

Ying Shao

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

2,943
citations

361413

20
h-index

454955

30
g-index

33
all docs

33
docs citations

33
times ranked

5969
citing authors

#	ARTICLE	IF	CITATIONS
1	EP300 Selectively Controls the Enhancer Landscape of <i>MYCN</i> -Amplified Neuroblastoma. <i>Cancer Discovery</i> , 2022, 12, 730-751.	9.4	64
2	SequencErr: measuring and suppressing sequencer errors in next-generation sequencing data. <i>Genome Biology</i> , 2021, 22, 37.	8.8	15
3	Exploration of Coding and Non-coding Variants in Cancer Using GenomePaint. <i>Cancer Cell</i> , 2021, 39, 83-95.e4.	16.8	18
4	Acute depletion of CTCF rewires genome-wide chromatin accessibility. <i>Genome Biology</i> , 2021, 22, 244.	8.8	29
5	The landscape of coding RNA editing events in pediatric cancer. <i>BMC Cancer</i> , 2021, 21, 1233.	2.6	7
6	Discovery of regulatory noncoding variants in individual cancer genomes by using cis-X. <i>Nature Genetics</i> , 2020, 52, 811-818.	21.4	47
7	Mutational Landscape and Patterns of Clonal Evolution in Relapsed Pediatric Acute Lymphoblastic Leukemia. <i>Blood Cancer Discovery</i> , 2020, 1, 96-111.	5.0	93
8	Relapse-Fated Latent Diagnosis Subclones in Acute B Lineage Leukemia Are Drug Tolerant and Possess Distinct Metabolic Programs. <i>Cancer Discovery</i> , 2020, 10, 568-587.	9.4	72
9	Therapy-induced mutations drive the genomic landscape of relapsed acute lymphoblastic leukemia. <i>Blood</i> , 2020, 135, 41-55.	1.4	171
10	Functional interrogation of HOXA9 regulome in MLLr leukemia via reporter-based CRISPR/Cas9 screen. <i>ELife</i> , 2020, 9, .	6.0	25
11	Multi-Omic Based Antigen Discovery for the Immunotherapy of Pediatric Acute T Cell Lymphoblastic Leukemia. <i>Blood</i> , 2020, 136, 17-18.	1.4	1
12	Mutational Landscape and Patterns of Clonal Evolution in Relapsed Pediatric Acute Lymphoblastic Leukemia. <i>Blood Cancer Discovery</i> , 2020, 1, 96-111.	5.0	3
13	Long-read sequencing unveils IGH-DUX4 translocation into the silenced IGH allele in B-cell acute lymphoblastic leukemia. <i>Nature Communications</i> , 2019, 10, 2789.	12.8	14
14	Nucleome Dynamics during Retinal Development. <i>Neuron</i> , 2019, 104, 512-528.e11.	8.1	70
15	Acute depletion of CTCF directly affects MYC regulation through loss of enhancer-promoter looping. <i>Nucleic Acids Research</i> , 2019, 47, 6699-6713.	14.5	98
16	Clinical genome sequencing uncovers potentially targetable truncations and fusions of MAP3K8 in spitzoid and other melanomas. <i>Nature Medicine</i> , 2019, 25, 597-602.	30.7	61
17	Analysis of error profiles in deep next-generation sequencing data. <i>Genome Biology</i> , 2019, 20, 50.	8.8	196
18	H3.3 K27M depletion increases differentiation and extends latency of diffuse intrinsic pontine glioma growth in vivo. <i>Acta Neuropathologica</i> , 2019, 137, 637-655.	7.7	85

#	ARTICLE	IF	CITATIONS
19	A <i>cis</i> -element within the <i>ARF</i> locus mediates repression of <i>p16</i> ^{INK4A} expression via long-range chromatin interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 26644-26652.	7.1	16
20	Structure and evolution of double minutes in diagnosis and relapse brain tumors. <i>Acta Neuropathologica</i> , 2019, 137, 123-137.	7.7	63
21	<i>MYC</i> Drives a Subset of High-Risk Pediatric Neuroblastomas and Is Activated through Mechanisms Including Enhancer Hijacking and Focal Enhancer Amplification. <i>Cancer Discovery</i> , 2018, 8, 320-335.	9.4	172
22	Mutational Landscape and Temporal Evolution during Treatment of Relapsed Acute Lymphoblastic Leukemia. <i>Blood</i> , 2018, 132, 917-917.	1.4	0
23	Relapse-Initiating Clones Preexisting at Diagnosis in B- Cell Acute Lymphoblastic Leukemia Help Predict Molecular Pathways of Relapse. <i>Blood</i> , 2018, 132, 915-915.	1.4	1
24	Targetable kinase gene fusions in high-risk B-ALL: a study from the Children's Oncology Group. <i>Blood</i> , 2017, 129, 3352-3361.	1.4	236
25	The genomic landscape of pediatric and young adult T-lineage acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2017, 49, 1211-1218.	21.4	693
26	Genomic analyses identify recurrent MEF2D fusions in acute lymphoblastic leukaemia. <i>Nature Communications</i> , 2016, 7, 13331.	12.8	218
27	Genetic alterations in uncommon low-grade neuroepithelial tumors: BRAF, FGFR1, and MYB mutations occur at high frequency and align with morphology. <i>Acta Neuropathologica</i> , 2016, 131, 833-845.	7.7	288
28	The landscape of fusion transcripts in spitzoid melanoma and biologically indeterminate spitzoid tumors by RNA sequencing. <i>Modern Pathology</i> , 2016, 29, 359-369.	5.5	61
29	Truncating Erythropoietin Receptor Rearrangements in Acute Lymphoblastic Leukemia. <i>Cancer Cell</i> , 2016, 29, 186-200.	16.8	118
30	Linking Subclonal Genetic Diversity with Functional Heterogeneity Identifies Diagnosis Subclones Destined to Relapse. <i>Blood</i> , 2016, 128, 605-605.	1.4	0
31	The Genomic Landscape of Childhood T-Lineage Acute Lymphoblastic Leukemia. <i>Blood</i> , 2015, 126, 691-691.	1.4	4
32	Genomic Landscape of Relapsed Acute Lymphoblastic Leukemia. <i>Blood</i> , 2015, 126, 692-692.	1.4	3