

# Huining Kang

## List of Publications by Year in descending order

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72  
papers

3,085  
citations

331670

21  
h-index

197818

49  
g-index

76  
all docs

76  
docs citations

76  
times ranked

4606  
citing authors

#	ARTICLE	IF	CITATIONS
1	Rearrangement of CRLF2 is associated with mutation of JAK kinases, alteration of IKZF1, Hispanic/Latino ethnicity, and a poor outcome in pediatric B-progenitor acute lymphoblastic leukemia. <i>Blood</i> , 2010, 115, 5312-5321.	1.4	503
2	Identification of novel cluster groups in pediatric high-risk B-precursor acute lymphoblastic leukemia with gene expression profiling: correlation with genome-wide DNA copy number alterations, clinical characteristics, and outcome. <i>Blood</i> , 2010, 116, 4874-4884.	1.4	370
3	Outcome modeling with CRLF2, IKZF1, JAK, and minimal residual disease in pediatric acute lymphoblastic leukemia: a Children's Oncology Group Study. <i>Blood</i> , 2012, 119, 3512-3522.	1.4	210
4	Gene expression classifiers for relapse-free survival and minimal residual disease improve risk classification and outcome prediction in pediatric B-precursor acute lymphoblastic leukemia. <i>Blood</i> , 2010, 115, 1394-1405.	1.4	192
5	Gene expression profiling of adult acute myeloid leukemia identifies novel biologic clusters for risk classification and outcome prediction. <i>Blood</i> , 2006, 108, 685-696.	1.4	180
6	Recurrent Fusions in <i>MYB</i> and <i>MYBL1</i> Define a Common, Transcription Factor-Driven Oncogenic Pathway in Salivary Gland Adenoid Cystic Carcinoma. <i>Cancer Discovery</i> , 2016, 6, 176-187.	9.4	179
7	Identification of serum metabolites associating with chronic kidney disease progression and anti-fibrotic effect of 5-methoxytryptophan. <i>Nature Communications</i> , 2019, 10, 1476.	12.8	171
8	Tyrosine kinome sequencing of pediatric acute lymphoblastic leukemia: a report from the Children's Oncology Group TARGET Project. <i>Blood</i> , 2013, 121, 485-488.	1.4	156
9	Biologic pathways associated with relapse in childhood acute lymphoblastic leukemia: a Children's Oncology Group study. <i>Blood</i> , 2006, 108, 711-717.	1.4	147
10	Gene expression profiles predictive of outcome and age in infant acute lymphoblastic leukemia: a Children's Oncology Group study. <i>Blood</i> , 2012, 119, 1872-1881.	1.4	110
11	Gene Expression Signatures Predictive of Early Response and Outcome in High-Risk Childhood Acute Lymphoblastic Leukemia: A Children's Oncology Group Study. <i>Journal of Clinical Oncology</i> , 2008, 26, 4376-4384.	1.6	102
12	BACH2 mediates negative selection and p53-dependent tumor suppression at the pre-B cell receptor checkpoint. <i>Nature Medicine</i> , 2013, 19, 1014-1022.	30.7	100
13	Multivitamins, Folate, and Green Vegetables Protect against Gene Promoter Methylation in the Aerodigestive Tract of Smokers. <i>Cancer Research</i> , 2010, 70, 568-574.	0.9	76
14	Development and Validation Of a Highly Sensitive and Specific Gene Expression Classifier To Prospectively Screen and Identify B-Precursor Acute Lymphoblastic Leukemia (ALL) Patients With a Philadelphia Chromosome-Like (Ph-like) or BCR-ABL1-Like Signature For Therapeutic Targeting and Clinical Intervention. <i>Blood</i> , 2013, 122, 826-826.	1.4	65
15	High Incidence of ErbB3, ErbB4, and MET Expression in Ovarian Cancer. <i>International Journal of Gynecological Pathology</i> , 2014, 33, 402-410.	1.4	45
16	A Novel Pharmacologic Activity of Ketorolac for Therapeutic Benefit in Ovarian Cancer Patients. <i>Clinical Cancer Research</i> , 2015, 21, 5064-5072.	7.0	40
17	Transcriptomes define distinct subgroups of salivary gland adenoid cystic carcinoma with different driver mutations and outcomes. <i>Oncotarget</i> , 2018, 9, 7341-7358.	1.8	38
18	Scoring of MYC protein expression in diffuse large B-cell lymphomas: concordance rate among hematopathologists. <i>Modern Pathology</i> , 2015, 28, 545-551.	5.5	33

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19	Polymorphisms in cytokine genes and serum cytokine levels among New Mexican women with and without breast cancer. <i>Cytokine</i> , 2010, 51, 18-24.	3.2	32
20	Advancing Pan-cancer Gene Expression Survival Analysis by Inclusion of Non-coding RNA. <i>RNA Biology</i> , 2020, 17, 1666-1673.	3.1	26
21	Epigenetic silencing of <i>SOCS5</i> potentiates <i>JAK</i> - <i>STAT</i> signaling and progression of T cell acute lymphoblastic leukemia. <i>Cancer Science</i> , 2019, 110, 1931-1946.	3.9	24
22	A Home-Based Mobile Health Intervention to Replace Sedentary Time With Light Physical Activity in Older Cancer Survivors: Randomized Controlled Pilot Trial. <i>JMIR Cancer</i> , 2021, 7, e18819.	2.4	24
23	Ovarian Tumor Microenvironment Signaling: Convergence on the Rac1 GTPase. <i>Cancers</i> , 2018, 10, 358.	3.7	23
24	Method of Detection and Breast Cancer Survival Disparities in Hispanic Women. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 2453-2460.	2.5	22
25	Identification of a Small Molecule Yeast TORC1 Inhibitor with a Multiplex Screen Based on Flow Cytometry. <i>ACS Chemical Biology</i> , 2012, 7, 715-722.	3.4	22
26	RUNX2 regulates leukemic cell metabolism and chemotaxis in high-risk T cell acute lymphoblastic leukemia. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	20
27	Pediatric B-lymphoblastic leukemia with RUNX1 amplification: clinicopathologic study of eight cases. <i>Modern Pathology</i> , 2011, 24, 1606-1611.	5.5	16
28	N-Terminal Truncated Myb with New Transcriptional Activity Produced Through Use of an Alternative MYB Promoter in Salivary Gland Adenoid Cystic Carcinoma. <i>Cancers</i> , 2020, 12, 45.	3.7	15
29	In Utero Exposure of Female CD-1 Mice to AZT and/or 3TC: II. Persistence of Functional Alterations in Cardiac Tissue. <i>Cardiovascular Toxicology</i> , 2010, 10, 87-99.	2.7	14
30	Default Patterning Produces Pan-cortical Glutamatergic and CGE/LGE-like GABAergic Neurons from Human Pluripotent Stem Cells. <i>Stem Cell Reports</i> , 2017, 9, 1463-1476.	4.8	14
31	MutEx: a multifaceted gateway for exploring integrative pan-cancer genomic data. <i>Briefings in Bioinformatics</i> , 2020, 21, 1479-1486.	6.5	12
32	Serum Occludin as a Biomarker to Predict the Severity of Acute Ischemic Stroke, Hemorrhagic Transformation, and Patient Prognosis. , 2020, 11, 1395.		12
33	CD34+ megakaryocytes (≈30%) are associated with megaloblastic anaemia and non-acute myeloid neoplasia. <i>Histopathology</i> , 2012, 61, 694-701.	2.9	9
34	Gene Expression Studies on Human Trisomy 21 iPSCs and Neurons: Towards Mechanisms Underlying Downâ€™s Syndrome and Early Alzheimerâ€™s Disease-Like Pathologies. <i>Methods in Molecular Biology</i> , 2016, 1303, 247-265.	0.9	9
35	Dietary Nutrient Intake, Ethnicity, and Epigenetic Silencing of Lung Cancer Genes Detected in Sputum in New Mexican Smokers. <i>Cancer Prevention Research</i> , 2018, 11, 93-102.	1.5	9
36	Dysregulated transcriptional networks in KMT2A- and MLLT10-rearranged T-ALL. <i>Biomarker Research</i> , 2018, 6, 27.	6.8	9

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37	Serum Occludin Level Combined With NIHSS Score Predicts Hemorrhage Transformation in Ischemic Stroke Patients With Reperfusion. <i>Frontiers in Cellular Neuroscience</i> , 2021, 15, 714171.	3.7	9
38	Accurate and efficient estimation of small $P$ -values with the cross-entropy method: applications in genomic data analysis. <i>Bioinformatics</i> , 2019, 35, 2441-2448.	4.1	6
39	Transcriptomic changes due to early, chronic intermittent alcohol exposure during forebrain development implicate WNT signaling, cell type specification, and cortical regionalization as primary determinants of fetal alcohol syndrome. <i>Alcoholism: Clinical and Experimental Research</i> , 2021, 45, 979-995.	2.4	6
40	Most Morphologic Features in Chronic Lymphocytic Leukemia/Small Lymphocytic Lymphoma (CLL/SLL) do not Reliably Predict Underlying FISH Genetics or Immunoglobulin Heavy Chain Variable Region Somatic Mutational Status. <i>Applied Immunohistochemistry and Molecular Morphology</i> , 2010, 18, 119-127.	1.2	5
41	Adherence to National Guidelines on Cervical Screening: A Population-Based Evaluation From a Statewide Registry. <i>Journal of the National Cancer Institute</i> , 2022, 114, 626-630.	6.3	5
42	Non-canonical RNA-DNA differences and other human genomic features are enriched within very short tandem repeats. <i>PLoS Computational Biology</i> , 2020, 16, e1007968.	3.2	4
43	A streamlined solution for processing, elucidating and quality control of cyclobutane pyrimidine dimer sequencing data. <i>Nature Protocols</i> , 2021, 16, 2190-2212.	12.0	3
44	Acceptability of Phone Calls and Texts to Promote Healthy Behaviors Among Spanish-Speaking Hispanics. <i>Hispanic Journal of Behavioral Sciences</i> , 2021, 43, 278-293.	0.5	3
45	A BCR-ABL1-Like Gene Expression Profile Confers a Poor Prognosis In Patients with High-Risk Acute Lymphoblastic Leukemia (HR-ALL): A Report From Children's Oncology Group (COG) AALL0232. <i>Blood</i> , 2011, 118, 743-743.	1.4	3
46	A Two-Part Mixed Model for Differential Expression Analysis in Single-Cell High-Throughput Gene Expression Data. <i>Genes</i> , 2022, 13, 377.	2.4	3
47	MetaGSCA: A tool for meta-analysis of gene set differential coexpression. <i>PLoS Computational Biology</i> , 2021, 17, e1008976.	3.2	2
48	Mixed Lineage Leukemia Rearrangements (MLL-R) Are Determinants of High Risk Disease in Homeobox A (HOXA)-deregulated T-Lineage Acute Lymphoblastic Leukemia: A Children's Oncology Group Study. <i>Blood</i> , 2015, 126, 694-694.	1.4	2
49	Self-Selected Walking Cadence after 16-Week Light-Intensity Physical Activity Intervention for Older Cancer Survivors. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 4768.	2.6	2
50	Global Autozygosity Is Associated with Cancer Risk, Mutational Signature and Prognosis. <i>Cancers</i> , 2020, 12, 3646.	3.7	1
51	Abstract 4129:RUNX2as a regulator of high-risk T-ALL. , 2018, , .		1
52	RUNX2 Regulates Cell Migration in T-Cell Lineage Acute Lymphoblastic Leukemia. <i>Blood</i> , 2019, 134, 3947-3947.	1.4	1
53	CD34+ Megakaryocytes (30%) are Unique to Megaloblastic Anemia and Myeloid Neoplasms. <i>American Journal of Clinical Pathology</i> , 2012, 138, A168-A168.	0.7	0
54	Plasma Cell Enrichment in the Detection of Genetic Abnormalities in Plasma Cell Myeloma by Fluorescence In Situ Hybridization: A Single-Center Experience. <i>American Journal of Clinical Pathology</i> , 2012, 138, A215-A215.	0.7	0

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55	Molecular Classifiers for Prediction of Minimal Residual Disease (MRD) and Event Free Survival (EFS) Improve Risk Assignment at Diagnosis in Pediatric High-Risk B Precursor Acute Lymphoblastic Leukemia (ALL): A Children's Oncology Group Study.. Blood, 2007, 110, 1422-1422.	1.4	0
56	Gene Expression Profiling Reveals Genes Predictive of Outcome In Infant Acute Lymphoblastic Leukemia (ALL) and Distinctive Age-Related Gene Expression Profiles (< 90 Days vs. > 90 Days): A Children's Oncology Group Study. Blood, 2010, 116, 412-412.	1.4	0
57	BACH2 Is Required for Pre-B Cell Receptor Checkpoint Control and p53-Dependent Tumor Surveillance. Blood, 2012, 120, 1300-1300.	1.4	0
58	Abstract C56: Relationship of ancestry and breast cancer subtypes in Hispanic women from New Mexico and Washington State. , 2016, , .		0
59	New Insights into Deregulated Gene Expression Pathways in MLL- and AF10-Rearranged T-Lineage Acute Lymphoblastic Leukemia. Blood, 2016, 128, 2906-2906.	1.4	0
60	Abstract LB-077: H1047R mutation of p110 alpha alters expression level of genes which are associated with cell migration & cancer metastasis. , 2017, , .		0
61	Abstract 3874: Epigenetic deregulation ofSOCS5expression in T cell lineage acute lymphoblastic leukemia. , 2017, , .		0
62	Self-selected Walking Cadence After Light-intensity Physical Activity Intervention For Older Cancer Survivors. Medicine and Science in Sports and Exercise, 2020, 52, 331-332.	0.4	0
63	Title is missing!. , 2020, 16, e1007968.		0
64	Title is missing!. , 2020, 16, e1007968.		0
65	Title is missing!. , 2020, 16, e1007968.		0
66	Title is missing!. , 2020, 16, e1007968.		0
67	Title is missing!. , 2020, 16, e1007968.		0
68	Title is missing!. , 2020, 16, e1007968.		0
69	Two-step mixed model approach to analyzing differential alternative RNA splicing. , 2020, 15, e0232646.		0
70	Two-step mixed model approach to analyzing differential alternative RNA splicing. , 2020, 15, e0232646.		0
71	Two-step mixed model approach to analyzing differential alternative RNA splicing. , 2020, 15, e0232646.		0
72	Two-step mixed model approach to analyzing differential alternative RNA splicing. , 2020, 15, e0232646.		0