Jianjun Chen

List of Publications by Year
in descending order

147 papers	17,041 citations	19608 61 h-index	16127 124 g-index
154 all docs	154 docs citations	154 times ranked	16999 citing authors

#	Article	IF	Citations
1	Recognition of RNA N6-methyladenosine by IGF2BP proteins enhances mRNA stability and translation. Nature Cell Biology, 2018, 20, 285-295.	4.6	1,650
2	FTO Plays an Oncogenic Role in Acute Myeloid Leukemia as a N 6 -Methyladenosine RNA Demethylase. Cancer Cell, 2017, 31, 127-141.	7.7	1,139
3	R-2HG Exhibits Anti-tumor Activity by Targeting FTO/m6A/MYC/CEBPA Signaling. Cell, 2018, 172, 90-105.e23.	13.5	794
4	METTL14 Inhibits Hematopoietic Stem/Progenitor Differentiation and Promotes Leukemogenesis via mRNA m6A Modification. Cell Stem Cell, 2018, 22, 191-205.e9.	5.2	749
5	m6A Modification in Coding and Non-coding RNAs: Roles and Therapeutic Implications in Cancer. Cancer Cell, 2020, 37, 270-288.	7.7	688
6	RNA N6-methyladenosine modification in cancers: current status and perspectives. Cell Research, 2018, 28, 507-517.	5.7	586
7	Small-Molecule Targeting of Oncogenic FTO Demethylase in Acute Myeloid Leukemia. Cancer Cell, 2019, 35, 677-691.e10.	7.7	516
8	Differential m6A, m6Am, and m1A Demethylation Mediated by FTO in the Cell Nucleus and Cytoplasm. Molecular Cell, 2018, 71, 973-985.e5.	4.5	506
9	Histone H3 trimethylation at lysine 36 guides m6A RNA modification co-transcriptionally. Nature, 2019, 567, 414-419.	13.7	452
10	MicroRNA expression signatures accurately discriminate acute lymphoblastic leukemia from acute myeloid leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 19971-19976.	3.3	435
11	miR-21 plays a pivotal role in gastric cancer pathogenesis and progression. Laboratory Investigation, 2008, 88, 1358-1366.	1.7	434
12	Distinct microRNA expression profiles in acute myeloid leukemia with common translocations. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15535-15540.	3.3	418
13	Targeting FTO Suppresses Cancer Stem Cell Maintenance and Immune Evasion. Cancer Cell, 2020, 38, 79-96.e11.	7.7	389
14	Over 20% of human transcripts might form sense-antisense pairs. Nucleic Acids Research, 2004, 32, 4812-4820.	6.5	287
15	Leukaemogenesis: more than mutant genes. Nature Reviews Cancer, 2010, 10, 23-36.	12.8	286
16	IGF2BP1 promotes SRF-dependent transcription in cancer in a m6A- and miRNA-dependent manner. Nucleic Acids Research, 2019, 47, 375-390.	6.5	256
17	MicroRNA and cancer: Current status and prospective. International Journal of Cancer, 2006, 120, 953-960.	2.3	231
18	HMGA2/TET1/HOXA9 signaling pathway regulates breast cancer growth and metastasis. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 9920-9925.	3.3	231

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19	RNA Demethylase ALKBH5 Selectively Promotes Tumorigenesis and Cancer Stem Cell Self-Renewal in Acute Myeloid Leukemia. Cell Stem Cell, 2020, 27, 64-80.e9.	5.2	225
20	Regulation of mir-196b by MLL and its overexpression by MLL fusions contributes to immortalization. Blood, 2009, 113, 3314-3322.	0.6	208
21	The Biogenesis and Precise Control of RNA m6A Methylation. Trends in Genetics, 2020, 36, 44-52.	2.9	198
22	<i>TET1</i> plays an essential oncogenic role in <i>MLL</i> -rearranged leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11994-11999.	3.3	185
23	Role of N6-methyladenosine modification in cancer. Current Opinion in Genetics and Development, 2018, 48, 1-7.	1.5	178
24	Oligo(dT) primer generates a high frequency of truncated cDNAs through internal poly(A) priming during reverse transcription. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 6152-6156.	3.3	168
25	Identification of a 24-Gene Prognostic Signature That Improves the European LeukemiaNet Risk Classification of Acute Myeloid Leukemia: An International Collaborative Study. Journal of Clinical Oncology, 2013, 31, 1172-1181.	0.8	164
26	R-2-hydroxyglutarate attenuates aerobic glycolysis in leukemia by targeting the FTO/m6A/PFKP/LDHB axis. Molecular Cell, 2021, 81, 922-939.e9.	4.5	157
27	Blockade of miR-150 Maturation by MLL-Fusion/MYC/LIN-28 Is Required for MLL-Associated Leukemia. Cancer Cell, 2012, 22, 524-535.	7.7	154
28	YTHDF1 Promotes Gastric Carcinogenesis by Controlling Translation of <i>FZD7</i>. Cancer Research, 2021, 81, 2651-2665.	0.4	150
29	Up-regulation of a HOXA-PBX3 homeobox-gene signature following down-regulation of miR-181 is associated with adverse prognosis in patients with cytogenetically abnormal AML. Blood, 2012, 119, 2314-2324.	0.6	145
30	Identifying novel transcripts and novel genes in the human genome by using novel SAGE tags. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 12257-12262.	3.3	143
31	METTL16 exerts an m6A-independent function to facilitate translation and tumorigenesis. Nature Cell Biology, 2022, 24, 205-216.	4.6	143
32	Aberrant overexpression and function of the miR-17-92 cluster in <i>MLL</i> -rearranged acute leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 3710-3715.	3.3	141
33	An Extensive Network of TET2-Targeting MicroRNAs Regulates Malignant Hematopoiesis. Cell Reports, 2013, 5, 471-481.	2.9	139
34	miR-196b directly targets both HOXA9/MEIS1 oncogenes and FAS tumour suppressor in MLL-rearranged leukaemia. Nature Communications, 2012, 3, 688.	5.8	138
35	Genome-wide analysis of coordinate expression and evolution of human encoded sense-antisense transcripts. Trends in Genetics, 2005, 21, 326-329.	2.9	133
36	MicroRNAs expression signatures are associated with lineage and survival in acute leukemias. Blood Cells, Molecules, and Diseases, 2010, 44, 191-197.	0.6	132

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37	FTO-Dependent <i>N</i>⁶-Methyladenosine Modifications Inhibit Ovarian Cancer Stem Cell Self-Renewal by Blocking cAMP Signaling. Cancer Research, 2020, 80, 3200-3214.	0.4	128
38	HIF-2Î± promotes conversion to a stem cell phenotype and induces chemoresistance in breast cancer cells by activating Wnt and Notch pathways. Journal of Experimental and Clinical Cancer Research, 2018, 37, 256.	3.5	124
39	PBX3 is an important cofactor of HOXA9 in leukemogenesis. Blood, 2013, 121, 1422-1431.	0.6	116
40	m6A RNA modifications are measured at single-base resolution across the mammalian transcriptome. Nature Biotechnology, 2022, 40, 1210-1219.	9.4	115
41	miR-22 has a potent anti-tumour role with therapeutic potential in acute myeloid leukaemia. Nature Communications, 2016, 7, 11452.	5.8	113
42	MicroRNAs in cancer biology and therapy: Current status and perspectives. Genes and Diseases, 2014, 1, 53-63.	1.5	111
43	miR-495 is a tumor-suppressor microRNA down-regulated in <i>MLL</i> -rearranged leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 19397-19402.	3.3	109
44	Crosstalk between epitranscriptomic and epigenetic mechanisms in gene regulation. Trends in Genetics, 2022, 38, 182-193.	2.9	108
45	The IRF4 Gene Regulatory Module Functions as a Read-Write Integrator to Dynamically Coordinate TÂHelper Cell Fate. Immunity, 2017, 47, 481-497.e7.	6.6	104
46	Critical Enzymatic Functions of FTO in Obesity and Cancer. Frontiers in Endocrinology, 2018, 9, 396.	1.5	102
47	Genomic DNA breakpoints in AML1/RUNX1 and ETO cluster with topoisomerase II DNA cleavage and DNase I hypersensitive sites in t(8;21) leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 3070-3075.	3.3	100
48	SAGE is far more sensitive than EST for detecting low-abundance transcripts. BMC Genomics, 2004, 5, 1.	1.2	98
49	miR-9 is an essential oncogenic microRNA specifically overexpressed in <i>mixed lineage leukemia</i> â€“rearranged leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11511-11516.	3.3	97
50	EGR1 recruits TET1 to shape the brain methylome during development and upon neuronal activity. Nature Communications, 2019, 10, 3892.	5.8	95
51	Epitranscriptomics in liver disease: Basic concepts and therapeutic potential. Journal of Hepatology, 2020, 73, 664-679.	1.8	92
52	YBX1 is required for maintaining myeloid leukemia cell survival by regulating <i>BCL2</i> stability in an m6A-dependent manner. Blood, 2021, 138, 71-85.	0.6	87
53	The RNA m6A reader YTHDF2 controls NK cell antitumor and antiviral immunity. Journal of Experimental Medicine, 2021, 218, .	4.2	82
54	Consistent Deregulation of Gene Expression between Human and Murine <i>MLL</i> Rearrangement Leukemias. Cancer Research, 2009, 69, 1109-1116.	0.4	81

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55	Co-inhibition of NF-Î°B and JNK is synergistic in TNF-expressing human AML. Journal of Experimental Medicine, 2014, 211, 1093-1108.	4.2	80
56	Evidence for a preferential targeting of 3'-UTRs by cis-encoded natural antisense transcripts. Nucleic Acids Research, 2005, 33, 5533-5543.	6.5	78
57	The dynamics of DNA methylation fidelity during mouse embryonic stem cell self-renewal and differentiation. Genome Research, 2014, 24, 1296-1307.	2.4	72
58	Identification of a circulating MicroRNA signature to distinguish recurrence in breast cancer patients. Oncotarget, 2016, 7, 55231-55248.	0.8	70
59	Critical role of miR-9 in myelopoiesis and EVI1-induced leukemogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5594-5599.	3.3	68
60	Therapeutic antagonists of microRNAs deplete leukemia-initiating cell activity. Journal of Clinical Investigation, 2014, 124, 222-236.	3.9	66
61	Overexpression and knockout of miR-126 both promote leukemogenesis. Blood, 2015, 126, 2005-2015.	0.6	65
62	Young intragenic miRNAs are less coexpressed with host genes than old ones: implications of miRNAâ€"host gene coevolution. Nucleic Acids Research, 2012, 40, 4002-4012.	6.5	63
63	FTO in cancer: functions, molecular mechanisms, and therapeutic implications. Trends in Cancer, 2022, 8, 598-614.	3.8	61
64	Human antisense genes have unusually short introns: evidence for selection for rapid transcription. Trends in Genetics, 2005, 21, 203-207.	2.9	60
65	RNA Modifications in Cancer: Functions, Mechanisms, and Therapeutic Implications. Annual Review of Cancer Biology, 2020, 4, 221-240.	2.3	60
66	N(6)â€methyladenosineâ€binding protein YTHDF1 suppresses EBV replication and promotes EBV RNA decay. EMBO Reports, 2021, 22, e50128.	2.0	59
67	IFITM3 functions as a PIP3 scaffold to amplify PI3K signalling in BÂcells. Nature, 2020, 588, 491-497.	13.7	57
68	FOXM1 regulates leukemia stem cell quiescence and survival in MLL-rearranged AML. Nature Communications, 2020, 11, 928.	5.8	54
69	High-throughput GLGI procedure for converting a large number of serial analysis of gene expression tag sequences into 3? complementary DNAs. Genes Chromosomes and Cancer, 2002, 33, 252-261.	1.5	51
70	The pathological role and prognostic impact of miR-181 in acute myeloid leukemia. Cancer Genetics, 2015, 208, 225-229.	0.2	49
71	Eradication of Acute Myeloid Leukemia with FLT3 Ligandâ€"Targeted miR-150 Nanoparticles. Cancer Research, 2016, 76, 4470-4480.	0.4	48
72	Hypoxiaâ€inducible factorâ€2Î± directly promotes <i><scp>BCRP</scp></i> expression and mediates the resistance of ovarian cancer stem cells to adriamycin. Molecular Oncology, 2019, 13, 403-421.	2.1	47

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73	PBX3 and MEIS1 Cooperate in Hematopoietic Cells to Drive Acute Myeloid Leukemias Characterized by a Core Transcriptome of the <i>MLL</i>-Rearranged Disease. Cancer Research, 2016, 76, 619-629.	0.4	45
74	Targeted inhibition of STAT/TET1 axis as a therapeutic strategy for acute myeloid leukemia. Nature Communications, 2017, 8, 2099.	5.8	45
75	Homoharringtonine exhibits potent anti-tumor effect and modulates DNA epigenome in acute myeloid leukemia by targeting SP1/TET1/5hmC. Haematologica, 2020, 105, 148-160.	1.7	41
76	Evidence for variation in abundance of antisense transcripts between multicellular animals but no relationship between antisense transcriptionand organismic complexity. Genome Research, 2006, 16, 922-933.	2.4	40
77	Molecular portraits of B cell lineage commitment. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 10014-10019.	3.3	39
78	<i>MIR29B</i> regulates expression of <i>MLLT11 (AF1Q),</i> an <i>MLL</i> fusion partner, and low <i>MIR29B expression</i> associates with adverse cytogenetics and poor overall survival in AML. British Journal of Haematology, 2011, 153, 753-757.	1.2	38
79	Signalling input from divergent pathways subverts BÂcell transformation. Nature, 2020, 583, 845-851.	13.7	37
80	Analysis of translocations that involve theNUP98 gene in patients with 11p15 chromosomal rearrangements. Genes Chromosomes and Cancer, 2004, 41, 339-352.	1.5	36
81	YTHDF1 promotes mRNA degradation via YTHDF1â€AGO2 interaction and phase separation. Cell Proliferation, 2022, 55, e13157.	2.4	36
82	RNA N 6-Methyladenosine Modification in Normal and Malignant Hematopoiesis. Advances in Experimental Medicine and Biology, 2019, 1143, 75-93.	0.8	35
83	Duplexes of 21-nucleotide RNAs mediate RNA interference in differentiated mouse ES cells. Biology of the Cell, 2003, 95, 365-371.	0.7	33
84	Gene expression profiles in acute myeloid leukemia with common translocations using SAGE. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 1030-1035.	3.3	32
85	PRDX4, a member of the peroxiredoxin family, is fused toAML1 (RUNX1) in an acute myeloid leukemia patient with a t(X;21)(p22;q22). Genes Chromosomes and Cancer, 2004, 40, 365-370.	1.5	31
86	Targeting PRMT1-mediated FLT3 methylation disrupts maintenance of MLL-rearranged acute lymphoblastic leukemia. Blood, 2019, 134, 1257-1268.	0.6	30
87	Frequency and spectrum of disease-causing variants in 1892 patients with suspected genetic HLH disorders. Blood Advances, 2020, 4, 2578-2594.	2.5	29
88	Sensitizing leukemia stem cells to NF-Î°B inhibitor treatment <i>in vivo</i> by inactivation of both TNF and IL-1 signaling. Oncotarget, 2017, 8, 8420-8435.	0.8	29
89	RNA-binding proteins in regulating mRNA stability and translation: roles and mechanisms in cancer. Seminars in Cancer Biology, 2022, 86, 664-677.	4.3	29
90	Correct Identification of Genes from Serial Analysis of Gene Expression Tag Sequences. Genomics, 2002, 79, 598-602.	1.3	28

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91	Characterization of genomic breakpoints inMLL andCBP in leukemia patients with t(11;16). Genes Chromosomes and Cancer, 2004, 41, 257-265.	1.5	26
92	ALOX5 exhibits anti-tumor and drug-sensitizing effects in MLL-rearranged leukemia. Scientific Reports, 2017, 7, 1853.	1.6	26
93	Identification of MLL-fusion/MYCâŠ£miR-26âŠ£TET1 signaling circuit in MLL-rearranged leukemia. Cancer Letters, 2016, 372, 157-165.	3.2	25
94	RNA modifications in hematopoietic malignancies: a new research frontier. Blood, 2021, 138, 637-648.	0.6	24
95	Transcriptional regulation of N6-methyladenosine orchestrates sex-dimorphic metabolic traits. Nature Metabolism, 2021, 3, 940-953.	5.1	24
96	High-resolution characterization of gene function using single-cell CRISPR tiling screen. Nature Communications, 2021, 12, 4063.	5.8	23
97	DNA N6-methyldeoxyadenosine in mammals and human disease. Trends in Genetics, 2022, 38, 454-467.	2.9	23
98	In Vitro Functional Study of miR-126 in Leukemia. Methods in Molecular Biology, 2011, 676, 185-195.	0.4	22
99	RNA N6-methyladenosine modification in solid tumors: new therapeutic frontiers. Cancer Gene Therapy, 2020, 27, 625-633.	2.2	22
100	TRAIL pathway is associated with inhibition of colon cancer by protopanaxadiol. Journal of Pharmacological Sciences, 2015, 127, 83-91.	1.1	20
101	The Small Introns of Antisense Genes Are Better Explained by Selection for Rapid Transcription Than by â€œGenomic Designâ€ Genetics, 2005, 171, 2151-2155.	1.2	17
102	Rationale for targeting BCL6 in <i>MLL</i>-rearranged acute lymphoblastic leukemia. Genes and Development, 2019, 33, 1265-1279.	2.7	17
103	Crosstalk Between DNA and Histones: Tetâ€™s New Role in Embryonic Stem Cells. Current Genomics, 2012, 13, 603-608.	0.7	14
104	Generation of longer 3' cDNA fragments from massively parallel signature sequencing tags. Nucleic Acids Research, 2004, 32, e94-e94.	6.5	12
105	Cytoplasmic FANCA-FANCC Complex Interacts and Stabilizes the Cytoplasm-dislocalized Leukemic Nucleophosmin Protein (NPMc). Journal of Biological Chemistry, 2010, 285, 37436-37444.	1.6	12
106	Two isoforms of HOXA9 function differently but work synergistically in human MLL-rearranged leukemia. Blood Cells, Molecules, and Diseases, 2012, 49, 102-106.	0.6	11
107	Systematic computation with functional gene-sets among leukemic and hematopoietic stem cells reveals a favorable prognostic signature for acute myeloid leukemia. BMC Bioinformatics, 2015, 16, 97.	1.2	11
108	miR-550-1 functions as a tumor suppressor in acute myeloid leukemia via the hippo signaling pathway. International Journal of Biological Sciences, 2020, 16, 2853-2867.	2.6	11

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109	Cytoplasmic DROSHA and non-canonical mechanisms of MiR-155 biogenesis in FLT3-ITD acute myeloid leukemia. Leukemia, 2021, 35, 2285-2298.	3.3	10
110	Lysine acetylation restricts mutant IDH2 activity to optimize transformation in AML cells. Molecular Cell, 2021, 81, 3833-3847.e11.	4.5	10
111	The Pattern of Gene Expression in Mouse Gr-1+ Myeloid Progenitor Cells. Genomics, 2001, 77, 149-162.	1.3	9
112	Breast Cancer Riskâ€“Associated SNPs in the <i>mTOR</i> Promoter Form <i>De Novo</i> KLF5- and ZEB1-Binding Sites that Influence the Cellular Response to Paclitaxel. Molecular Cancer Research, 2019, 17, 2244-2256.	1.5	8
113	Glycoproteome remodeling in MLL-rearranged B-cell precursor acute lymphoblastic leukemia. Theranostics, 2021, 11, 9519-9537.	4.6	8
114	Construction of novel tumor necrosis factor-alpha mutants with reduced toxicity and higher cytotoxicity on human tumor cells. Science in China Series C: Life Sciences, 2003, 46, 1-9.	1.3	6
115	Opioid receptor signaling suppresses leukemia through both catalytic and non-catalytic functions of TET2. Cell Reports, 2022, 38, 110253.	2.9	6
116	Effective Novel Fto Inhibitors Show Potent Anti-Cancer Efficacy and Suppress Drug Resistance. Blood, 2019, 134, 233-233.	0.6	5
117	Recent Patents on the Identification and Clinical Application of microRNAs and Target Genes. Recent Patents on DNA & Gene Sequences, 2007, 1, 116-24.	0.7	4
118	Targeting differentiation blockade in AML: New hope from cell-surface-based CRISPR screens. Cell Stem Cell, 2021, 28, 585-587.	5.2	4
119	Targeting FTO for cancer therapy and more. Aging, 2021, 13, 19080-19082.	1.4	4
120	Ten-eleven translocation protein 1 modulates medulloblastoma progression. Genome Biology, 2021, 22, 125.	3.8	3
121	miR-150: targeting MLL leukemia. Oncotarget, 2012, 3, 1268-1269.	0.8	3
122	Co-culture Systems of Drug-Treated Acute Myeloid Leukemia Cells and T Cells for In Vitro and In Vivo Study. STAR Protocols, 2020, 1, 100097.	0.5	2
123	Evaluation of glycolytic rates in human hematopoietic stem/progenitor cells after target gene depletion. STAR Protocols, 2021, 2, 100603.	0.5	1
124	The N6-Adenine Methyltransferase METTL14 Plays an Oncogenic Role in Acute Myeloid Leukemia. Blood, 2016, 128, 1536-1536.	0.6	1
125	Blockade of Mir-150 Maturation by MLL-Fusion/MYC/Lin-28 Is Required for MLL-Associated Leukemia. Blood, 2012, 120, 3499-3499.	0.6	1
126	Overexpression and Knockout of Mir-126 Both Promote Leukemogenesis through Targeting Distinct Gene Signaling. Blood, 2015, 126, 3667-3667.	0.6	1

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127	Targeted Inhibition of STAT/TET1 Axis As a Potent Therapeutic Strategy for Acute Myeloid Leukemia. Blood, 2017, 130, 857-857.	0.6	1
128	Ifitm3 Is Essential for PI(3,4,5)P3-Dependent B-Cell Activation and Leukemogenesis. Blood, 2019, 134, 2782-2782.	0.6	1
129	RNA Modification in Cancer. FASEB Journal, 2021, 35, .	0.2	0
130	Gene Expression Profiles in Acute Myeloid Leukemia (AML): From Diagnosis to Prognosis.. Blood, 2005, 106, 2996-2996.	0.6	0
131	Identification of Genes Abnormally Expressed in Human MLL-AF4 Leukemia.. Blood, 2006, 108, 4314-4314.	0.6	0
132	Identification of Genes Abnormally Expressed in Both Human and Murine MLL-ELL and/or MLL-ENL Leukemia.. Blood, 2006, 108, 2249-2249.	0.6	0
133	MicroRNA Expression Profiles in Acute Myeloid Leukemia with Common Translocations.. Blood, 2007, 110, 3181-3181.	0.6	0
134	Repression of Mir-495, a Microrna Associated with Favorable Outcome of Acute Myeloid Leukemia Patients, Is Required for the MLL-Associated Leukemogenesis,. Blood, 2011, 118, 3462-3462.	0.6	0
135	Activation of a Mir-181-Targeting HOXA-PBX3 Homeobox Gene Signature Is Associated with Adverse Prognosis of Cytogenetically Abnormal Acute Myeloid Leukemia. Blood, 2011, 118, 236-236.	0.6	0
136	The HOXA/PBX3 Pathway Is an Attractive Therapeutic Target in MLL-Rearranged Acute Leukemia. Blood, 2012, 120, 3522-3522.	0.6	0
137	MLL-Associated Leukemias Drive Expression of MiR-9, Required for Tumorigenesis. Blood, 2012, 120, 525-525.	0.6	0
138	AML Cells Utilize TNF-Driven JNK Signaling As a Critical NF-Î°B-Independent Survival Signal. Blood, 2013, 122, 2890-2890.	0.6	0
139	MLL-Rearranged Acute Myeloid Leukemias Drive Expression Of Mir-9, a Critical Oncogene In Leukemogenesis. Blood, 2013, 122, 3740-3740.	0.6	0
140	Alox5 Functions As Both Tumor Suppressor and Drug Sensitizer in AML. Blood, 2016, 128, 2851-2851.	0.6	0
141	Downregulation of Mir-142 Promotes Leukemia Growth in Philadelphia Chromosome-Positive (Ph+) Acute Lymphoblastic Leukemia (ALL): A Possible Novel Therapeutic Target?. Blood, 2018, 132, 1338-1338.	0.6	0
142	ALKBH5 Functions As an Oncogene in Acute Myeloid Leukemia. Blood, 2018, 132, 3910-3910.	0.6	0
143	TET1 Modulates DNA Replication in Leukemia Cells Via a Catalytic-Independent Mechanism through Cooperating with KAT8. Blood, 2019, 134, 1249-1249.	0.6	0
144	Identification of ZNF217 As an Essential Oncogenic Gene in B-Cell Acute Lymphoblastic Leukemia By CRISPR/Cas9-Based Library Screening. Blood, 2019, 134, 1465-1465.	0.6	0

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145	METTL3 Dysregulates RNA Splicing by Translational Control of Splicing Factors via m 6A Modification in CLL. Blood, 2021, 138, 499-499.	0.6	0
146	Integrative Transcriptome and Quantitative Proteome Analyses Identify METTL3 As a Key Regulator for Aberrant RNA Processing in Chronic Lymphocytic Leukemia. Blood, 2020, 136, 12-12.	0.6	0
147	Epitranscriptomics in myeloid malignancies. Blood Science, 0, Publish Ahead of Print, .	0.4	0