Lili

List of Publications by Year
in descending order

27 papers	256 citations	1040056 9 h-index	996975 15 g-index
27 all docs	27 docs citations	27 times ranked	333 citing authors

#	Article	IF	Citations
1	A Murine Model of Chronic Lymphocytic Leukemia Based on B Cell-Restricted Expression of Sf3b1 Mutation and Atm Deletion. Cancer Cell, 2019, 35, 283-296.e5.	16.8	71
2	Genomic and transcriptomic profiling reveals distinct molecular subsets associated with outcomes in mantle cell lymphoma. Journal of Clinical Investigation, 2022, 132, .	8.2	30
3	A hotspot mutation in transcription factor IKZF3 drives B cell neoplasia via transcriptional dysregulation. Cancer Cell, 2021, 39, 380-393.e8.	16.8	27
4	High-dimension single-cell analysis applied to cancer. Molecular Aspects of Medicine, 2018, 59, 70-84.	6.4	19
5	Developmental partitioning of SYK and ZAP70 prevents autoimmunity and cancer. Molecular Cell, 2021, 81, 2094-2111.e9.	9.7	17
6	Preneoplastic Alterations Define CLL DNA Methylome and Persist through Disease Progression and Therapy. Blood Cancer Discovery, 2021, 2, 54-69.	5.0	16
7	High incidence of MYD88 and KMT2D mutations in Chinese with chronic lymphocytic leukemia. Leukemia, 2021, 35, 2412-2415.	7.2	15
8	Genomic profiling identifies distinct genetic subtypes in extra-nodal natural killer/T-cell lymphoma. Leukemia, 2022, 36, 2064-2075.	7.2	15
9	Coactivation of NF-ÎºB and Notch signaling is sufficient to induce B-cell transformation and enables B-myeloid conversion. Blood, 2020, 135, 108-120.	1.4	14
10	Activation of <i>Notch</i> and <i>Myc</i> Signaling via B-cellâ€"Restricted Depletion of <i>Dnmt3a</i> Generates a Consistent Murine Model of Chronic Lymphocytic Leukemia. Cancer Research, 2021, 81, 6117-6130.	0.9	10
11	98% IGHV gene identity is the optimal cutoff to dichotomize the prognosis of Chinese patients with chronic lymphocytic leukemia. Cancer Medicine, 2020, 9, 999-1007.	2.8	8
12	<i>RPS15</i> and <i>TP53</i> Co-Mutation Drives B Cell Malignancy through Altered Translation and MYC Activation in a Murine Model. Blood, 2020, 136, 28-29.	1.4	4
13	A Phase I Trial of PI3KÎ±Î´ Inhibitor Copanlisib in Combination with Nivolumab in Patients with Richter's Transformation (RT) or Transformed Non-Hodgkin Lymphoma (tNHL). Blood, 2021, 138, 3558-3558.	1.4	3
14	Genomic and Transcriptomic Profiling Reveals Distinct Subsets Associated with Outcomes in Mantle Cell Lymphoma. Blood, 2020, 136, 28-29.	1.4	2
15	Portending death in germinal centers â€" when B cells know their time is up. Cell Research, 2018, 28, 5-6.	12.0	1
16	CLL dedifferentiation to clonally related myeloid cells. Blood Advances, 2020, 4, 6169-6174.	5.2	1
17	MGA deletion Leads to Richter's Transformation Via NME1. Blood, 2021, 138, 252-252.	1.4	1
18	Expression of Sf3b1-K700E accelerates the Development of Chronic Lymphocytic Leukemia in a Del(13q) Murine Model. Blood, 2020, 136, 4-5.	1.4	1

#	Article	IF	Citations
19	Multiplexed CRISPR *In Vivo* Editing of CLL Loss-of-Function Lesions Models Transformation of Chronic Lymphocytic Leukemia into Richter's Syndrome. Blood, 2020, 136, 2-3.	1.4	1
20	KZF-L162R Mutation Affects Splenic Mature B Cell Development and Alters Expression of Aiolos Target Genes. Blood, 2018, 132, 668-668.	1.4	0
21	Richter's Transformation after CD-19 Directed CAR-T Cells for Relapsed/Refractory Chronic Lymphocytic Leukemia (CLL). Blood, 2021, 138, 1430-1430.	1.4	0
22	METTL3 Dysregulates RNA Splicing by Translational Control of Splicing Factors via m 6A Modification in CLL. Blood, 2021, 138, 499-499.	1.4	0
23	B Cell-Restricted Depletion of Dnmt3a Activates Notch Signaling and Causes Chronic Lymphocytic Leukemia. Blood, 2021, 138, 249-249.	1.4	0
24	Nedd8-Activating Enzyme Inhibition Enhances Anti-Tumor Immunity and PD1 Blockade in *In Vivo* lymphoma Models. Blood, 2021, 138, 2414-2414.	1.4	0
25	R-Loop Associated Mitotic Stress Confers Vulnerabilities in Splicing Factor Mutant Leukemia. Blood, 2021, 138, 3713-3713.	1.4	0
26	Pre-Existing T Cell Subsets Determine Anti-PD1 Blockade Response in Richter's Transformation. Blood, 2020, 136, 42-43.	1.4	0
27	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.	1.4	0