

# Qian-Fei Wang

## List of Publications by Year in descending order

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Version: 2024-02-01

40  
papers

1,094  
citations

361045

20  
h-index

414034

32  
g-index

41  
all docs

41  
docs citations

41  
times ranked

2541  
citing authors

#	ARTICLE	IF	CITATIONS
1	Common Postzygotic Mutational Signatures in Healthy Adult Tissues Related to Embryonic Hypoxia. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 177-191.	3.0	1
2	Single-cell Transcriptomic Analysis Reveals the Cellular Heterogeneity of Mesenchymal Stem Cells. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 70-86.	3.0	27
3	Prednisone plus IVIg compared with prednisone or IVIg for immune thrombocytopenia in pregnancy: a national retrospective cohort study. <i>Therapeutic Advances in Hematology</i> , 2022, 13, 204062072210952.	1.1	5
4	Benzene induces rapid leukemic transformation after prolonged hematotoxicity in a murine model. <i>Leukemia</i> , 2021, 35, 595-600.	3.3	8
5	Risk stratification and outcomes of intracranial hemorrhage in patients with immune thrombocytopenia under 60 years of age. <i>Platelets</i> , 2021, 32, 633-641.	1.1	6
6	Minimally myelosuppressive regimen for remission induction in pediatric AML: long-term results of an observational study. <i>Blood Advances</i> , 2021, 5, 1837-1847.	2.5	4
7	Germline variants in UNC13D and AP3B1 are enriched in COVID-19 patients experiencing severe cytokine storms. <i>European Journal of Human Genetics</i> , 2021, 29, 1312-1315.	1.4	21
8	Single-cell analysis of ploidy and the transcriptome reveals functional and spatial divergency in murine megakaryopoiesis. <i>Blood</i> , 2021, 138, 1211-1224.	0.6	59
9	Machine-Learning Model for Resistance/Relapse Prediction in Immune Thrombocytopenia Using Gut Microbiota and Function Signatures. <i>Blood</i> , 2021, 138, 18-18.	0.6	1
10	A promising iPSC-based single-cell cloning strategy revealing signatures of somatic mutations in heterogeneous normal cells. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2326-2335.	1.9	0
11	A risk score for predicting hospitalization for community-acquired pneumonia in ITP using nationally representative data. <i>Blood Advances</i> , 2020, 4, 5846-5857.	2.5	5
12	Development and validation of a prediction model (AHC) for early identification of refractory thrombotic thrombocytopenic purpura using nationally representative data. <i>British Journal of Haematology</i> , 2020, 191, 269-281.	1.2	5
13	Empowering host immunity by kinase-targeting in LSC. <i>Blood Science</i> , 2020, 2, 107-108.	0.4	0
14	Identification of Chemo-Resistant Residual Cell Population in Pediatric AML of Complete Remission By Single Cell RNA Sequencing. <i>Blood</i> , 2020, 136, 25-26.	0.6	0
15	Evolutionary transition between invertebrates and vertebrates via methylation reprogramming in embryogenesis. <i>National Science Review</i> , 2019, 6, 993-1003.	4.6	58
16	SETD2 mutations confer chemoresistance in acute myeloid leukemia partly through altered cell cycle checkpoints. <i>Leukemia</i> , 2019, 33, 2585-2598.	3.3	29
17	Benzene metabolite hydroquinone promotes DNA homologous recombination repair via the NF- $\kappa$ B pathway. <i>Carcinogenesis</i> , 2019, 40, 1021-1030.	1.3	12
18	Ecological principle meets cancer treatment: treating children with acute myeloid leukemia with low-dose chemotherapy. <i>National Science Review</i> , 2019, 6, 469-479.	4.6	9

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19	Tumor heterogeneity of acute myeloid leukemia: insights from single-cell sequencing. <i>Blood Science</i> , 2019, 1, 73-76.	0.4	5
20	Transcriptional and Spatial Heterogeneity of Mouse Megakaryocytes at Single-Cell Resolution. <i>Blood</i> , 2019, 134, 275-275.	0.6	4
21	Setd2 regulates quiescence and differentiation of adult hematopoietic stem cells by restricting RNA polymerase II elongation. <i>Haematologica</i> , 2018, 103, 1110-1123.	1.7	27
22	ANP32A regulates histone H3 acetylation and promotes leukemogenesis. <i>Leukemia</i> , 2018, 32, 1587-1597.	3.3	25
23	Whole exome sequencing identifies novel mutations of epigenetic regulators in chemorefractory pediatric acute myeloid leukemia. <i>Leukemia Research</i> , 2018, 65, 20-24.	0.4	24
24	Human NOTCH4 is a key target of RUNX1 in megakaryocytic differentiation. <i>Blood</i> , 2018, 131, 191-201.	0.6	31
25	Integrated genomic analysis identifies deregulated JAK/STAT-MYC-biosynthesis axis in aggressive NK-cell leukemia. <i>Cell Research</i> , 2018, 28, 172-186.	5.7	62
26	Chromatin regulator Asx1 loss and Nf1 haploinsufficiency cooperate to accelerate myeloid malignancy. <i>Journal of Clinical Investigation</i> , 2018, 128, 5383-5398.	3.9	25
27	Histone variants H2A.Z and H3.3 coordinately regulate PRC2-dependent H3K27me3 deposition and gene expression regulation in mES cells. <i>BMC Biology</i> , 2018, 16, 107.	1.7	54
28	Synthetic lethality between HER2 and transaldolase in intrinsically resistant HER2-positive breast cancers. <i>Nature Communications</i> , 2018, 9, 4274.	5.8	25
29	Pathobiological Pseudohypoxia as a Putative Mechanism Underlying Myelodysplastic Syndromes. <i>Cancer Discovery</i> , 2018, 8, 1438-1457.	7.7	38
30	Expression profiling-based clustering of healthy subjects recapitulates classifications defined by clinical observation in Chinese medicine. <i>Journal of Genetics and Genomics</i> , 2017, 44, 191-197.	1.7	22
31	Loss of Asx2 leads to myeloid malignancies in mice. <i>Nature Communications</i> , 2017, 8, 15456.	5.8	23
32	Loss of Asx1 Alters Self-Renewal and Cell Fate of Bone Marrow Stromal Cells, Leading to Bohring-Opitz-like Syndrome in Mice. <i>Stem Cell Reports</i> , 2016, 6, 914-925.	2.3	18
33	ATF4 plays a pivotal role in the development of functional hematopoietic stem cells in mouse fetal liver. <i>Blood</i> , 2015, 126, 2383-2391.	0.6	58
34	The priming induction regimen of HAG as a low dose chemotherapy strategy in AML clonal evolution. <i>Science China Life Sciences</i> , 2015, 58, 1302-1305.	2.3	0
35	Cell Type-Specific Expression Profile and Signaling Requirements in Early Hematopoietic Reprogramming. <i>Stem Cells and Development</i> , 2015, 24, 1483-1492.	1.1	0
36	Identification of functional cooperative mutations of SETD2 in human acute leukemia. <i>Nature Genetics</i> , 2014, 46, 287-293.	9.4	213

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37	Whole-Genome Sequencing Identifies Genetic Variances in Culture-Expanded Human Mesenchymal Stem Cells. <i>Stem Cell Reports</i> , 2014, 3, 227-233.	2.3	42
38	MLL fusion proteins preferentially regulate a subset of wild-type MLL target genes in the leukemic genome. <i>Blood</i> , 2011, 117, 6895-6905.	0.6	103
39	Methylation and expression analysis of tumor suppressor genes p15 and p16 in benzene poisoning. <i>Chemico-Biological Interactions</i> , 2010, 184, 306-309.	1.7	44
40	Developing and validating a mortality prediction model for ICH in ITP: a nationwide representative multicenter study. <i>Blood Advances</i> , 0, , .	2.5	1