

# Zhi-hui Zhang

## List of Publications by Year in descending order

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93  
papers

1,814  
citations

279798

23  
h-index

330143

37  
g-index

102  
all docs

102  
docs citations

102  
times ranked

2274  
citing authors

#	ARTICLE	IF	CITATIONS
1	Recurrent DNMT3A R882 Mutations in Chinese Patients with Acute Myeloid Leukemia and Myelodysplastic Syndrome. PLoS ONE, 2011, 6, e26906.	2.5	110
2	IDH1 and IDH2 mutation analysis in Chinese patients with acute myeloid leukemia and myelodysplastic syndrome. Annals of Hematology, 2012, 91, 519-525.	1.8	96
3	H19 overexpression promotes leukemogenesis and predicts unfavorable prognosis in acute myeloid leukemia. Clinical Epigenetics, 2018, 10, 47.	4.1	79
4	U2AF1 Mutations in Chinese Patients with Acute Myeloid Leukemia and Myelodysplastic Syndrome. PLoS ONE, 2012, 7, e45760.	2.5	75
5	miR-374a-5p: A New Target for Diagnosis and Drug Resistance Therapy in Gastric Cancer. Molecular Therapy - Nucleic Acids, 2019, 18, 320-331.	5.1	64
6	RAS mutation analysis in a large cohort of Chinese patients with acute myeloid leukemia. Clinical Biochemistry, 2013, 46, 579-583.	1.9	60
7	Efficacy and safety of decitabine in treatment of elderly patients with acute myeloid leukemia: A systematic review and meta-analysis. Oncotarget, 2017, 8, 41498-41507.	1.8	58
8	Overexpressed let-7a-3 is associated with poor outcome in acute myeloid leukemia. Leukemia Research, 2013, 37, 1642-1647.	0.8	57
9	Overexpression of miR-378 is frequent and may affect treatment outcomes in patients with acute myeloid leukemia. Leukemia Research, 2013, 37, 765-768.	0.8	49
10	Circ-Foxo3 is positively associated with the Foxo3 gene and leads to better prognosis of acute myeloid leukemia patients. BMC Cancer, 2019, 19, 930.	2.6	46
11	Aberrant methylation of the death-associated protein kinase 1 ( <i>DAPK1</i> ) CpG island in chronic myeloid leukemia. European Journal of Haematology, 2009, 82, 119-123.	2.2	43
12	Epigenetic dysregulation of <i>ID4</i> predicts disease progression and treatment outcome in myeloid malignancies. Journal of Cellular and Molecular Medicine, 2017, 21, 1468-1481.	3.6	43
13	BCL2 overexpression: clinical implication and biological insights in acute myeloid leukemia. Diagnostic Pathology, 2019, 14, 68.	2.0	41
14	Double CEBPA mutations are prognostically favorable in non-M3 acute myeloid leukemia patients with wild-type NPM1 and FLT3-ITD. International Journal of Clinical and Experimental Pathology, 2014, 7, 6832-40.	0.5	41
15	<i>KRAS</i> overexpression independent of <i>RAS</i> mutations confers an adverse prognosis in cytogenetically normal acute myeloid leukemia. Oncotarget, 2017, 8, 66087-66097.	1.8	34
16	Dysregulation of miR-124-1 predicts favorable prognosis in acute myeloid leukemia. Clinical Biochemistry, 2014, 47, 63-66.	1.9	29
17	Reduced <i>miR-215</i> expression predicts poor prognosis in patients with acute myeloid leukemia. Japanese Journal of Clinical Oncology, 2016, 46, 350-356.	1.3	29
18	Identification and validation of SRY-box containing gene family member SOX30 methylation as a prognostic and predictive biomarker in myeloid malignancies. Clinical Epigenetics, 2018, 10, 92.	4.1	27

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19	Increased MCL-1 expression predicts poor prognosis and disease recurrence in acute myeloid leukemia. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 3295-3304.	2.0	27
20	Overexpression of BAALC: clinical significance in Chinese de novo acute myeloid leukemia. <i>Medical Oncology</i> , 2015, 32, 386.	2.5	25
21	Hypomethylation-mediated H19 overexpression increases the risk of disease evolution through the association with BCR-ABL transcript in chronic myeloid leukemia. <i>Journal of Cellular Physiology</i> , 2018, 233, 2444-2450.	4.1	25
22	Detection of SRSF2-P95 Mutation by High-Resolution Melting Curve Analysis and Its Effect on Prognosis in Myelodysplastic Syndrome. <i>PLoS ONE</i> , 2014, 9, e115693.	2.5	25
23	Identification and validation of prognosis-related DLX5 methylation as an epigenetic driver in myeloid neoplasms. <i>Clinical and Translational Medicine</i> , 2020, 10, e29.	4.0	24
24	Rapid detection of JAK2 V617F mutation using high-resolution melting analysis with LightScanner platform. <i>Clinica Chimica Acta</i> , 2010, 411, 2097-2100.	1.1	23
25	TET2 expression is a potential prognostic and predictive biomarker in cytogenetically normal acute myeloid leukemia. <i>Journal of Cellular Physiology</i> , 2018, 233, 5838-5846.	4.1	23
26	GPX3 methylation in bone marrow predicts adverse prognosis and leukemia transformation in myelodysplastic syndrome. <i>Cancer Medicine</i> , 2017, 6, 267-274.	2.8	22
27	Over-expression of miR-98 in FFPE tissues might serve as a valuable source for biomarker discovery in breast cancer patients. <i>International Journal of Clinical and Experimental Pathology</i> , 2014, 7, 1166-71.	0.5	21
28	The prognostic implication of SRSF2 mutations in Chinese patients with acute myeloid leukemia. <i>Tumor Biology</i> , 2016, 37, 10107-10114.	1.8	20
29	CDH1 (E-cadherin) expression independently affects clinical outcome in acute myeloid leukemia with normal cytogenetics. <i>Clinical Chemistry and Laboratory Medicine</i> , 2017, 55, 123-131.	2.3	20
30	Association between mir-24 and mir-378 in formalin-fixed paraffin-embedded tissues of breast cancer. <i>International Journal of Clinical and Experimental Pathology</i> , 2014, 7, 4261-7.	0.5	20
31	Methylation-independent ITGA2 overexpression is associated with poor prognosis in de novo acute myeloid leukemia. <i>Journal of Cellular Physiology</i> , 2018, 233, 9584-9593.	4.1	19
32	MiR-378 promoted cell proliferation and inhibited apoptosis by enhanced stem cell properties in chronic myeloid leukemia K562 cells. <i>Biomedicine and Pharmacotherapy</i> , 2019, 112, 108623.	5.6	19
33	Decreased SCIN expression, associated with promoter methylation, is a valuable predictor for prognosis in acute myeloid leukemia. <i>Molecular Carcinogenesis</i> , 2018, 57, 735-744.	2.7	18
34	High bone marrow miR-19b level predicts poor prognosis and disease recurrence in de novo acute myeloid leukemia. <i>Gene</i> , 2018, 640, 79-85.	2.2	18
35	Genome-wide methylation sequencing identifies progression-related epigenetic drivers in myelodysplastic syndromes. <i>Cell Death and Disease</i> , 2020, 11, 997.	6.3	18
36	Epigenetic inactivation of DLX4 is associated with disease progression in chronic myeloid leukemia. <i>Biochemical and Biophysical Research Communications</i> , 2015, 463, 1250-1256.	2.1	17

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37	Overexpression of <i>miR-216b</i> : Prognostic and predictive value in acute myeloid leukemia. <i>Journal of Cellular Physiology</i> , 2018, 233, 3274-3281.	4.1	17
38	DDX43 promoter is frequently hypomethylated and may predict a favorable outcome in acute myeloid leukemia. <i>Leukemia Research</i> , 2014, 38, 601-607.	0.8	16
39	High expression of OCT4 is frequent and may cause undesirable treatment outcomes in patients with acute myeloid leukemia. <i>Tumor Biology</i> , 2015, 36, 9711-9716.	1.8	16
40	Association Analyses of TP53 Mutation With Prognosis, Tumor Mutational Burden, and Immunological Features in Acute Myeloid Leukemia. <i>Frontiers in Immunology</i> , 2021, 12, 717527.	4.8	16
41	DLX4 hypermethylation is a prognostically adverse indicator in de novo acute myeloid leukemia. <i>Tumor Biology</i> , 2016, 37, 8951-8960.	1.8	15
42	Dose-adjusted EPOCH regimen as first-line treatment for non-Hodgkin lymphoma-associated hemophagocytic lymphohistiocytosis: a single-arm, open-label, phase II trial. <i>Haematologica</i> , 2020, 105, e29-e32.	3.5	15
43	Methotrexate therapy of T-cell large granular lymphocytic leukemia impact of STAT3 mutation. <i>Oncotarget</i> , 2016, 7, 61419-61425.	1.8	14
44	Hypomethylation of <i>let-7a-3</i> is associated with poor prognosis in myelodysplastic syndrome. <i>Leukemia and Lymphoma</i> , 2017, 58, 96-103.	1.3	13
45	Pseudogene <i>BMI1P1</i> expression as a novel predictor for acute myeloid leukemia development and prognosis. <i>Oncotarget</i> , 2016, 7, 47376-47386.	1.8	13
46	Reduced expression of chemerin is associated with poor clinical outcome in acute myeloid leukemia. <i>Oncotarget</i> , 2017, 8, 92536-92544.	1.8	13
47	Increased expression of miR-24 is associated with acute myeloid leukemia with t(8;21). <i>International Journal of Clinical and Experimental Pathology</i> , 2014, 7, 8032-8.	0.5	13
48	Abnormal methylation of GRAF promoter Chinese patients with acute myeloid leukemia. <i>Leukemia Research</i> , 2011, 35, 783-786.	0.8	12
49	Establishment and molecular characterization of decitabine-resistant K562 cells. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 3317-3324.	3.6	12
50	Low Expression of Pseudogene POU5F1B Affects Diagnosis and Prognosis in Acute Myeloid Leukemia (AML). <i>Medical Science Monitor</i> , 2019, 25, 4952-4959.	1.1	12
51	Reduced intensity conditioning of allogeneic hematopoietic stem cell transplantation for myelodysplastic syndrome and acute myeloid leukemia in patients older than 50 years of age: a systematic review and meta-analysis. <i>Journal of Cancer Research and Clinical Oncology</i> , 2017, 143, 1853-1864.	2.5	11
52	Identification and validation of obesity-related gene LEP methylation as a prognostic indicator in patients with acute myeloid leukemia. <i>Clinical Epigenetics</i> , 2021, 13, 16.	4.1	11
53	High bone marrow <i>ID2</i> expression predicts poor chemotherapy response and prognosis in acute myeloid leukemia. <i>Oncotarget</i> , 2017, 8, 91979-91989.	1.8	11
54	Efficacy and Safety of Lenalidomide for Treatment of Low-/Intermediate-1-Risk Myelodysplastic Syndromes with or without 5q Deletion: A Systematic Review and Meta-Analysis. <i>PLoS ONE</i> , 2016, 11, e0165948.	2.5	10

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55	GPX3 promoter is methylated in chronic myeloid leukemia. <i>International Journal of Clinical and Experimental Pathology</i> , 2015, 8, 6450-7.	0.5	10
56	Aberrant hypomethylation of <i>DDX43</i> promoter in myelodysplastic syndrome. <i>British Journal of Haematology</i> , 2012, 158, 293-296.	2.5	9
57	Epigenetic dysregulation of NKD2 is a valuable predictor assessing treatment outcome in acute myeloid leukemia. <i>Journal of Cancer</i> , 2017, 8, 460-468.	2.5	9
58	Low NKD1 expression predicts adverse prognosis in cytogenetically normal acute myeloid leukemia. <i>Tumor Biology</i> , 2017, 39, 101042831769912.	1.8	8
59	Dysregulation of miR-200s clusters as potential prognostic biomarkers in acute myeloid leukemia. <i>Journal of Translational Medicine</i> , 2018, 16, 135.	4.4	8
60	<i>SOX30</i> methylation correlates with disease progression in patients with chronic myeloid leukemia. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 4789-4794.	2.0	8
61	Hypermethylation of <i>ITGBL1</i> is associated with poor prognosis in acute myeloid leukemia. <i>Journal of Cellular Physiology</i> , 2019, 234, 9438-9446.	4.1	8
62	EZH2 dysregulation: Potential biomarkers predicting prognosis and guiding treatment choice in acute myeloid leukaemia. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 1640-1649.	3.6	8
63	Methylation of <i>CTNNA1</i> promoter: Frequent but not an adverse prognostic factor in acute myeloid leukemia. <i>Leukemia Research</i> , 2014, 38, 613-618.	0.8	7
64	BP1 overexpression is associated with adverse prognosis in de novo acute myeloid leukemia. <i>Leukemia and Lymphoma</i> , 2016, 57, 828-834.	1.3	7
65	Down-regulation of miR-29c is a prognostic biomarker in acute myeloid leukemia and can reduce the sensitivity of leukemic cells to decitabine. <i>Cancer Cell International</i> , 2019, 19, 177.	4.1	7
66	Clinical significance of up-regulated <i>ID1</i> expression in Chinese de novo acute myeloid leukemia. <i>International Journal of Clinical and Experimental Pathology</i> , 2015, 8, 5336-44.	0.5	7
67	High expression of dual-specificity phosphatase 5 pseudogene 1 ( <i>DUSP5P1</i> ) is associated with poor prognosis in acute myeloid leukemia. <i>International Journal of Clinical and Experimental Pathology</i> , 2015, 8, 16073-80.	0.5	7
68	Let-7a-3 hypomethylation is associated with favorable/intermediate karyotypes but not with survival in acute myeloid leukemia. <i>Tumor Biology</i> , 2016, 37, 491-501.	1.8	6
69	Methylation-independent <i>CHFR</i> expression is a potential biomarker affecting prognosis in acute myeloid leukemia. <i>Journal of Cellular Physiology</i> , 2018, 233, 4707-4714.	4.1	6
70	GPX3 hypermethylation serves as an independent prognostic biomarker in non-M3 acute myeloid leukemia. <i>American Journal of Cancer Research</i> , 2015, 5, 1786-94.	1.4	6
71	GPX3 hypermethylation serves as an independent prognostic biomarker in non-M3 acute myeloid leukemia. <i>American Journal of Cancer Research</i> , 2015, 5, 2047-55.	1.4	6
72	Intragenic hypomethylation of <i>DNMT3A</i> in patients with myelodysplastic syndrome. <i>Clinical Chemistry and Laboratory Medicine</i> , 2018, 56, 485-491.	2.3	5

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73	Bone marrow miR-10a overexpression is associated with genetic events but not affects clinical outcome in acute myeloid leukemia. <i>Pathology Research and Practice</i> , 2018, 214, 169-173.	2.3	5
74	Decreased SFRP2 expression is associated with intermediate and poor karyotypes in de novo acute myeloid leukemia. <i>International Journal of Clinical and Experimental Pathology</i> , 2014, 7, 4695-703.	0.5	5
75	Down-regulation of GPX3 is associated with favorable/intermediate karyotypes in de novo acute myeloid leukemia. <i>International Journal of Clinical and Experimental Pathology</i> , 2015, 8, 2384-91.	0.5	5
76	Expression characteristic of <i>CD44</i> and <i>CD24</i> in acute myeloid leukemia. <i>Bioengineered</i> , 2021, 12, 11987-12002.	3.2	5
77	Pan-cancer analysis identifies <i>CD300</i> molecules as potential immune regulators and promising therapeutic targets in acute myeloid leukemia. <i>Cancer Medicine</i> , 2023, 12, 789-807.	2.8	5
78	DNMT3A intragenic hypomethylation is associated with adverse prognosis in acute myeloid leukemia. <i>Leukemia Research</i> , 2015, 39, 1041-1047.	0.8	4
79	Lower expression of bone marrow miR-122 is an independent risk factor for overall survival in cytogenetically normal acute myeloid leukemia. <i>Pathology Research and Practice</i> , 2018, 214, 896-901.	2.3	4
80	Abnormal expression and methylation of <i>PRR34</i> and <i>AS1</i> are associated with adverse outcomes in acute myeloid leukemia. <i>Cancer Medicine</i> , 2021, 10, 5283-5296.	2.8	4
81	Cardiac resynchronization therapy for heart failure induced by left bundle branch block after transcatheter closure of ventricular septal defect. <i>Journal of Geriatric Cardiology</i> , 2014, 11, 357-62.	0.2	4
82	Kinetic analysis of the immunity in a pregnant patient infected with avian influenza H7N9. <i>International Journal of Clinical and Experimental Medicine</i> , 2014, 7, 1768-74.	1.3	4
83	MOK overexpression is associated with promoter hypomethylation in patients with acute myeloid leukemia. <i>International Journal of Clinical and Experimental Pathology</i> , 2015, 8, 127-36.	0.5	4
84	The 5' flanking region of miR-378 is hypomethylated in acute myeloid leukemia. <i>International Journal of Clinical and Experimental Pathology</i> , 2015, 8, 4321-31.	0.5	4
85	The novel structure make LDM effectively remove CD123+ AML stem cells in combination with interleukin 3. <i>Cancer Biology and Therapy</i> , 2015, 16, 1514-1525.	3.4	3
86	SETBP1 mutations in Chinese patients with acute myeloid leukemia and myelodysplastic syndrome. <i>Pathology Research and Practice</i> , 2018, 214, 706-712.	2.3	3
87	A three-gene signature might predict prognosis in patients with acute myeloid leukemia. <i>Bioscience Reports</i> , 2020, 40, .	2.4	3
88	Promoter methylation of the candidate tumor suppressor gene TCF21 in myelodysplastic syndrome and acute myeloid leukemia. <i>American Journal of Translational Research (discontinued)</i> , 2019, 11, 3450-3460.	0.0	3
89	SOX7 methylation is an independent prognostic factor in myelodysplastic syndromes. <i>Pathology Research and Practice</i> , 2019, 215, 322-328.	2.3	2
90	Hypomethylation of MIR-378 5' flanking region predicts poor survival in young patients with myelodysplastic syndrome. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2020, 8, e1067.	1.2	2

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91	Clinical and prognostic relevance of <i>CXCL12</i> expression in acute myeloid leukemia. PeerJ, 2021, 9, e11820.	2.0	2
92	Reduced expression of lncRNA <i>DLEU7-AS1</i> is a novel favorable prognostic factor in acute myeloid leukemia. Bioscience Reports, 2022, 42, .	2.4	1
93	Methylation-independent expression is a potential biomarker affecting prognosis in cytogenetically normal acute myeloid leukemia. American Journal of Translational Research (discontinued), 2020, 12, 4840-4852.	0.0	0