Wen Tan

List of Publications by Year
in descending order

50 papers	2,994 citations	236925 25 h-index	182427 51 g-index
51 all docs	51 docs citations	51 times ranked	5883 citing authors

#	Article	IF	Citations
1	Excessive miR-25-3p maturation via N6-methyladenosine stimulated by cigarette smoke promotes pancreatic cancer progression. Nature Communications, 2019, 10, 1858.	12.8	242
2	Pancreatic cancer risk variant in LINC00673 creates a miR-1231 binding site and interferes with PTPN11 degradation. Nature Genetics, 2016, 48, 747-757.	21.4	237
3	Genomic analysis of oesophageal squamous-cell carcinoma identifies alcohol drinking-related mutation signature and genomic alterations. Nature Communications, 2017, 8, 15290.	12.8	195
4	Identification of risk loci and a polygenic risk score for lung cancer: a large-scale prospective cohort study in Chinese populations. Lancet Respiratory Medicine,the, 2019, 7, 881-891.	10.7	167
5	Genome-wide association study identifies five loci associated with susceptibility to pancreatic cancer in Chinese populations. Nature Genetics, 2012, 44, 62-66.	21.4	164
6	Joint analysis of three genome-wide association studies of esophageal squamous cell carcinoma in Chinese populations. Nature Genetics, 2014, 46, 1001-1006.	21.4	148
7	PIWI-interacting RNA-36712 restrains breast cancer progression and chemoresistance by interaction with SEPW1 pseudogene SEPW1P RNA. Molecular Cancer, 2019, 18, 9.	19.2	139
8	CYP 1A1 polymorphism and risk of lung cancer in relation to tobacco smoking: a case-control study in China. Carcinogenesis, 2001, 22, 11-16.	2.8	131
9	Frequency ofCYP2A6 gene deletion and its relation to risk of lung and esophageal cancer in the Chinese population. International Journal of Cancer, 2001, 95, 96-101.	5.1	115
10	PIWI-interacting RNA-54265 is oncogenic and a potential therapeutic target in colorectal adenocarcinoma. Theranostics, 2018, 8, 5213-5230.	10.0	115
11	Dissecting esophageal squamous-cell carcinoma ecosystem by single-cell transcriptomic analysis. Nature Communications, 2021, 12, 5291.	12.8	98
12	Genome-wide association study identifies common variants in SLC39A6 associated with length of survival in esophageal squamous-cell carcinoma. Nature Genetics, 2013, 45, 632-638.	21.4	97
13	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. Human Molecular Genetics, 2014, 23, 6616-6633.	2.9	90
14	Associations of functional polymorphisms in cyclooxygenase-2 and platelet 12-lipoxygenase with risk of occurrence and advanced disease status of colorectal cancer. Carcinogenesis, 2007, 28, 1197-1201.	2.8	89
15	Genetic risk of extranodal natural killer T-cell lymphoma: a genome-wide association study. Lancet Oncology, The, 2016, 17, 1240-1247.	10.7	84
16	<scp>G</scp>enetic 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. International Journal of Cancer, 2015, 137, 311-319.	5.1	72
17	Serum piRNA-54265 is a New Biomarker for early detection and clinical surveillance of Human Colorectal Cancer. Theranostics, 2020, 10, 8468-8478.	10.0	58
18	A Genome Wide Association Study Identifies Common Variants Associated with Lipid Levels in the Chinese Population. PLoS ONE, 2013, 8, e82420.	2.5	57

#	Article	IF	Citations
19	Genome-wide association study identifies three susceptibility loci for laryngeal squamous cell carcinoma in the Chinese population. Nature Genetics, 2014, 46, 1110-1114.	21.4	57
20	Association between GWAS-identified lung adenocarcinoma susceptibility loci and EGFR mutations in never-smoking Asian women, and comparison with findings from Western populations. Human Molecular Genetics, 2016, 26, ddw414.	2.9	50
21	Meta-analysis of genome-wide association studies identifies multiple lung cancer susceptibility loci in never-smoking Asian women. Human Molecular Genetics, 2016, 25, 620-629.	2.9	50
22	Genetic risk of extranodal natural killer T-cell lymphoma: a genome-wide association study in multiple populations. Lancet Oncology, The, 2020, 21, 306-316.	10.7	49
23	Metformin inhibits pancreatic cancer metastasis caused by SMAD4 deficiency and consequent HNF4G upregulation. Protein and Cell, 2021, 12, 128-144.	11.0	41
24	Solute Carrier Family 39 Member 6 Gene Promotes Aggressiveness of Esophageal Carcinoma Cells by Increasing Intracellular Levels of Zinc, Activating Phosphatidylinositol 3-Kinase Signaling, and Up-regulating Genes That Regulate Metastasis. Gastroenterology, 2017, 152, 1985-1997.e12.	1.3	40
25	Significant increase in risk of gastroesophageal cancer is associated with interaction between promoter polymorphisms in thymidylate synthase and serum folate status. Carcinogenesis, 2005, 26, 1430-1435.	2.8	37
26	Genome landscapes of rectal cancer before and after preoperative chemoradiotherapy. Theranostics, 2019, 9, 6856-6866.	10.0	27
27	Metabolic remodeling by TIGAR overexpression is a therapeutic target in esophageal squamous-cell carcinoma. Theranostics, 2020, 10, 3488-3502.	10.0	27
28	Regulatory T cells promote pulmonary repair by modulating T helper cell immune responses in lipopolysaccharide induced acute respiratory distress syndrome. Immunology, 2019, 157, 151-162.	4.4	26
29	BRCA1-Associated Protein Increases Invasiveness of Esophageal Squamous Cell Carcinoma. Gastroenterology, 2017, 153, 1304-1319.e5.	1.3	23
30	Multi-omic characterization of genome-wide abnormal DNA methylation reveals diagnostic and prognostic markers for esophageal squamous-cell carcinoma. Signal Transduction and Targeted Therapy, 2022, 7, 53.	17.1	22
31	Genomic and transcriptomic alterations associated with drug vulnerabilities and prognosis in adenocarcinoma at the gastroesophageal junction. Nature Communications, 2020, 11, 6091.	12.8	21
32	Functional role of BTB and CNC Homology 1 gene in pancreatic cancer and its association with survival in patients treated with gemcitabine. Theranostics, 2018, 8, 3366-3379.	10.0	19
33	CCGD-ESCC: A Comprehensive Database for Genetic Variants Associated with Esophageal Squamous Cell Carcinoma in Chinese Population. Genomics, Proteomics and Bioinformatics, 2018, 16, 262-268.	6.9	17
34	Genetic variant repressing ADH1A expression confers susceptibility to esophageal squamous-cell carcinoma. Cancer Letters, 2018, 421, 43-50.	7.2	16
35	Pulmonary expression of *CYP2A13* and *ABCB1* is regulated by FOXA2, and their genetic interaction is associated with lung cancer. FASEB Journal, 2015, 29, 1986-1998.	0.5	15
36	Tuberculosis infection and lung adenocarcinoma: Mendelian randomization and pathway analysis of genome-wide association study data from never-smoking Asian women. Genomics, 2020, 112, 1223-1232.	2.9	15

#	Article	IF	Citations
37	Reply to â€A promoter polymorphism in the CASP8 gene is not associated with cancer riskâ€• Nature Genetics, 2008, 40, 260-261.	21.4	14
38	Integrative analysis of gene expression profiles reveals specific signaling pathways associated with pancreatic duct adenocarcinoma. Cancer Communications, 2018, 38, 1-12.	9.2	14
39	VAV2 is required for DNA repair and implicated in cancer radiotherapy resistance. Signal Transduction and Targeted Therapy, 2021, 6, 322.	17.1	14
40	CstF64-Induced Shortening of the *BID* 3â€²UTR Promotes Esophageal Squamous Cell Carcinoma Progression by Disrupting ceRNA Cross-talk with *ZFP36L2*. Cancer Research, 2021, 81, 5638-5651.	0.9	13
41	Two Novel Variants on 13q22.1 Are Associated with Risk of Esophageal Squamous Cell Carcinoma. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1774-1780.	2.5	12
42	Protectin DX Exhibits Protective Effects in Mouse Model of Lipopolysaccharide-Induced Acute Lung Injury. Chinese Medical Journal, 2018, 131, 1167-1173.	2.3	12
43	Remote Ischemic Preconditioning has a Cardioprotective Effect in Children in the Early Postoperative Phase: A Meta-Analysis of Randomized Controlled Trials. Pediatric Cardiology, 2018, 39, 617-626.	1.3	11
44	Associations of Genetic Variations in Mismatch Repair Genes MSH3 and PMS1 with Acute Adverse Events and Survival in Patients with Rectal Cancer Receiving Postoperative Chemoradiotherapy. Cancer Research and Treatment, 2019, 51, 1198-1206.	3.0	10
45	Interleukin-33-Dependent Accumulation of Regulatory T Cells Mediates Pulmonary Epithelial Regeneration During Acute Respiratory Distress Syndrome. Frontiers in Immunology, 2021, 12, 653803.	4.8	9
46	Functional role of PLCE1 intronic insertion variant associated with susceptibility to esophageal squamous cell carcinoma. Carcinogenesis, 2018, 39, 191-201.	2.8	5
47	Functional XPF polymorphisms associated with lung cancer susceptibility in a Chinese population. Frontiers of Medicine in China, 2010, 4, 82-89.	0.1	4
48	Associations of ATM Polymorphisms With Survival in Advanced Esophageal Squamous Cell Carcinoma Patients Receiving Radiation Therapy. International Journal of Radiation Oncology Biology Physics, 2015, 93, 181-189.	0.8	4
49	Associations of Genetic Variations in MicroRNA Seed Regions With Acute Adverse Events and Survival in Patients With Rectal Cancer Receiving Postoperative Chemoradiation Therapy. International Journal of Radiation Oncology Biology Physics, 2018, 100, 1026-1033.	0.8	3
50	Relatively Small Contribution of Methylation and Genomic Copy Number Aberration to the Aberrant Expression of Inflammation-Related Genes in HBV-Related Hepatocellular Carcinoma. PLoS ONE, 2015, 10, e0126836.	2.5	1