List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Epigenetic changes in human model KMT2A leukemias highlight early events during leukemogenesis. Haematologica, 2022, 107, 86-99.	3.5	10
2	Vesicular trafficking is a key determinant of the statin response in acute myeloid leukemia. Blood Advances, 2022, 6, 509-514.	5.2	4
3	CDK7/12/13 inhibition targets an oscillating leukemia stem cell network and synergizes with venetoclax in acute myeloid leukemia. EMBO Molecular Medicine, 2022, 14, e14990.	6.9	14
4	Monoallelic Heb/Tcf12 Deletion Reduces the Requirement for NOTCH1 Hyperactivation in T-Cell Acute Lymphoblastic Leukemia. Frontiers in Immunology, 2022, 13, 867443.	4.8	4
5	HMGA2 expression defines a subset of human AML with immature transcriptional signature and vulnerability to G2/M inhibition. Blood Advances, 2022, 6, 4793-4806.	5.2	5
6	The uracil-DNA glycosylase UNG protects the fitness of normal and cancer B cells expressing AID. NAR Cancer, 2021, 2, zcaa019.	3.1	10
7	Apoptotic Blocks in Primary Non-Hodgkin B Cell Lymphomas Identified by BH3 Profiling. Cancers, 2021, 13, 1002.	3.7	9
8	Human pluripotent stem cells identify molecular targets of trisomy 12 in chronic lymphocytic leukemia patients. Cell Reports, 2021, 34, 108845.	6.4	3
9	Atypical acute myeloid leukemia-specific transcripts generate shared and immunogenic MHC class-l-associated epitopes. Immunity, 2021, 54, 737-752.e10.	14.3	58
10	Legal and Ethical Considerations for the Design and Use of Web Portals for Researchers, Clinicians, and Patients: Scoping Literature Review. Journal of Medical Internet Research, 2021, 23, e26450.	4.3	3
11	Efficacy, Toxicity and Cost of Venetoclax-Based Combinations for the Treatment of Acute Myeloid Leukemia: Real-World Evidence from a Canadian Academic Center. Blood, 2021, 138, 1253-1253.	1.4	0
12	Genetic characterization of ABT-199 sensitivity in human AML. Leukemia, 2020, 34, 63-74.	7.2	58
13	Cryptic recurrent <i>ACIN1</i> â€ <i>NUTM1</i> fusions in nonâ€ <i>KMT2A</i> â€rearranged infant acute lymphoblastic leukemia. Genes Chromosomes and Cancer, 2020, 59, 125-130.	2.8	16
14	High frequency of germline <i>RUNX1</i> mutations in patients with <i> RUNX1</i> -mutated AML. Blood, 2020, 135, 1882-1886.	1.4	63
15	Cost-Effectiveness Analysis of a HMGA2 Prognostic Test for Acute Myeloid Leukemia in a Canadian Setting. Applied Health Economics and Health Policy, 2019, 17, 827-839.	2.1	3
16	Mubritinib Targets the Electron Transport Chain Complex I and Reveals the Landscape of OXPHOS Dependency in Acute Myeloid Leukemia. Cancer Cell, 2019, 36, 84-99.e8.	16.8	163
17	IDH1 as a Cooperating Mutation in AML Arising in the Context of Shwachman-Diamond Syndrome. Frontiers in Oncology, 2019, 9, 772.	2.8	8
18	The neuropeptide receptor calcitonin receptor-like (CALCRL) is a potential therapeutic target in acute myeloid leukemia. Leukemia, 2019, 33, 2830-2841.	7.2	30

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19	Hepatic leukemia factor is a novel leukemic stem cell regulator in DNMT3A, NPM1, and FLT3-ITD triple-mutated AML. Blood, 2019, 134, 263-276.	1.4	41
20	Human models of NUP98-KDM5A megakaryocytic leukemia in mice contribute to uncovering new biomarkers and therapeutic vulnerabilities. Blood Advances, 2019, 3, 3307-3321.	5.2	23
21	Complex karyotype AML displays G2/M signature and hypersensitivity to PLK1 inhibition. Blood Advances, 2019, 3, 552-563.	5.2	24
22	Targeted variant detection using unaligned RNA-Seq reads. Life Science Alliance, 2019, 2, e201900336.	2.8	14
23	Transcriptomic landscape of acute promyelocytic leukemia reveals aberrant surface expression of the platelet aggregation agonist Podoplanin. Leukemia, 2018, 32, 1349-1357.	7.2	31
24	GFI1 facilitates efficient DNA repair by regulating PRMT1 dependent methylation of MRE11 and 53BP1. Nature Communications, 2018, 9, 1418.	12.8	42
25	MEF2C Phosphorylation Is Required forÂChemotherapy Resistance in Acute Myeloid Leukemia. Cancer Discovery, 2018, 8, 478-497.	9.4	59
26	<i>NUP98â€BPTF</i> gene fusion identified in primary refractory acute megakaryoblastic leukemia of infancy. Genes Chromosomes and Cancer, 2018, 57, 311-319.	2.8	18
27	The genomic landscape of two Burkitt lymphoma cases and derived cell lines: comparison between primary and relapse samples. Leukemia and Lymphoma, 2018, 59, 2159-2174.	1.3	6
28	The Adhesion G Protein-Coupled Receptor GPR97/ADGRG3 Is Expressed in Human Granulocytes and Triggers Antimicrobial Effector Functions. Frontiers in Immunology, 2018, 9, 2830.	4.8	27
29	High expression of HMGA2 independently predicts poor clinical outcomes in acute myeloid leukemia. Blood Cancer Journal, 2018, 8, 68.	6.2	36
30	Genetic Characterization of ABT-199 Sensitivity in Human AML. Blood, 2018, 132, 283-283.	1.4	37
31	Reduced Intensity Conditioned Sibling Transplantation Versus No Transplant in Intermediate or High Risk Acute Myeloid Leukemia: A Prospective Multi-Center Study in Patients 50-70 Years in First Complete Remission and with at Least One Potential Sibling Donor (ClinTrialGov 00342316). Blood, 2018, 132, 205-205	1.4	2
32	Chemogenomic Approach Unveils the Increased Susceptibility of RUNX1-Mutated AML to Glucocorticoids. Blood, 2018, 132, 4675-4675.	1.4	0
33	Apoptotic Blocks in Primary Non-Hodgkin B-Cell Lymphomas Identified By BH3 Profiling. Blood, 2018, 132, 4126-4126.	1.4	0
34	MiSTIC, an integrated platform for the analysis of heterogeneity in large tumour transcriptome datasets. Nucleic Acids Research, 2017, 45, e122-e122.	14.5	14
35	Chemogenomic Landscape of <i>RUNX1</i> -mutated AML Reveals Importance of <i>RUNX1</i> Allele Dosage in Genetics and Glucocorticoid Sensitivity. Clinical Cancer Research, 2017, 23, 6969-6981.	7.0	36
36	H3 K27M/I mutations promote context-dependent transformation in acute myeloid leukemia with RUNX1 alterations. Blood, 2017, 130, 2204-2214.	1.4	62

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37	Identification of novel biomarkers for MLL-translocated acute myeloid leukemia. Experimental Hematology, 2017, 56, 58-63.	0.4	5
38	AML1-ETO requires enhanced C/D box snoRNA/RNP formation to induce self-renewal and leukaemia. Nature Cell Biology, 2017, 19, 844-855.	10.3	132
39	Adhesion GPCRs in Regulating Immune Responses and Inflammation. Advances in Immunology, 2017, 136, 163-201.	2.2	59
40	GPR56 identifies primary human acute myeloid leukemia cells with high repopulating potential in vivo. Blood, 2016, 127, 2018-2027.	1.4	148
41	RNA-sequencing analysis of core binding factor AML identifies recurrent ZBTB7A mutations and defines RUNX1-CBFA2T3 fusion signature. Blood, 2016, 127, 2498-2501.	1.4	60
42	Chemo-genomic interrogation of CEBPA mutated AML reveals recurrent CSF3R mutations and subgroup sensitivity to JAK inhibitors. Blood, 2016, 127, 3054-3061.	1.4	70
43	Expression of immunoproteasome genes is regulated by cell-intrinsic and –extrinsic factors in human cancers. Scientific Reports, 2016, 6, 34019.	3.3	67
44	UTX inhibition as selective epigenetic therapy against TAL1-driven T-cell acute lymphoblastic leukemia. Genes and Development, 2016, 30, 508-521.	5.9	104
45	High-throughput screening in niche-based assay identifies compounds to target preleukemic stem cells. Journal of Clinical Investigation, 2016, 126, 4569-4584.	8.2	49
46	Targeting Pre-Leukemic Stem Cells in T-Acute Lymphoblastic Leukemia. Blood, 2016, 128, 527-527.	1.4	0
47	EVI1-rearranged acute myeloid leukemias are characterized by distinct molecular alterations. Blood, 2015, 125, 140-143.	1.4	68
48	The transcriptomic landscape and directed chemical interrogation of MLL-rearranged acute myeloid leukemias. Nature Genetics, 2015, 47, 1030-1037.	21.4	132
49	Transcriptome Analysis Reveals That G Protein-Coupled Receptors Are Potential Diagnostic Markers or Therapeutic Targets in Acute Myeloid Leukemia. Blood, 2015, 126, 3855-3855.	1.4	2
50	The Novel Leukemia Stem Cell Marker GPR56 Discriminates Leukemic Subclones with Divergent Stem Cell Properties in Human Acute Myeloid Leukemia. Blood, 2015, 126, 1859-1859.	1.4	0
51	Essential role of BRG, the ATPase subunit of BAF chromatin remodeling complexes, in leukemia maintenance. Blood, 2014, 123, 1720-1728.	1.4	97
52	SCL, LMO1 and Notch1 Reprogram Thymocytes into Self-Renewing Cells. PLoS Genetics, 2014, 10, e1004768.	3.5	57
53	Identification of small molecules that support human leukemia stem cell activity ex vivo. Nature Methods, 2014, 11, 436-442.	19.0	115
54	Tumor suppressor and deubiquitinase BAP1 promotes DNA double-strand break repair. Proceedings of the United States of America, 2014, 111, 285-290.	7.1	300

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55	UBAP2L is a novel BMI1-interacting protein essential for hematopoietic stem cell activity. Blood, 2014, 124, 2362-2369.	1.4	30
56	Presence of alternative lengthening of telomeres associated circular extrachromosome telomere repeats in primary leukemia cells of chronic myeloid leukemia. Journal of Hematology and Oncology, 2013, 6, 26.	17.0	10
57	Nuclear remodeling of telomeres in chronic myeloid leukemia. Genes Chromosomes and Cancer, 2013, 52, 495-502.	2.8	7
58	ldentification of a novel fusion gene involving <i>RUNX1</i> and the antisense strand of <i>SV2B</i> in a <i>BCRâ€ABL1</i> â€positive acute leukemia. Genes Chromosomes and Cancer, 2013, 52, 1114-1122.	2.8	9
59	RNA-Seq Reveals Spliceosome and Proteasome Genes as Most Consistent Transcripts in Human Cancer Cells. PLoS ONE, 2013, 8, e72884.	2.5	46
60	Ezh2 Is An Essential Regulator Of T-Cell Development and Oncogenic Transformation. Blood, 2013, 122, 3729-3729.	1.4	0
61	A key role for <i>EZH2</i> and associated genes in mouse and human adult T-cell acute leukemia. Genes and Development, 2012, 26, 651-656.	5.9	238
62	A role for GPx3 in activity of normal and leukemia stem cells. Journal of Experimental Medicine, 2012, 209, 895-901.	8.5	83
63	The MRE11 GAR motif regulates DNA double-strand break processing and ATR activation. Cell Research, 2012, 22, 305-320.	12.0	68
64	Chromosome Arm-Specific Long Telomeres: A New Clonal Event in Primary Chronic Myelogenous Leukemia Cells. Neoplasia, 2011, 13, 550-IN17.	5.3	12
65	RNA-seq analysis of 2 closely related leukemia clones that differ in their self-renewal capacity. Blood, 2011, 117, e27-e38.	1.4	57
66	Microhomologies and topoisomerase II consensus sequences identified near the breakpoint junctions of the recurrent t(7;21)(p22;q22) translocation in acute myeloid leukemia. Genes Chromosomes and Cancer, 2011, 50, 228-238.	2.8	15
67	An anticlastogenic function for the Polycomb Group gene Bmi1. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5284-5289.	7.1	61
68	CLCA2, a novel RUNX1 partner gene in a therapy-related leukemia with t(1;21)(p22;q22). Cancer Genetics and Cytogenetics, 2010, 202, 94-100.	1.0	8
69	Modeling T-cell acute lymphoblastic leukemia induced by the <i>SCL</i> and <i>LMO1</i> oncogenes. Genes and Development, 2010, 24, 1093-1105.	5.9	104
70	Genome-Wide Interrogation of Mammalian Stem Cell Fate Determinants by Nested Chromosome Deletions. PLoS Genetics, 2010, 6, e1001241.	3.5	5
71	A Mouse <i>PRMT1</i> Null Allele Defines an Essential Role for Arginine Methylation in Genome Maintenance and Cell Proliferation. Molecular and Cellular Biology, 2009, 29, 2982-2996.	2.3	160
72	Individual Telomere Lengths in Chronic Myeloid Leukemia. Neoplasia, 2009, 11, 1146-IN6.	5.3	24

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73	Quantitative expression profiling guided by common retroviral insertion sites reveals novel and cell type–specific cancer genes in leukemia. Blood, 2008, 111, 790-799.	1.4	32
74	Deregulated Expression of Ubiquitin-Specific Peptidase Genes in Myeloid Leukemia. Blood, 2008, 112, 4481-4481.	1.4	1
75	BMI1 Interacts with FANCD2 at DNA Lesions and Prevents Chromosome Breaks. Blood, 2008, 112, 3099-3099.	1.4	11
76	A retroviral strategy that efficiently creates chromosomal deletions in mammalian cells. Nature Methods, 2007, 4, 263-268.	19.0	14
77	Overexpression of PRDM16 in the presence and absence of the RUNX1/PRDM16 fusion gene in myeloid leukemias. Genes Chromosomes and Cancer, 2006, 45, 1072-1076.	2.8	15
78	Overexpression of MEL1 as a Novel Fusion Partner of AML1 in the Blastic Phase of Chronic Myeloid Leukemia with the Recurrent Cryptic Translocation t(1;21)(p36.3;q22) Blood, 2005, 106, 4332-4332.	1.4	0