Yiping Fan

List of Publications by Year in descending order

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73 papers	4,493 citations	159525 30 h-index	118793 62 g-index
80 all docs	80 docs citations	80 times ranked	8709 citing authors

#	Article	IF	Citations
1	Antigen cross-presentation in young tumor-bearing hosts promotes CD8 ⁺ T cell terminal differentiation. Science Immunology, 2022, 7, eabf6136.	5.6	5
2	Special Issue on Bioinformatics and Machine Learning for Cancer Biology. Biology, 2022, 11, 361.	1.3	0
3	Genomic profiling identifies genes and pathways dysregulated by HEY1â€“NCOA2 fusion and shines a light on mesenchymal chondrosarcoma tumorigenesis. Journal of Pathology, 2022, 257, 579-592.	2.1	7
4	The myokine Fibcd1 is an endogenous determinant of myofiber size and mitigates cancer-induced myofiber atrophy. Nature Communications, 2022, 13, 2370.	5.8	14
5	Acute lymphoblastic leukemia displays a distinct highly methylated genome. Nature Cancer, 2022, 3, 768-782.	5.7	15
6	Targeting KDM4 for treating PAX3-FOXO1â€“driven alveolar rhabdomyosarcoma. Science Translational Medicine, 2022, 14, .	5.8	16
7	FBXO11-mediated proteolysis of BAHD1 relieves PRC2-dependent transcriptional repression in erythropoiesis. Blood, 2021, 137, 155-167.	0.6	22
8	MEK inhibition reprograms CD8+ T lymphocytes into memory stem cells with potent antitumor effects. Nature Immunology, 2021, 22, 53-66.	7.0	95
9	Regnase-1 suppresses TCF-1+ precursor exhausted T-cell formation to limit CARâ€“T-cell responses against ALL. Blood, 2021, 138, 122-135.	0.6	28
10	A distal Foxp3 enhancer enables interleukin-2 dependent thymic Treg cell lineage commitment for robust immune tolerance. Immunity, 2021, 54, 931-946.e11.	6.6	46
11	An age-downregulated ribosomal RpS28 protein variant regulates the muscle proteome. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	11
12	Identification of small molecules that mitigate vincristineâ€induced neurotoxicity while sensitizing leukemia cells to vincristine. Clinical and Translational Science, 2021, 14, 1490-1504.	1.5	12
13	Proteasome stress in skeletal muscle mounts a long-range protective response that delays retinal and brain aging. Cell Metabolism, 2021, 33, 1137-1154.e9.	7.2	45
14	Foxp3 enhancers synergize to maximize regulatory T cell suppressive capacity. Journal of Experimental Medicine, 2021, 218, .	4.2	5
15	Abstract 2093: Alternative splicing in hematopoietic stem cells is affected by the loss of DNMT3A. , 2021, , .		0
16	Acute depletion of CTCF rewires genome-wide chromatin accessibility. Genome Biology, 2021, 22, 244.	3.8	29
17	A genetic mouse model with postnatalNf1andp53loss recapitulates the histology and transcriptome of human malignant peripheral nerve sheath tumor. Neuro-Oncology Advances, 2021, 3, vdab129.	0.4	3
18	YAP/TAZ maintain the proliferative capacity and structural organization of radial glial cells during brain development. Developmental Biology, 2021, 480, 39-49.	0.9	9

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19	CD19-CAR TÂcells undergo exhaustion DNA methylation programming in patients with acute lymphoblastic leukemia. Cell Reports, 2021, 37, 110079.	2.9	48
20	CD19-CAR T Cells Develop Exhaustion Epigenetic Programs during a Clinical Response. Blood, 2021, 138, 2782-2782.	0.6	0
21	Mapping the Glucocorticoid Gene Regulatory Network and Alterations That Contribute to Steroid Resistance in Childhood Acute Lymphoblastic Leukemia. Blood, 2021, 138, 674-674.	0.6	1
22	Integrated genomic and proteomic analyses identify stimulus-dependent molecular changes associated with distinct modes of skeletal muscle atrophy. Cell Reports, 2021, 37, 109971.	2.9	32
23	Targeting the spliceosome through RBM39 degradation results in exceptional responses in high-risk neuroblastoma models. Science Advances, 2021, 7, eabj5405.	4.7	32
24	Deleting DNMT3A in CAR T cells prevents exhaustion and enhances antitumor activity. Science Translational Medicine, 2021, 13, eabh0272.	5.8	123
25	Unifying heterogeneous expression data to predict targets for CAR-T cell therapy. OncoImmunology, 2021, 10, 2000109.	2.1	1
26	Control of Foxp3 induction and maintenance by sequential histone acetylation and DNA demethylation. Cell Reports, 2021, 37, 110124.	2.9	13
27	A six-gene leukemic stem cell score identifies high risk pediatric acute myeloid leukemia. Leukemia, 2020, 34, 735-745.	3.3	56
28	ChIPseqSpikeInFree: a ChIP-seq normalization approach to reveal global changes in histone modifications without spike-in. Bioinformatics, 2020, 36, 1270-1272.	1.8	25
29	Muscle-derived Dpp regulates feeding initiation via endocrine modulation of brain dopamine biosynthesis. Genes and Development, 2020, 34, 37-52.	2.7	15
30	UTX/KDM6A suppresses AP-1 and a gliogenesis program during neural differentiation of human pluripotent stem cells. Epigenetics and Chromatin, 2020, 13, 38.	1.8	5
31	Ybx1 fine-tunes PRC2 activities to control embryonic brain development. Nature Communications, 2020, 11, 4060.	5.8	29
32	Beta cell-specific CD8+ T cells maintain stem cell memory-associated epigenetic programs during type 1 diabetes. Nature Immunology, 2020, 21, 578-587.	7.0	63
33	MYCN amplification and ATRX mutations are incompatible in neuroblastoma. Nature Communications, 2020, 11, 913.	5.8	66
34	Developmental plasticity allows outside-in immune responses by resident memory T cells. Nature Immunology, 2020, 21, 412-421.	7.0	191
35	Mutational Landscape and Patterns of Clonal Evolution in Relapsed Pediatric Acute Lymphoblastic Leukemia. Blood Cancer Discovery, 2020, 1, 96-111.	2.6	93
36	Relapse-Fated Latent Diagnosis Subclones in Acute B Lineage Leukemia Are Drug Tolerant and Possess Distinct Metabolic Programs. Cancer Discovery, 2020, 10, 568-587.	7.7	72

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37	The histone deacetylase complex MiDAC regulates a neurodevelopmental gene expression program to control neurite outgrowth. ELife, 2020, 9, .	2.8	23
38	Processing Millions of Single Cells by SHARP. , 2020, , .		0
39	A Key Role for the Ubiquitin Ligase UBR4 in Myofiber Hypertrophy in Drosophila and Mice. Cell Reports, 2019, 28, 1268-1281.e6.	2.9	56
40	Circadian gene variants and the skeletal muscle circadian clock contribute to the evolutionary divergence in longevity across Drosophila populations. Genome Research, 2019, 29, 1262-1276.	2.4	20
41	TOX reinforces the phenotype and longevity of exhausted T cells in chronic viral infection. Nature, 2019, 571, 265-269.	13.7	581
42	Tissue-specific alteration of gene expression and function by RU486 and the GeneSwitch system. Npj Aging and Mechanisms of Disease, 2019, 5, 6.	4.5	20
43	H3.3 K27M depletion increases differentiation and extends latency of diffuse intrinsic pontine glioma growth in vivo. Acta Neuropathologica, 2019, 137, 637-655.	3.9	85
44	Metabolic heterogeneity underlies reciprocal fates of TH17 cell stemness and plasticity. Nature, 2019, 565, 101-105.	13.7	141
45	Histone H3.3 K27M Accelerates Spontaneous Brainstem Glioma and Drives Restricted Changes in Bivalent Gene Expression. Cancer Cell, 2019, 35, 140-155.e7.	7.7	194
46	Differentiation of human pluripotent stem cells into neurons or cortical organoids requires transcriptional co-regulation by UTX and 53BP1. Nature Neuroscience, 2019, 22, 362-373.	7.1	33
47	Engineering Naturally Occurring CD7 Negative Cells for the Immunotherapy of CD7 Positive Leukemia. Blood, 2019, 134, 868-868.	0.6	1
48	The Genomic Landscape of Childhood Acute Lymphoblastic Leukemia. Blood, 2019, 134, 649-649.	0.6	5
49	KDM5A Regulates a Translational Program that Controls p53 Protein Expression. IScience, 2018, 9, 84-100.	1.9	25
50	The Hippo Pathway Prevents YAP/TAZ-Driven Hypertranscription and Controls Neural Progenitor Number. Developmental Cell, 2018, 47, 576-591.e8.	3.1	80
51	Identification of Therapeutic Targets in Rhabdomyosarcoma through Integrated Genomic, Epigenomic, and Proteomic Analyses. Cancer Cell, 2018, 34, 411-426.e19.	7.7	106
52	Inactivation of Ezh2 Upregulates Gfi1 and Drives Aggressive Myc-Driven Group 3 Medulloblastoma. Cell Reports, 2017, 18, 2907-2917.	2.9	61
53	Human memory CD8 T cell effector potential is epigenetically preserved during in vivo homeostasis. Journal of Experimental Medicine, 2017, 214, 1593-1606.	4.2	123
54	De Novo Epigenetic Programs Inhibit PD-1 Blockade-Mediated T Cell Rejuvenation. Cell, 2017, 170, 142-157.e19.	13.5	536

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55	Effector CD8 T cells dedifferentiate into long-lived memory cells. Nature, 2017, 552, 404-409.	13.7	378
56	Msh2 deficiency leads to dysmyelination of the corpus callosum, impaired locomotion and altered sensory function in mice. Scientific Reports, 2016, 6, 30757.	1.6	3
57	Evaluation of artemisinins for the treatment of acute myeloid leukemia. Cancer Chemotherapy and Pharmacology, 2016, 77, 1231-1243.	1.1	41
58	Binding of estrogen receptors to switch sites and regulatory elements in the immunoglobulin heavy chain locus of activated B cells suggests a direct influence of estrogen on antibody expression. Molecular Immunology, 2016, 77, 97-102.	1.0	42
59	Telomerase Expression by Aberrant Methylation of the TERT Promoter in Melanoma Arising in Giant Congenital Nevi. Journal of Investigative Dermatology, 2016, 136, 339-342.	0.3	36
60	Hotspots for Vitaminâ€“Steroidâ€“Thyroid Hormone Response Elements Within Switch Regions of Immunoglobulin Heavy Chain Loci Predict a Direct Influence of Vitamins and Hormones on B Cell Class Switch Recombination. Viral Immunology, 2016, 29, 132-136.	0.6	23
61	c-Fos Repression by Piwi Regulates Drosophila Ovarian Germline Formation and Tissue Morphogenesis. PLoS Genetics, 2016, 12, e1006281.	1.5	31
62	Outcome of children with hypodiploid ALL treated with risk-directed therapy based on MRD levels. Blood, 2015, 126, 2896-2899.	0.6	76
63	Quantification of Retinogenesis in 3D Cultures Reveals Epigenetic Memory and Higher Efficiency in iPSCs Derived from Rod Photoreceptors. Cell Stem Cell, 2015, 17, 101-115.	5.2	88
64	Association of an Inherited Genetic Variant With Vincristine-Related Peripheral Neuropathy in Children With Acute Lymphoblastic Leukemia. JAMA - Journal of the American Medical Association, 2015, 313, 815.	3.8	234
65	NALP3 inflammasome upregulation and CASP1 cleavage of the glucocorticoid receptor cause glucocorticoid resistance in leukemia cells. Nature Genetics, 2015, 47, 607-614.	9.4	126
66	TheCYP2C19Intron 2 Branch Point SNP is the Ancestral Polymorphism Contributing to the Poor Metabolizer Phenotype in Livers withCYP2C19*35andCYP2C19*2Alleles. Drug Metabolism and Disposition, 2015, 43, 1226-1235.	1.7	23
67	The glucose-sensing transcription factor MLX promotes myogenesis via myokine signaling. Genes and Development, 2015, 29, 2475-2489.	2.7	38
68	Molecular mechanisms for telomere maintenance in neuroblastoma.. Journal of Clinical Oncology, 2015, 33, 10041-10041.	0.8	0
69	Survival analysis of infected mice reveals pathogenic variations in the genome of avian H1N1 viruses. Scientific Reports, 2014, 4, 7455.	1.6	13
70	Genome-Wide Association Analyses Identify Susceptibility Loci For Vincristine-Induced Peripheral Neuropathy In Children With Acute Lymphoblastic Leukemia. Blood, 2013, 122, 618-618.	0.6	6
71	A Genome-Wide Analysis of Variants Influencing Methotrexate Clearance Replicates SLCO1B1.. Blood, 2012, 120, 2466-2466.	0.6	5
72	Genome-Wide Association Study Identifies Germline Polymorphisms Associated with Relapse of Childhood Acute Lymphoblastic Leukemia. Blood, 2012, 120, 878-878.	0.6	0

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73	SLCO1B1 Variation and Methotrexate Disposition in Children with Acute Lymphoblastic Leukemia: The Importance of Rare Variants in Pharmacogenetics. Blood, 2011, 118, 571-571.	0.6	0