

# The reference epigenome and regulatory chromatin landscape in acute leukemia

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Enhancer Architecture and Essential Core Regulatory Circuitry of Chronic Lymphocytic Leukemia. <i>Cancer Cell</i> , 2018, 34, 982-995.e7.	7.7	101
2	Insight into origins, mechanisms, and utility of DNA methylation in B-cell malignancies. <i>Blood</i> , 2018, 132, 999-1006.	0.6	24
3	Insight into genetic predisposition to chronic lymphocytic leukemia from integrative epigenomics. <i>Nature Communications</i> , 2019, 10, 3615.	5.8	32
4	Nuclear factor of activated T-cells, NFATC1, governs FLT3ITD-driven hematopoietic stem cell transformation and a poor prognosis in AML. <i>Journal of Hematology and Oncology</i> , 2019, 12, 72.	6.9	12
5	Chronic lymphocytic leukaemia: from genetics to treatment. <i>Nature Reviews Clinical Oncology</i> , 2019, 16, 684-701.	12.5	154
6	Clonal Evolution in Chronic Lymphocytic Leukemia. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, S16-S19.	0.2	0
7	IL-10-producing regulatory B cells and plasmacytes: Molecular mechanisms and disease relevance. <i>Seminars in Immunology</i> , 2019, 44, 101323.	2.7	39
8	The Mithralog EC-7072 Induces Chronic Lymphocytic Leukemia Cell Death by Targeting Tonic B-Cell Receptor Signaling. <i>Frontiers in Immunology</i> , 2019, 10, 2455.	2.2	4
9	The Open Chromatin Landscape of Non-Small Cell Lung Carcinoma. <i>Cancer Research</i> , 2019, 79, 4840-4854.	0.4	24
10	Linking aberrant chromatin features in chronic lymphocytic leukemia to transcription factor networks. <i>Molecular Systems Biology</i> , 2019, 15, e8339.	3.2	39
11	Epigenetic evolution and lineage histories of chronic lymphocytic leukaemia. <i>Nature</i> , 2019, 569, 576-580.	13.7	195
12	Ibrutinib induces chromatin reorganisation of chronic lymphocytic leukaemia cells. <i>Oncogenesis</i> , 2019, 8, 32.	2.1	10
13	Corrupted coordination of epigenetic modifications leads to diverging chromatin states and transcriptional heterogeneity in CLL. <i>Nature Communications</i> , 2019, 10, 1874.	5.8	63
14	Dissecting CLL through high-dimensional single-cell technologies. <i>Blood</i> , 2019, 133, 1446-1456.	0.6	5
15	Clinical significance of DNA methylation in chronic lymphocytic leukemia patients: results from 3 UK clinical trials. <i>Blood Advances</i> , 2019, 3, 2474-2481.	2.5	25
16	Clonal dynamics in chronic lymphocytic leukemia. <i>Blood Advances</i> , 2019, 3, 3759-3769.	2.5	23
17	Advances in Epigenetics and Epigenomics in Chronic Lymphocytic Leukemia. <i>Current Genetic Medicine Reports</i> , 2019, 7, 214-226.	1.9	5
18	DNA methylation profiles in chronic lymphocytic leukemia patients treated with chemoimmunotherapy. <i>Clinical Epigenetics</i> , 2019, 11, 177.	1.8	15

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19	CCND2 and CCND3 hijack immunoglobulin light-chain enhancers in cyclin D1 <sup>hi</sup> mantle cell lymphoma. <i>Blood</i> , 2019, 133, 940-951.	0.6	77
20	Epigenetic dynamics in normal and malignant B cells: die a hero or live to become a villain. <i>Current Opinion in Immunology</i> , 2019, 57, 15-22.	2.4	4
21	Foundations and Application of Precision Medicine. , 2019, , 21-45.		0
22	Dynamic changes in intron retention are tightly associated with regulation of splicing factors and proliferative activity during B-cell development. <i>Nucleic Acids Research</i> , 2020, 48, 1327-1340.	6.5	49
23	Evolution of the Epigenetic Landscape in Childhood B Acute Lymphoblastic Leukemia and Its Role in Drug Resistance. <i>Cancer Research</i> , 2020, 80, 5189-5202.	0.4	9
24	SOHO State of the Art Updates and Next Questions: Clonal Evolution in Chronic Lymphocytic Leukemia. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2020, 20, 779-784.	0.2	4
25	Determinants and role of chromatin organization in acute leukemia. <i>Leukemia</i> , 2020, 34, 2561-2575.	3.3	16
26	Educational Updates in Hematology Book: 25th Congress of the European Hematology Association, Virtual Edition 2020. <i>HemaSphere</i> , 2020, 4, .	1.2	2
27	Chromatin network markers of leukemia. <i>Bioinformatics</i> , 2020, 36, i455-i463.	1.8	8
28	Molecular tumor classification using DNA methylome analysis. <i>Human Molecular Genetics</i> , 2020, 29, R205-R213.	1.4	10
29	Chromatin accessibility landscape of pediatric T <sup>h</sup> 1 lymphoblastic leukemia and human T <sup>h</sup> 1 cell precursors. <i>EMBO Molecular Medicine</i> , 2020, 12, e12104.	3.3	13
30	Advances in whole genome methylomic sequencing. , 2020, , 213-233.		2
31	The proliferative history shapes the DNA methylome of B-cell tumors and predicts clinical outcome. <i>Nature Cancer</i> , 2020, 1, 1066-1081.	5.7	51
32	VRK1 Phosphorylates Tip60/KAT5 and Is Required for H4K16 Acetylation in Response to DNA Damage. <i>Cancers</i> , 2020, 12, 2986.	1.7	17
33	Assessing prognosis of chronic lymphocytic leukemia using biomarkers and genetics. <i>Expert Opinion on Orphan Drugs</i> , 2020, 8, 329-342.	0.5	2
34	Chromatin activation as a unifying principle underlying pathogenic mechanisms in multiple myeloma. <i>Genome Research</i> , 2020, 30, 1217-1227.	2.4	35
35	DNA methylation of chronic lymphocytic leukemia with differential response to chemotherapy. <i>Scientific Data</i> , 2020, 7, 133.	2.4	6
36	Chronic lymphocytic leukemias with trisomy 12 show a distinct DNA methylation profile linked to altered chromatin activation. <i>Haematologica</i> , 2020, 105, 2864-2867.	1.7	11

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37	Genomic deregulation of PRMT5 supports growth and stress tolerance in chronic lymphocytic leukemia. <i>Scientific Reports</i> , 2020, 10, 9775.	1.6	5
38	Using GARDEN-NET and ChAseR to explore human haematopoietic 3D chromatin interaction networks. <i>Nucleic Acids Research</i> , 2020, 48, 4066-4080.	6.5	18
39	Tumor Suppressors in Chronic Lymphocytic Leukemia: From Lost Partners to Active Targets. <i>Cancers</i> , 2020, 12, 629.	1.7	6
40	Precision Medicine Management of Chronic Lymphocytic Leukemia. <i>Cancers</i> , 2020, 12, 642.	1.7	28
41	IgCaller for reconstructing immunoglobulin gene rearrangements and oncogenic translocations from whole-genome sequencing in lymphoid neoplasms. <i>Nature Communications</i> , 2020, 11, 3390.	5.8	24
42	Chronic lymphocytic leukemia: from molecular pathogenesis to novel therapeutic strategies. <i>Haematologica</i> , 2020, 105, 2205-2217.	1.7	47
43	A lncRNA-SWI/SNF complex crosstalk controls transcriptional activation at specific promoter regions. <i>Nature Communications</i> , 2020, 11, 936.	5.8	69
44	Altered chromatin landscape and enhancer engagement underlie transcriptional dysregulation in MED12 mutant uterine leiomyomas. <i>Nature Communications</i> , 2020, 11, 1019.	5.8	34
45	Genomic and Epigenomic Alterations in Chronic Lymphocytic Leukemia. <i>Annual Review of Pathology: Mechanisms of Disease</i> , 2020, 15, 149-177.	9.6	17
46	Sexual-dimorphism in human immune system aging. <i>Nature Communications</i> , 2020, 11, 751.	5.8	316
47	Molecular networks in Network Medicine: Development and applications. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2020, 12, e1489.	6.6	128
48	CLL intraclonal fractions exhibit established and recently acquired patterns of DNA methylation. <i>Blood Advances</i> , 2020, 4, 893-905.	2.5	5
49	Genomic and transcriptomic correlates of Richter transformation in chronic lymphocytic leukemia. <i>Blood</i> , 2021, 137, 2800-2816.	0.6	51
50	Preneoplastic Alterations Define CLL DNA Methylome and Persist through Disease Progression and Therapy. <i>Blood Cancer Discovery</i> , 2021, 2, 54-69.	2.6	16
51	Integrating genetic and non-genetic determinants of cancer evolution by single-cell multi-omics. <i>Nature Reviews Genetics</i> , 2021, 22, 3-18.	7.7	228
52	shinyPICo: a graphical pipeline to analyze Illumina DNA methylation arrays. <i>Bioinformatics</i> , 2021, 37, 257-259.	1.8	19
53	Dynamics of genome architecture and chromatin function during human B cell differentiation and neoplastic transformation. <i>Nature Communications</i> , 2021, 12, 651.	5.8	67
54	Genomic Instability and Clonal Evolution in Chronic Lymphocytic Leukemia: Clinical Relevance. <i>Journal of the National Comprehensive Cancer Network: JNCCN</i> , 2021, 19, 227-233.	2.3	2

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55	Characterization of complete lncRNAs transcriptome reveals the functional and clinical impact of lncRNAs in multiple myeloma. <i>Leukemia</i> , 2021, 35, 1438-1450.	3.3	28
56	lncRNAs activate longevity regulation pathway due to aging of Leydig cells caused by DEHP exposure: A transcriptome-based study. <i>Ecotoxicology and Environmental Safety</i> , 2021, 209, 111798.	2.9	8
57	FoxO1-GAB1 axis regulates homing capacity and tonic AKT activity in chronic lymphocytic leukemia. <i>Blood</i> , 2021, 138, 758-772.	0.6	19
58	EOMES is essential for antitumor activity of CD8+ T cells in chronic lymphocytic leukemia. <i>Leukemia</i> , 2021, 35, 3152-3162.	3.3	26
59	Human pluripotent stem cells identify molecular targets of trisomy 12 in chronic lymphocytic leukemia patients. <i>Cell Reports</i> , 2021, 34, 108845.	2.9	3
61	Clonal evolution in chronic lymphocytic leukemia is scant in relapsed but accelerated in refractory cases after chemo(immune) therapy. <i>Haematologica</i> , 2022, 107, 604-614.	1.7	11
62	The Role of lncRNAs in the Pathobiology and Clinical Behavior of Multiple Myeloma. <i>Cancers</i> , 2021, 13, 1976.	1.7	9
63	Role of NFAT in Chronic Lymphocytic Leukemia and Other B-Cell Malignancies. <i>Frontiers in Oncology</i> , 2021, 11, 651057.	1.3	5
65	Gene expression derived from alternative promoters improves prognostic stratification in multiple myeloma. <i>Leukemia</i> , 2021, 35, 3012-3016.	3.3	11
66	The Evolving Landscape of Chronic Lymphocytic Leukemia on Diagnosis, Prognosis and Treatment. <i>Diagnostics</i> , 2021, 11, 853.	1.3	15
67	Transcriptome Analysis Reveals the Profile of Long Non-coding RNAs During Chicken Muscle Development. <i>Frontiers in Physiology</i> , 2021, 12, 660370.	1.3	3
68	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. <i>Leukemia</i> , 2021, 35, 2002-2016.	3.3	34
69	Challenges with Approved Targeted Therapies against Recurrent Mutations in CLL: A Place for New Actionable Targets. <i>Cancers</i> , 2021, 13, 3150.	1.7	1
70	Antioxidant stress and anticancer activity of peptide-chelated selenium <i>in vitro</i> . <i>International Journal of Molecular Medicine</i> , 2021, 48, .	1.8	8
71	Exploring the pathways to chronic lymphocytic leukemia. <i>Blood</i> , 2021, 138, 827-835.	0.6	20
73	Leveraging three-dimensional chromatin architecture for effective reconstruction of enhancer-target gene regulatory interactions. <i>Nucleic Acids Research</i> , 2021, 49, e97-e97.	6.5	6
74	Genetics of Chronic Lymphocytic Leukemia. <i>Cancer Journal (Sudbury, Mass )</i> , 2021, 27, 259-265.	1.0	1
75	The Biology of Chronic Lymphocytic Leukemia. <i>Cancer Journal (Sudbury, Mass )</i> , 2021, 27, 266-274.	1.0	3

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76	The DNA methylation landscape of multiple myeloma shows extensive inter- and inpatient heterogeneity that fuels transcriptomic variability. <i>Genome Medicine</i> , 2021, 13, 127.	3.6	9
77	CRIS: complete reconstruction of immunoglobulin <i>V-D-J</i> sequences from RNA-seq data. <i>Bioinformatics Advances</i> , 2021, 1, vbab021.	0.9	4
78	Chromatin-based, in cis and in trans regulatory rewiring underpins distinct oncogenic transcriptomes in multiple myeloma. <i>Nature Communications</i> , 2021, 12, 5450.	5.8	19
79	Loss of synergistic transcriptional feedback loops drives diverse B-cell cancers. <i>EBioMedicine</i> , 2021, 71, 103559.	2.7	1
80	Biomimetic Ti6Al4V alloy/gelatin methacrylate hybrid scaffold with enhanced osteogenic and angiogenic capabilities for large bone defect restoration. <i>Bioactive Materials</i> , 2021, 6, 3437-3448.	8.6	43
81	Chromatin accessibility profiling methods. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	95
82	Novel genes exhibiting DNA methylation alterations in Korean patients with chronic lymphocytic leukaemia: a methyl-CpG-binding domain sequencing study. <i>Scientific Reports</i> , 2020, 10, 1085.	1.6	3
83	Ribosomal RNA 2'-O-methylation as a novel layer of inter-tumour heterogeneity in breast cancer. <i>NAR Cancer</i> , 2020, 2, zcaa036.	1.6	40
87	Pathogenesis of chronic lymphocytic leukemia and the development of novel therapeutic strategies. <i>Journal of Clinical and Experimental Hematopathology: JCEH</i> , 2020, 60, 146-158.	0.3	20
88	Robust Glycogene-Based Prognostic Signature for Proficient Mismatch Repair Colorectal Adenocarcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 727752.	1.3	2
89	Chronic lymphocytic leukemia: 2022 update on diagnostic and therapeutic procedures. <i>American Journal of Hematology</i> , 2021, 96, 1679-1705.	2.0	150
93	Clonal dynamics in chronic lymphocytic leukemia. <i>Hematology American Society of Hematology Education Program</i> , 2019, 2019, 466-475.	0.9	0
97	Epigenetic Trajectories of the Premalignant-to-Malignant Transition of Chronic Lymphocytic Leukemia. <i>Blood Cancer Discovery</i> , 2021, 2, 6-8.	2.6	0
98	Rare t(X;14)(q28;q32) translocation reveals link between MTCP1 and chronic lymphocytic leukemia. <i>Nature Communications</i> , 2021, 12, 6338.	5.8	3
99	Towards precision medicine in lymphoid malignancies. <i>Journal of Internal Medicine</i> , 2022, 292, 221-242.	2.7	9
100	InterTADs: integration of multi-omics data on topologically associated domains, application to chronic lymphocytic leukemia. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqab121.	1.5	2
101	Super enhancers as master gene regulators in the pathogenesis of hematologic malignancies. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2022, 1877, 188697.	3.3	8
102	Dissecting TET2 Regulatory Networks in Blood Differentiation and Cancer. <i>Cancers</i> , 2022, 14, 830.	1.7	9

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103	Transcriptome Analysis Reveals the Gene Expression Changes in the Silkworm ( <i>Bombyx mori</i> ) in Response to Hydrogen Sulfide Exposure. <i>Insects</i> , 2021, 12, 1110.	1.0	11
104	Targets Exploration of Hydroxychloroquine for Pigmentation and Cell Protection Effect in Melanocytes: The Clue for Vitiligo Treatment. <i>Drug Design, Development and Therapy</i> , 2022, Volume 16, 1011-1024.	2.0	2
105	Lift the curtain on long non-coding RNAs in hematological malignancies: Pathogenic elements and potential targets. <i>Cancer Letters</i> , 2022, 536, 215645.	3.2	7
106	Clonal Evolution of High-Risk Chronic Lymphocytic Leukemia: A Contemporary Perspective. <i>Frontiers in Oncology</i> , 2021, 11, 790004.	1.3	11
107	Understanding CLL biology through mouse models of human genetics. <i>Blood</i> , 2021, 138, 2621-2631.	0.6	11
110	A leukemia-protective germline variant mediates chromatin module formation via transcription factor nucleation. <i>Nature Communications</i> , 2022, 13, 2042.	5.8	6
114	The International Consensus Classification of Mature Lymphoid Neoplasms: a report from the Clinical Advisory Committee. <i>Blood</i> , 2022, 140, 1229-1253.	0.6	512
116	B cell receptor signaling drives APOBEC3 expression via direct enhancer regulation in chronic lymphocytic leukemia B cells. <i>Blood Cancer Journal</i> , 2022, 12, .	2.8	2
117	Genomic profiling for clinical decision making in lymphoid neoplasms. <i>Blood</i> , 2022, 140, 2193-2227.	0.6	63
118	Drug microenvironment perturbations reveal resistance mechanisms and prognostic subgroups in <scp>CLL</scp>. <i>Molecular Systems Biology</i> , 2022, 18, .	3.2	8
119	Detection of early seeding of Richter transformation in chronic lymphocytic leukemia. <i>Nature Medicine</i> , 2022, 28, 1662-1671.	15.2	53
120	Integrative epigenomics in chronic lymphocytic leukaemia: Biological insights and clinical applications. <i>British Journal of Haematology</i> , 2023, 200, 280-290.	1.2	4
121	Genome-wide Analyses of Histone Modifications in the Mammalian Genome. , 2023, , 137-161.		1
122	The end of the beginning: application of single-cell sequencing to chronic lymphocytic leukemia. <i>Blood</i> , 2023, 141, 369-379.	0.6	4
123	Characterization of differentially expressed and lipid metabolism-related lncRNA-mRNA interaction networks during the growth of liver tissue through rabbit models. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	0
124	Molecular map of chronic lymphocytic leukemia and its impact on outcome. <i>Nature Genetics</i> , 2022, 54, 1664-1674.	9.4	52
125	scTAM-seq enables targeted high-confidence analysis of DNA methylation in single cells. <i>Genome Biology</i> , 2022, 23, .	3.8	7
126	Viral transduction of primary human lymphoma B cells reveals mechanisms of NOTCH-mediated immune escape. <i>Nature Communications</i> , 2022, 13, .	5.8	8

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127	Expression of long noncoding RNAs in the ovarian granulosa cells of women with diminished ovarian reserve using high-throughput sequencing. <i>Journal of Ovarian Research</i> , 2022, 15, .	1.3	6
128	CD160 receptor in CLL: Current state and future avenues. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	4
129	Whole-genome sequencing of chronic lymphocytic leukemia identifies subgroups with distinct biological and clinical features. <i>Nature Genetics</i> , 2022, 54, 1675-1689.	9.4	21
131	Genetics and epigenetics of CLL. <i>Leukemia and Lymphoma</i> , 2023, 64, 551-563.	0.6	1
132	Tumorigenic role of Musashi-2 in aggressive mantle cell lymphoma. <i>Leukemia</i> , 0, , .	3.3	1
133	Genome-wide DNA methylation profiling in chronic lymphocytic leukaemia. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
135	The immunomodulatory molecule TIGIT is expressed by chronic lymphocytic leukemia cells and contributes to anergy. <i>Haematologica</i> , 2023, 108, 2101-2115.	1.7	4
136	Molecular characterization of Richter syndrome identifies de novo diffuse large B-cell lymphomas with poor prognosis. <i>Nature Communications</i> , 2023, 14, .	5.8	13
137	Chronic Lymphocytic Leukemia: Current Knowledge and Future Advances in Cytogenomic Testing. , 0, , 93-106.		0
138	Identification of two unannotated miRNAs in classic Hodgkin lymphoma cell lines. <i>PLoS ONE</i> , 2023, 18, e0283186.	1.1	0
148	Recurrent DNMT3B rearrangements are associated with unfavorable outcome in dicentric (9;20)-positive pediatric BCP-ALL. <i>Leukemia</i> , 0, , .	3.3	0
152	Clinical Studies and Epi-Drugs in Various Cancer Types. <i>Epigenetics and Human Health</i> , 2023, , 165-212.	0.2	0