Gong-Hong Wei

List of Publications by Year
in descending order

51	3,953	304368	205818
papers	citations	22 h-index	48 g-index

54	54	54	8191
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	DNA-Binding Specificities of Human Transcription Factors. Cell, 2013, 152, 327-339.	13.5	1,085
2	Genome-wide analysis of ETS-family DNA-binding in vitro and in vivo. EMBO Journal, 2010, 29, 2147-2160.	3.5	497
3	The common colorectal cancer predisposition SNP rs6983267 at chromosome 8q24 confers potential to enhanced Wnt signaling. Nature Genetics, 2009, 41, 885-890.	9.4	463
4	Multiplexed massively parallel SELEX for characterization of human transcription factor binding specificities. Genome Research, 2010, 20, 861-873.	2.4	382
5	A prostate cancer susceptibility allele at 6q22 increases RFX6 expression by modulating HOXB13 chromatin binding. Nature Genetics, 2014, 46, 126-135.	9.4	182
6	Whole-genome and Transcriptome Sequencing of Prostate Cancer Identify New Genetic Alterations Driving Disease Progression. European Urology, 2018, 73, 322-339.	0.9	130
7	Gene regulatory mechanisms underpinning prostate cancer susceptibility. Nature Genetics, 2016, 48, 387-397.	9.4	119
8	Biology and Clinical Implications of the 19q13 Aggressive Prostate Cancer Susceptibility Locus. Cell, 2018, 174, 576-589.e18.	13.5	116
9	The Role of HOX Transcription Factors in Cancer Predisposition and Progression. Cancers, 2019, 11, 528.	1.7	86
10	Systematic identification of regulatory variants associated with cancer risk. Genome Biology, 2017, 18, 194.	3.8	79
11	Charting gene regulatory networks: strategies, challenges and perspectives. Biochemical Journal, 2004, 381, 1-12.	1.7	73
12	Genomic Insight into the Role of lncRNAs in Cancer Susceptibility. International Journal of Molecular Sciences, 2017, 18, 1239.	1.8	71
13	High-throughput screening of prostate cancer risk loci by single nucleotide polymorphisms sequencing. Nature Communications, 2018, 9, 2022.	5.8	66
14	Human transcription factor protein interaction networks. Nature Communications, 2022, 13, 766.	5.8	59
15	Structural basis for DNA recognition by STAT6. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13015-13020.	3.3	46
16	A long hypoxia-inducible factor 3 isoform 2 is a transcription activator that regulates erythropoietin. Cellular and Molecular Life Sciences, 2020, 77, 3627-3642.	2.4	40
17	Systematic enrichment analysis of potentially functional regions for 103 prostate cancer risk-associated loci. Prostate, 2015, 75, 1264-1276.	1.2	37
18	Chromatin interactions and candidate genes at ten prostate cancer risk loci. Scientific Reports, 2016, 6, 23202.	1.6	36

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19	Comprehensive assessment of cellular senescence in the tumor microenvironment. Briefings in Bioinformatics, 2022, 23, .	3.2	33
20	CRISPRi screens reveal a DNA methylation-mediated 3D genome dependent causal mechanism in prostate cancer. Nature Communications, 2021, 12, 1781.	5.8	32
21	ANO7 is associated with aggressive prostate cancer. International Journal of Cancer, 2018, 143, 2479-2487.	2.3	31
22	SIRT1 deacetylates the cardiac transcription factor Nkx2.5 and inhibits its transcriptional activity. Scientific Reports, 2016, 6, 36576.	1.6	29
23	Identification of several potential chromatin binding sites of HOXB7 and its downstream target genes in breast cancer. International Journal of Cancer, 2015, 137, 2374-2383.	2.3	28
24	Exploring cellular memory molecules marking competent and active transcriptions. BMC Molecular Biology, 2007, 8, 31.	3.0	24
25	A Large-Scale, Exome-Wide Association Study of Han Chinese Women Identifies Three Novel Loci Predisposing to Breast Cancer. Cancer Research, 2018, 78, 3087-3097.	0.4	19
26	Mechanisms of human Î³-globin transcriptional induction by apicidin involves p38 signaling to chromatin. Biochemical and Biophysical Research Communications, 2007, 363, 889-894.	1.0	17
27	Synergistic Interaction of HOXB13 and CIP2A Predisposes to Aggressive Prostate Cancer. Clinical Cancer Research, 2018, 24, 6265-6276.	3.2	17
28	Genetic association analysis of the RTK/ERK pathway with aggressive prostate cancer highlights the potential role of CCND2 in disease progression. Scientific Reports, 2017, 7, 4538.	1.6	15
29	Enhancer Dysfunction in 3D Genome and Disease. Cells, 2019, 8, 1281.	1.8	15
30	Unravelling the world of cis-regulatory elements. Medical and Biological Engineering and Computing, 2007, 45, 709-718.	1.6	13
31	Clinical characteristics and risk factors of COVID-19 patients with chronic hepatitis B: a multi-center retrospective cohort study. Frontiers of Medicine, 2021, , 1.	1.5	13
32	Association between homocysteine, vitamin B_{₁₂}, folic acid and erectile dysfunction: a cross-sectional study in China. BMJ Open, 2019, 9, e023003.	0.8	12
33	SATB1 regulates Î²-like globin genes through matrix related nuclear relocation of the cluster. Biochemical and Biophysical Research Communications, 2009, 383, 11-15.	1.0	10
34	The Amino-Terminal Oligomerization Domain of Angiopoietin-2 Affects Vascular Remodeling, Mammary Gland Tumor Growth, and Lung Metastasis in Mice. Cancer Research, 2021, 81, 129-143.	0.4	10
35	Disassembly of Î±6Î²4-mediated hemidesmosomal adhesions promotes tumorigenesis in PTEN-negative prostate cancer by targeting plectin to focal adhesions. Oncogene, 2022, 41, 3804-3820.	2.6	9
36	TP53 supports basal-like differentiation of mammary epithelial cells by preventing translocation of deltaNp63 into nucleoli. Scientific Reports, 2015, 4, 4663.	1.6	8

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37	Mechanistic insights into genetic susceptibility to prostate cancer. Cancer Letters, 2021, 522, 155-163.	3.2	7
38	Whole exome sequencing in Finnish families identifies new candidate genes for osteoarthritis. PLoS ONE, 2018, 13, e0203313.	1.1	6
39	An enhancer variant at 16q22.1 predisposes to hepatocellular carcinoma via regulating PRMT7 expression. Nature Communications, 2022, 13, 1232.	5.8	6
40	Oncogenic regulatory circuits driven by 19q13 rs11672691 underlies prostate cancer aggressiveness. Molecular and Cellular Oncology, 2018, 5, e1516451.	0.3	5
41	Optimized CRISPR/Cas9-mediated single nucleotide mutation in adherent cancer cell lines. STAR Protocols, 2021, 2, 100419.	0.5	5
42	Meta-analysis of gene expression and integrin-associated signaling pathways in papillary renal cell carcinoma subtypes. Oncotarget, 2016, 7, 84178-84189.	0.8	4
43	Multi-factors including Inflammatory/Immune, Hormones, Tumor-related Proteins and Nutrition associated with Chronic Prostatitis NIH IIIa+b and IV based on FAMHES project. Scientific Reports, 2017, 7, 9143.	1.6	4
44	Exome Sequencing Reveals a Phenotype Modifying Variant in <scp>ZNF528</scp> in Primary Osteoporosis With a <scp>COL1A2</scp> Deletion. Journal of Bone and Mineral Research, 2020, 35, 2381-2392.	3.1	4
45	VHL Ser65 mutations enhance HIF2Î± signaling and promote epithelial-mesenchymal transition of renal cancer cells. Cell and Bioscience, 2022, 12, 52.	2.1	4
46	Large Multicohort Study Reveals a Prostate Cancer Susceptibility Allele at 5p15 Regulating TERT via Androgen Signaling-Orchestrated Chromatin Binding of E2F1 and MYC. Frontiers in Oncology, 2021, 11, 754206.	1.3	2
47	Ataxin-10 is involved in Golgi membrane dynamics. Journal of Genetics and Genomics, 2017, 44, 549-552.	1.7	1
48	Illumination of cell cycle progression by multi-fluorescent sensing system. Cell Cycle, 2019, 18, 1364-1378.	1.3	1
49	Combined immunotherapy for advanced prostate cancer: Empowering the T cell army. Asian Journal of Urology, 2017, 4, 199-200.	0.5	0
50	Expanding luminal epitheliums as cells of origin for prostate cancer. Asian Journal of Urology, 2021, 8, 238-240.	0.5	0
51	Single-cell transcriptomics reveals cell type diversity of human prostate. Journal of Genetics and Genomics, 2022, , .	1.7	0