

# Weiqun Peng

## List of Publications by Year in descending order

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57  
papers

10,990  
citations

117453

34  
h-index

155451

55  
g-index

62  
all docs

62  
docs citations

62  
times ranked

18551  
citing authors

#	ARTICLE	IF	CITATIONS
1	Tcf1 preprograms the mobilization of glycolysis in central memory CD8 <sup>+</sup> T cells during recall responses. <i>Nature Immunology</i> , 2022, 23, 386-398.	7.0	26
2	Interplay of BAF and MLL4 promotes cell type-specific enhancer activation. <i>Nature Communications</i> , 2021, 12, 1630.	5.8	38
3	Arid1a-Plagl1-Hh signaling is indispensable for differentiation-associated cell cycle arrest of tooth root progenitors. <i>Cell Reports</i> , 2021, 35, 108964.	2.9	6
4	Tcf1 and Lef1 provide constant supervision to mature CD8 <sup>+</sup> T cell identity and function by organizing genomic architecture. <i>Nature Communications</i> , 2021, 12, 5863.	5.8	41
5	Sepsis leads to lasting changes in phenotype and function of memory CD8 T cells. <i>ELife</i> , 2021, 10, .	2.8	19
6	Evidence of Superior and Inferior Sinoatrial Nodes in the Mammalian Heart. <i>JACC: Clinical Electrophysiology</i> , 2020, 6, 1827-1840.	1.3	44
7	Transcriptome-wide stability analysis uncovers LARP4-mediated NF- $\kappa$ B1 mRNA stabilization during T cell activation. <i>Nucleic Acids Research</i> , 2020, 48, 8724-8739.	6.5	10
8	RECOGNICER: A coarse-graining approach for identifying broad domains from ChIP-seq data. <i>Quantitative Biology</i> , 2020, 8, 359-368.	0.3	1
9	HDAC10 Regulates Cancer Stem-Like Cell Properties in KRAS-Driven Lung Adenocarcinoma. <i>Cancer Research</i> , 2020, 80, 3265-3278.	0.4	30
10	Tcf1 and Lef1 are required for the immunosuppressive function of regulatory T cells. <i>Journal of Experimental Medicine</i> , 2019, 216, 847-866.	4.2	72
11	miR-137 mediates the functional link between c-Myc and EZH2 that regulates cisplatin resistance in ovarian cancer. <i>Oncogene</i> , 2019, 38, 564-580.	2.6	103
12	Autocrine activation of JAK2 by IL-11 promotes platinum drug resistance. <i>Oncogene</i> , 2018, 37, 3981-3997.	2.6	31
13	DUOX1-mediated ROS production promotes cisplatin resistance by activating ATR-Chk1 pathway in ovarian cancer. <i>Cancer Letters</i> , 2018, 428, 104-116.	3.2	60
14	Loss of KDM6A Activates Super-Enhancers to Induce Gender-Specific Squamous-like Pancreatic Cancer and Confers Sensitivity to BET Inhibitors. <i>Cancer Cell</i> , 2018, 33, 512-526.e8.	7.7	223
15	Ezh2 programs TFH differentiation by integrating phosphorylation-dependent activation of Bcl6 and polycomb-dependent repression of p19Arf. <i>Nature Communications</i> , 2018, 9, 5452.	5.8	53
16	Predicting CTCF-mediated chromatin interactions by integrating genomic and epigenomic features. <i>Nature Communications</i> , 2018, 9, 4221.	5.8	45
17	Tle corepressors are differentially partitioned to instruct CD8 <sup>+</sup> T cell lineage choice and identity. <i>Journal of Experimental Medicine</i> , 2018, 215, 2211-2226.	4.2	32
18	Rapid Recall Ability of Memory T cells is Encoded in their Epigenome. <i>Scientific Reports</i> , 2017, 7, 39785.	1.6	39

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19	Deficiency of microRNA <i>miR-34a</i> expands cell fate potential in pluripotent stem cells. <i>Science</i> , 2017, 355, .	6.0	129
20	MLL3/MLL4 are required for CBP/p300 binding on enhancers and super-enhancer formation in brown adipogenesis. <i>Nucleic Acids Research</i> , 2017, 45, 6388-6403.	6.5	131
21	The transcription factor Runx3 guards cytotoxic CD8+ effector T cells against deviation towards follicular helper T cell lineage. <i>Nature Immunology</i> , 2017, 18, 931-939.	7.0	113
22	Differential Requirements for Tcf1 Long Isoforms in CD8+ and CD4+ T Cell Responses to Acute Viral Infection. <i>Journal of Immunology</i> , 2017, 199, 911-919.	0.4	53
23	Brd4 binds to active enhancers to control cell identity gene induction in adipogenesis and myogenesis. <i>Nature Communications</i> , 2017, 8, 2217.	5.8	161
24	Global intron retention mediated gene regulation during CD4 <sup>+</sup> T cell activation. <i>Nucleic Acids Research</i> , 2016, 44, 6817-6829.	6.5	96
25	Hematopoietic and Leukemic Stem Cells Have Distinct Dependence on Tcf1 and Lef1 Transcription Factors. <i>Journal of Biological Chemistry</i> , 2016, 291, 11148-11160.	1.6	33
26	Tcf1 and Lef1 transcription factors establish CD8+ T cell identity through intrinsic HDAC activity. <i>Nature Immunology</i> , 2016, 17, 695-703.	7.0	188
27	Lineage relationship of CD8+ T cell subsets is revealed by progressive changes in the epigenetic landscape. <i>Cellular and Molecular Immunology</i> , 2016, 13, 502-513.	4.8	99
28	Enhancer priming by H3K4 methyltransferase MLL4 controls cell fate transition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 11871-11876.	3.3	172
29	A PTIP-PA1 subcomplex promotes transcription for IgH class switching independently from the associated MLL3/MLL4 methyltransferase complex. <i>Genes and Development</i> , 2016, 30, 149-163.	2.7	27
30	Histone demethylase KDM2B regulates lineage commitment in normal and malignant hematopoiesis. <i>Journal of Clinical Investigation</i> , 2016, 126, 905-920.	3.9	80
31	LEF-1 and TCF-1 orchestrate TFH differentiation by regulating differentiation circuits upstream of the transcriptional repressor Bcl6. <i>Nature Immunology</i> , 2015, 16, 980-990.	7.0	272
32	Gcn5 and PCAF negatively regulate interferon $\gamma$ production through HAT-independent inhibition of TBK1. <i>EMBO Reports</i> , 2014, 15, 1192-1201.	2.0	31
33	Spatial Clustering for Identification of ChIP-Enriched Regions (SICER) to Map Regions of Histone Methylation Patterns in Embryonic Stem Cells. <i>Methods in Molecular Biology</i> , 2014, 1150, 97-111.	0.4	206
34	Identification of an ABCB1 (P-glycoprotein)-positive carfilzomib-resistant myeloma subpopulation by the pluripotent stem cell fluorescent dye CDy1. <i>American Journal of Hematology</i> , 2013, 88, 265-272.	2.0	79
35	PfSETvs methylation of histone H3K36 represses virulence genes in <i>Plasmodium falciparum</i> . <i>Nature</i> , 2013, 499, 223-227.	13.7	219
36	H3K4 mono- and di-methyltransferase MLL4 is required for enhancer activation during cell differentiation. <i>ELife</i> , 2013, 2, e01503.	2.8	369

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37	Transcriptional Regulation of Rod Photoreceptor Homeostasis Revealed by In Vivo NRL Targetome Analysis. <i>PLoS Genetics</i> , 2012, 8, e1002649.	1.5	99
38	The DNA Damage- and Transcription-Associated Protein Paxip1 Controls Thymocyte Development and Emigration. <i>Immunity</i> , 2012, 37, 971-985.	6.6	35
39	Histone H3K9 methyltransferase G9a represses PPAR $\gamma$ expression and adipogenesis. <i>EMBO Journal</i> , 2012, 32, 45-59.	3.5	162
40	An integrated strategy for identification of both sharp and broad peaks from next-generation sequencing data. <i>Genome Biology</i> , 2011, 12, 120.	13.9	3
41	Discrete Roles of STAT4 and STAT6 Transcription Factors in Tuning Epigenetic Modifications and Transcription during T Helper Cell Differentiation. <i>Immunity</i> , 2010, 32, 840-851.	6.6	290
42	PTIP Promotes Chromatin Changes Critical for Immunoglobulin Class Switch Recombination. <i>Science</i> , 2010, 329, 917-923.	6.0	137
43	Single-walled carbon nanotube/poly(methyl methacrylate) composites for electromagnetic interference shielding. <i>Polymer Engineering and Science</i> , 2009, 49, 1627-1634.	1.5	191
44	H3.3/H2A.Z double variant-containing nucleosomes mark 'nucleosome-free regions' of active promoters and other regulatory regions. <i>Nature Genetics</i> , 2009, 41, 941-945.	9.4	679
45	Global Mapping of H3K4me3 and H3K27me3 Reveals Specificity and Plasticity in Lineage Fate Determination of Differentiating CD4 <sup>+</sup> T Cells. <i>Immunity</i> , 2009, 30, 155-167.	6.6	1,005
46	Genome-wide Analysis of Histone Methylation Reveals Chromatin State-Based Regulation of Gene Transcription and Function of Memory CD8 <sup>+</sup> T Cells. <i>Immunity</i> , 2009, 30, 912-925.	6.6	256
47	A clustering approach for identification of enriched domains from histone modification ChIP-Seq data. <i>Bioinformatics</i> , 2009, 25, 1952-1958.	1.8	936
48	Genome-wide Mapping of HATs and HDACs Reveals Distinct Functions in Active and Inactive Genes. <i>Cell</i> , 2009, 138, 1019-1031.	13.5	1,174
49	Chromatin Signatures in Multipotent Human Hematopoietic Stem Cells Indicate the Fate of Bivalent Genes during Differentiation. <i>Cell Stem Cell</i> , 2009, 4, 80-93.	5.2	548
50	Combinatorial patterns of histone acetylations and methylations in the human genome. <i>Nature Genetics</i> , 2008, 40, 897-903.	9.4	2,034
51	Capsid Proteins from Human Immunodeficiency Virus Type 1 and Simian Immunodeficiency Virus SIV <sub>mac</sub> Can Coassemble into Mature Cores of Infectious Viruses. <i>Journal of Virology</i> , 2008, 82, 8253-8261.	1.5	3
52	Pathway Switching Explains the Sharp Response Characteristic of Hypoxia Response Network. <i>PLoS Computational Biology</i> , 2007, 3, e171.	1.5	21
53	Interplay of crystallization and liquid-liquid phase separation in polyolefin blends: A thermal history dependence study. <i>Polymer</i> , 2007, 48, 4226-4234.	1.8	25
54	Pathway Switching Explains the Sharp Response Characteristic of Hypoxia Response Network. <i>PLoS Computational Biology</i> , 2005, preprint, e171.	1.5	0

#	ARTICLE	IF	CITATIONS
55	Renormalization-group approach to the vulcanization transition. Physical Review E, 2000, 61, 3339-3357.	0.8	13
56	Universality and its origins at the amorphous solidification transition. Physical Review B, 1998, 57, 839-847.	1.1	25
57	Lineage relationship of CD8+ T cell subsets is revealed by progressive changes in the epigenetic landscape. Cellular and Molecular Immunology, 0, , .	4.8	7