

StÃ©phanie Sungalee

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/303177/publications.pdf>

Version: 2024-02-01

15
papers

1,044
citations

623734

14
h-index

1058476

14
g-index

15
all docs

15
docs citations

15
times ranked

2074
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomics and drug profiling of fatal TCF3-HLF ⁺ positive acute lymphoblastic leukemia identifies recurrent mutation patterns and therapeutic options. <i>Nature Genetics</i> , 2015, 47, 1020-1029.	21.4	190
2	t(14;18) Translocation: A Predictive Blood Biomarker for Follicular Lymphoma. <i>Journal of Clinical Oncology</i> , 2014, 32, 1347-1355.	1.6	115
3	EZH2 oncogenic mutations drive epigenetic, transcriptional, and structural changes within chromatin domains. <i>Nature Genetics</i> , 2019, 51, 517-528.	21.4	102
4	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. <i>Nature Communications</i> , 2019, 10, 1459.	12.8	99
5	Germinal center reentries of BCL2-overexpressing B cells drive follicular lymphoma progression. <i>Journal of Clinical Investigation</i> , 2014, 124, 5337-5351.	8.2	96
6	Early Steps of Follicular Lymphoma Pathogenesis. <i>Advances in Immunology</i> , 2011, 111, 1-46.	2.2	91
7	Cathepsin S Regulates Antigen Processing and T Cell Activity in Non-Hodgkin Lymphoma. <i>Cancer Cell</i> , 2020, 37, 674-689.e12.	16.8	55
8	Genetic and epigenetic inactivation of <i>SESTRIN1</i> controls mTORC1 and response to EZH2 inhibition in follicular lymphoma. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	52
9	The genomic and transcriptional landscape of primary central nervous system lymphoma. <i>Nature Communications</i> , 2022, 13, 2558.	12.8	52
10	Systematic inference and comparison of multi-scale chromatin sub-compartments connects spatial organization to cell phenotypes. <i>Nature Communications</i> , 2021, 12, 2439.	12.8	50
11	Alterations of microRNA and microRNA-regulated messenger RNA expression in germinal center B-cell lymphomas determined by integrative sequencing analysis. <i>Haematologica</i> , 2016, 101, 1380-1389.	3.5	43
12	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. <i>Leukemia</i> , 2021, 35, 2002-2016.	7.2	34
13	Histone acetylation dynamics modulates chromatin conformation and allele-specific interactions at oncogenic loci. <i>Nature Genetics</i> , 2021, 53, 650-662.	21.4	34
14	Extensive molecular mapping of TCR α ⁺ β ⁻ and TCR α ² -involved chromosomal translocations reveals distinct mechanisms of oncogene activation in T-ALL. <i>Blood</i> , 2012, 120, 3298-3309.	1.4	31
15	Determinants of the t(14;18) translocation and their role in t(14;18)-positive follicular lymphoma. <i>Cancer Causes and Control</i> , 2015, 26, 1845-1855.	1.8	0