478.	1.8	47
32	Genetic variants of BLM interact with RAD51 to increase breast cancer susceptibility. Carcinogenesis, 2009, 30, 43-49.	2.8	46
33	Increased expression of SRp40 affecting CD44 splicing is associated with the clinical outcome of lymph node metastasis in human breast cancer. Clinica Chimica Acta, 2007, 384, 69-74.	1.1	45
34	The clinical implications of MMP-11 and CK-20 expression in human breast cancer. Clinica Chimica Acta, 2010, 411, 234-241.	1.1	45
35	Association betweenN-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. , 1999, 82, 175-179.		44
36	Allelic loss of theBRCA1 andBRCA2 genes and other regions on 17q and 13q in breast cancer among women from Taiwan (area of low incidence but early onset). International Journal of Cancer, 1998, 79, 580-587.	5.1	43

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37	Synergistic Effects of Polymorphisms in DNA Repair Genes and Endogenous Estrogen Exposure on Female Breast Cancer Risk. Annals of Surgical Oncology, 2010, 17, 760-771.	1.5	43
38	Unique features of breast cancer in Asian womenâ€"Breast cancer in Taiwan as an example. Journal of Steroid Biochemistry and Molecular Biology, 2010, 118, 300-303.	2.5	42
39	Genetic Variation in the Premature Aging Gene WRN: A Case-Control Study on Breast Cancer Susceptibility. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 263-269.	2.5	41
40	Polymorphism of cytosolic serine hydroxymethyltransferase, estrogen and breast cancer risk among Chinese women in Taiwan. Breast Cancer Research and Treatment, 2008, 111, 145-155.	2.5	41
41	Increased Cellular Levels of MicroRNA-9 and MicroRNA-221 Correlate with Cancer Stemness and Predict Poor Outcome in Human Breast Cancer. Cellular Physiology and Biochemistry, 2018, 48, 2205-2218.	1.6	41
42	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	6.2	39
43	Aberrant expression of cell-cycle regulator cyclin D1 in breast cancer is related to chromosomal genomic instability. Genes Chromosomes and Cancer, 2002, 34, 276-284.	2.8	38
44	Genetic susceptibility to the development and progression of breast cancer associated with polymorphism of cell cycle and ubiquitin ligase genes. Carcinogenesis, 2009, 30, 1562-1570.	2.8	37
45	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. American Journal of Human Genetics, 2015, 97, 22-34.	6.2	37
46	The Effect of MicroRNA-124 Overexpression on Anti-Tumor Drug Sensitivity. PLoS ONE, 2015, 10, e0128472.	2.5	37
47	Initiation of the ATM-Chk2 DNA damage response through the base excision repair pathway. Carcinogenesis, 2015, 36, 832-840.	2.8	35
48	High-resolution 19p13.2-13.3 allelotyping of breast carcinomas demonstrates frequent loss of heterozygosity. Genes Chromosomes and Cancer, 2004, 41, 250-256.	2.8	33
49	Genetic variation in the genome-wide predicted estrogen response element-related sequences is associated with breast cancer development. Breast Cancer Research, 2011, 13, R13.	5.0	30
50	Prognostic Significance of cyclin D1, Î²-catenin, and MTA1 in Patients with Invasive Ductal Carcinoma of the Breast. Annals of Surgical Oncology, 2012, 19, 4129-4139.	1.5	28
51	Diverse Associations between ESR1 Polymorphism and Breast Cancer Development and Progression. Clinical Cancer Research, 2010, 16, 3473-3484.	7.0	26
52	B-Myb Induces APOBEC3B Expression Leading to Somatic Mutation in Multiple Cancers. Scientific Reports, 2017, 7, 44089.	3.3	26
53	Breast cancer risk associated with genotypic polymorphism of the genes involved in the estrogen-receptor-signaling pathway: a multigenic study on cancer susceptibility. Journal of Biomedical Science, 2006, 13, 419-432.	7.0	25
54	Breast cancer risk associated with genotypic polymorphism of the mitotic checkpoint genes: a multigenic study on cancer susceptibility. Carcinogenesis, 2006, 28, 1079-1086.	2.8	25

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55	Novel patterns of p53 abnormality in breast cancer from Taiwan: experience from a low-incidence area. British Journal of Cancer, 1997, 75, 746-751.	6.4	24
56	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1680-1691.	2.5	24
57	FGFR2 regulates Mre11 expression and double-strand break repair via the MEK-ERK-POU1F1 pathway in breast tumorigenesis. Human Molecular Genetics, 2015, 24, 3506-3517.	2.9	19
58	Expression of estrogen receptor-Î± and Ki67 in relation to pathological and molecular features in early-onset infiltrating ductal carcinoma. Journal of Biomedical Science, 2004, 11, 911-919.	7.0	18
59	Protein deficiency after gastric bypass: The role of common limb length in revision surgery. Surgery for Obesity and Related Diseases, 2019, 15, 441-446.	1.2	18
60	'Hide-then-hit' to explain the importance of genotypic polymorphism of DNA repair genes in determining susceptibility to cancer. Journal of Molecular Cell Biology, 2011, 3, 59-65.	3.3	17
61	The human NANOS3 gene contributes to lung tumour invasion by inducing epithelialâ€“mesenchymal transition. Journal of Pathology, 2015, 237, 25-37.	4.5	17
62	Clinical Relevance of Liver Kinase B1(LKB1) Protein and Gene Expression in Breast Cancer. Scientific Reports, 2016, 6, 21374.	3.3	17
63	Hantavirus infection in Taiwan: The experience of a geographically unique area. , 2000, 60, 237-247.		16
64	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. Nature Communications, 2014, 5, 4051.	12.8	16
65	Fanconi anemia genes in lung adenocarcinoma- a pathway-wide study on cancer susceptibility. Journal of Biomedical Science, 2016, 23, 23.	7.0	16
66	A high-resolution HLA imputation system for the Taiwanese population: a study of the Taiwan Biobank. Pharmacogenomics Journal, 2020, 20, 695-704.	2.0	16
67	A functional variant near XCL1 gene improves breast cancer survival via promoting cancer immunity. International Journal of Cancer, 2020, 146, 2182-2193.	5.1	15
68	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. Breast Cancer Research, 2014, 16, R51.	5.0	14
69	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. EBioMedicine, 2019, 48, 203-211.	6.1	14
70	Rare variants discovery by extensive whole-genome sequencing of the Han Chinese population in Taiwan: Applications to cardiovascular medicine. Journal of Advanced Research, 2021, 30, 147-158.	9.5	13
71	Detecting Genetic Ancestry and Adaptation in the Taiwanese Han People. Molecular Biology and Evolution, 2021, 38, 4149-4165.	8.9	12
72	The Causal Relationship of Circulating Triglyceride and Glycated Hemoglobin: A Mendelian Randomization Study. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 908-919.	3.6	10

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73	MiR-139 Modulates Cancer Stem Cell Function of Human Breast Cancer through Targeting CXCR4. Cancers, 2021, 13, 2582.	3.7	10
74	High Prevalence of the BIM Deletion Polymorphism in Young Female Breast Cancer in an East Asian Country. PLoS ONE, 2015, 10, e0124908.	2.5	9
75	A common variant in 11q23.3 associated with hyperlipidemia is mediated by the binding and regulation of GATA4. Npj Genomic Medicine, 2022, 7, 4.	3.8	7
76	Blood multiomics reveal insights into population clusters with low prevalence of diabetes, dyslipidemia and hypertension. PLoS ONE, 2020, 15, e0229922.	2.5	6
77	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. American Journal of Human Genetics, 2021, 108, 1190-1203.	6.2	6
78	Genome-wide association study identifies genetic risk loci for adiposity in a Taiwanese population. PLoS Genetics, 2022, 18, e1009952.	3.5	6
79	[12] Laser capture microdissection in carcinoma analysis. Methods in Enzymology, 2002, 356, 137-144.	1.0	5
80	Functional variants at the 21q22.3 locus involved in breast cancer progression identified by screening of genome-wide estrogen response elements. Breast Cancer Research, 2014, 16, 455.	5.0	5
81	Gene-Environment Interactions Relevant to Estrogen and Risk of Breast Cancer: Can Gene-Environment Interactions Be Detected Only among Candidate SNPs from Genome-Wide Association Studies?. Cancers, 2021, 13, 2370.	3.7	4
82	Humoral immune responses and cytomegalovirus excretion in children with asymptomatic infection. Journal of Medical Virology, 1994, 44, 37-42.	5.0	3
83	Relevance of the MHC region for breast cancer susceptibility in Asians. Breast Cancer, 2022, 29, 869-879.	2.9	1
84	Body mass index and type 2 diabetes and breast cancer survival: a Mendelian randomization study. American Journal of Cancer Research, 2021, 11, 3921-3934.	1.4	0
85	Title is missing!. , 2020, 15, e0229922.		0
86	Title is missing!. , 2020, 15, e0229922.		0
87	Title is missing!. , 2020, 15, e0229922.		0
88	Title is missing!. , 2020, 15, e0229922.		0