Tongwu Zhang

List of Publications by Year
in descending order

61 papers	2,499 citations	201658 27 h-index	233409 45 g-index
67 all docs	67 docs citations	67 times ranked	5664 citing authors

#	Article	IF	Citations
1	Loci associated with skin pigmentation identified in African populations. Science, 2017, 358, .	12.6	260
2	The genomic landscape of cutaneous melanoma. Pigment Cell and Melanoma Research, 2016, 29, 266-283.	3.3	144
3	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. Nature Genetics, 2020, 52, 494-504.	21.4	138
4	Genomic Analysis of the Multidrug-Resistant Acinetobacter baumannii Strain MDR-ZJ06 Widely Spread in China. Antimicrobial Agents and Chemotherapy, 2011, 55, 4506-4512.	3.2	116
5	Gut microbiota dependent anti-tumor immunity restricts melanoma growth in Rnf5âˆ'/âˆ' mice. Nature Communications, 2019, 10, 1492.	12.8	114
6	A Complete Sequence and Transcriptomic Analyses of Date Palm (Phoenix dactylifera L.) Mitochondrial Genome. PLoS ONE, 2012, 7, e37164.	2.5	106
7	Epigenome-wide analysis of DNA methylation in lung tissue shows concordance with blood studies and identifies tobacco smoke-inducible enhancers. Human Molecular Genetics, 2017, 26, 3014-3027.	2.9	97
8	Genomic and evolutionary classification of lung cancer in never smokers. Nature Genetics, 2021, 53, 1348-1359.	21.4	81
9	The Complete Chloroplast and Mitochondrial Genome Sequences of Boea hygrometrica: Insights into the Evolution of Plant Organellar Genomes. PLoS ONE, 2012, 7, e30531.	2.5	79
10	Genetic and epigenetic intratumor heterogeneity impacts prognosis of lung adenocarcinoma. Nature Communications, 2020, 11, 2459.	12.8	77
11	Cell-typeâ€"specific eQTL of primary melanocytes facilitates identification of melanoma susceptibility genes. Genome Research, 2018, 28, 1621-1635.	5.5	67
12	Genetic Heterogeneity of BRAF Fusion Kinases in Melanoma Affects Drug Responses. Cell Reports, 2019, 29, 573-588.e7.	6.4	62
13	Mapping clustered mutations in cancer reveals APOBEC3 mutagenesis of ecDNA. Nature, 2022, 602, 510-517.	27.8	60
14	A Transcriptome-Wide Association Study Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer. Journal of the National Cancer Institute, 2020, 112, 1003-1012.	6.3	59
15	Downregulation of the Ubiquitin Ligase RNF125 Underlies Resistance of Melanoma Cells to BRAF Inhibitors via JAK1 Deregulation. Cell Reports, 2015, 11, 1458-1473.	6.4	55
16	Whole genome sequencing of skull-base chordoma reveals genomic alterations associated with recurrence and chordoma-specific survival. Nature Communications, 2021, 12, 757.	12.8	55
17	Massively parallel reporter assays of melanoma risk variants identify MX2 as a gene promoting melanoma. Nature Communications, 2020, 11, 2718.	12.8	53
18	A common intronic variant of PARP1 confers melanoma risk and mediates melanocyte growth via regulation of MITF. Nature Genetics, 2017, 49, 1326-1335.	21.4	51

#	ARTICLE	IF	CITATIONS
19	PDK1 and SGK3 Contribute to the Growth of BRAF-Mutant Melanomas and Are Potential Therapeutic Targets. Cancer Research, 2015, 75, 1399-1412.	0.9	50
20	An interaction proteomics survey of transcription factor binding at recurrent TERT promoter mutations. Proteomics, 2016, 16, 417-426.	2.2	50
21	Immune gene expression profiling reveals heterogeneity in luminal breast tumors. Breast Cancer Research, 2019, 21, 147.	5.0	43
22	Functional characterization of a multi-cancer risk locus on chr5p15.33 reveals regulation of TERT by ZNF148. Nature Communications, 2017, 8, 15034.	12.8	40
23	Regulation of S100A8 Stability by RNF5 in Intestinal Epithelial Cells Determines Intestinal Inflammation and Severity of Colitis. Cell Reports, 2018, 24, 3296-3311.e6.	6.4	39
24	SHARPIN-mediated regulation of protein arginine methyltransferase 5 controls melanoma growth. Journal of Clinical Investigation, 2017, 128, 517-530.	8.2	36
25	Combining common genetic variants and non-genetic risk factors to predict risk of cutaneous melanoma. Human Molecular Genetics, 2018, 27, 4145-4156.	2.9	34
26	Microparticles from tumors exposed to radiation promote immune evasion in part by PD-L1. Oncogene, 2020, 39, 187-203.	5.9	34
27	Meta-analysis of GWA studies provides new insights on the genetic architecture of skin pigmentation in recently admixed populations. BMC Genetics, 2019, 20, 59.	2.7	32
28	Analysis of DNA methylation patterns in the tumor immune microenvironment of metastatic melanoma. Molecular Oncology, 2020, 14, 933-950.	4.6	29
29	SBI-0640756 Attenuates the Growth of Clinically Unresponsive Melanomas by Disrupting the eIF4F Translation Initiation Complex. Cancer Research, 2015, 75, 5211-5218.	0.9	28
30	BIGpre: A Quality Assessment Package for Next-Generation Sequencing Data. Genomics, Proteomics and Bioinformatics, 2011, 9, 238-244.	6.9	26
31	Large-scale collection and annotation of gene models for date palm (Phoenix dactylifera, L.). Plant Molecular Biology, 2012, 79, 521-536.	3.9	26
32	Characterising <i>cis</i>-regulatory variation in the transcriptome of histologically normal and tumour-derived pancreatic tissues. Gut, 2018, 67, 521-533.	12.1	26
33	A Transcriptionally Inactive ATF2 Variant Drives Melanomagenesis. Cell Reports, 2016, 15, 1884-1892.	6.4	21
34	The ubiquitin ligase RNF5 determines acute myeloid leukemia growth and susceptibility to histone deacetylase inhibitors. Nature Communications, 2021, 12, 5397.	12.8	20
35	Nucleotide compositional asymmetry between the leading and lagging strands of eubacterial genomes. Research in Microbiology, 2010, 161, 838-846.	2.1	19
36	The genomic and epigenomic evolutionary history of papillary renal cell carcinomas. Nature Communications, 2020, 11, 3096.	12.8	19

#	Article	IF	Citations
37	IL-6 contributes to metastatic switch via the differentiation of monocytic-dendritic progenitors into prometastatic immune cells. , 2021, 9, e002856.		19
38	ezQTL: A Web Platform for Interactive Visualization and Colocalization of QTLs and GWAS Loci. Genomics, Proteomics and Bioinformatics, 2022, 20, 541-548.	6.9	17
39	Tracing Lung Cancer Risk Factors Through Mutational Signatures in Never-Smokers. American Journal of Epidemiology, 2021, 190, 962-976.	3.4	16
40	Siah2 control of T-regulatory cells limits anti-tumor immunity. Nature Communications, 2020, 11, 99.	12.8	15
41	A 584Âbp deletion in CTRB2 inhibits chymotrypsin B2 activity and secretion and confers risk of pancreatic cancer. American Journal of Human Genetics, 2021, 108, 1852-1865.	6.2	15
42	Evaluation of the contribution of germline variants in BRCA1 and BRCA2 to uveal and cutaneous melanoma. Melanoma Research, 2019, 29, 483-490.	1.2	13
43	SPANX Control of Lamin A/C Modulates Nuclear Architecture and Promotes Melanoma Growth. Molecular Cancer Research, 2020, 18, 1560-1573.	3.4	13
44	Regulation of eIF2Î± by RNF4 Promotes Melanoma Tumorigenesis and Therapy Resistance. Journal of Investigative Dermatology, 2020, 140, 2466-2477.	0.7	13
45	Cell-type-specific meQTLs extend melanoma GWAS annotation beyond eQTLs and inform melanocyte gene-regulatory mechanisms. American Journal of Human Genetics, 2021, 108, 1631-1646.	6.2	12
46	A large Canadian cohort provides insights into the genetic architecture of human hair colour. Communications Biology, 2021, 4, 1253.	4.4	11
47	<i>SDHD</i>Promoter Mutations Ablate GABP Transcription Factor Binding in Melanoma. Cancer Research, 2017, 77, 1649-1661.	0.9	9
48	Contribution of Common Genetic Variants to Familial Aggregation of Disease and Implications for Sequencing Studies. PLoS Genetics, 2019, 15, e1008490.	3.5	8
49	Clinical Implications of Inter- and Intratumor Heterogeneity of Immune Cell Markers in Lung Cancer. Journal of the National Cancer Institute, 2022, 114, 280-289.	6.3	8
50	A UVB-responsive common variant at chromosome band 7p21.1 confers tanning response and melanoma risk via regulation of the aryl hydrocarbon receptor, AHR. American Journal of Human Genetics, 2021, 108, 1611-1630.	6.2	7
51	Sequencing and analysis of four BAC clones containing innate immune genes from the Zhikong scallop (Chlamys farreri). Gene, 2012, 502, 9-15.	2.2	6
52	Rare germline deleterious variants increase susceptibility for lung cancer. Human Molecular Genetics, 2022, 31, 3558-3565.	2.9	5
53	Integrated Analysis of Coexpression and Exome Sequencing to Prioritize Susceptibility Genes for Familial Cutaneous Melanoma. Journal of Investigative Dermatology, 2022, 142, 2464-2475.e5.	0.7	4
54	Comparison of somatic mutation landscapes in Chinese versus European breast cancer patients. Human Genetics and Genomics Advances, 2021, 3, 100076.	1.7	3

#	Article	IF	Citations
55	Defining novel causal SNPs and linked phenotypes at melanoma-associated loci. Human Molecular Genetics, 2022, 31, 2845-2856.	2.9	3
56	Investigating the genetic architecture of eye colour in a Canadian cohort. IScience, 2022, 25, 104485.	4.1	2
57	Novel MAPK/AKT-impairing germline NRAS variant identified in a melanoma-prone family. Familial Cancer, 2022, 21, 347-355.	1.9	1
58	Arginyl‑tRNA‑protein transferase 1 (ATE1) promotes melanoma cell growth and migration. FEBS Letters, 2022, 596, 1468-1480.	2.8	1
59	A Unique Crosstalk between Tumor Cells and Hematopoietic Stem Cells Reveals a Myeloid Differentiation Pattern Signature Contributing to Metastasis. Blood, 2019, 134, 2465-2465.	1.4	0
60	Germline-Somatic Interactions in Myelofibrosis Susceptibility. Blood, 2021, 138, 313-313.	1.4	0
61	RNF5 Defines Acute Myeloid Leukemia Growth and Susceptibility to Histone Deacetylase Inhibitors. Blood, 2020, 136, 31-32.	1.4	0