

Jiantao Shi

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

1,233
citations

758635

12
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839053

18
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docs citations

22
times ranked

3082
citing authors

#	ARTICLE	IF	CITATIONS
1	Clonal Hematopoiesis Associated With Adverse Outcomes After Autologous Stem-Cell Transplantation for Lymphoma. <i>Journal of Clinical Oncology</i> , 2017, 35, 1598-1605.	0.8	339
2	Prognostic role of circulating exosomal miRNAs in multiple myeloma. <i>Blood</i> , 2017, 129, 2429-2436.	0.6	214
3	Epigenetic restriction of extraembryonic lineages mirrors the somatic transition to cancer. <i>Nature</i> , 2017, 549, 543-547.	13.7	146
4	CXCR4 Regulates Extra-Medullary Myeloma through Epithelial-Mesenchymal-Transition-like Transcriptional Activation. <i>Cell Reports</i> , 2015, 12, 622-635.	2.9	123
5	The Mutational Landscape of Circulating Tumor Cells in Multiple Myeloma. <i>Cell Reports</i> , 2017, 19, 218-224.	2.9	92
6	Blocking IFNAR1 inhibits multiple myeloma-driven Treg expansion and immunosuppression. <i>Journal of Clinical Investigation</i> , 2018, 128, 2487-2499.	3.9	80
7	Inhibiting the oncogenic translation program is an effective therapeutic strategy in multiple myeloma. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	53
8	Cancer Cell Dissemination and Homing to the Bone Marrow in a Zebrafish Model. <i>Cancer Research</i> , 2016, 76, 463-471.	0.4	39
9	Mutational Profile and Prognostic Relevance of Circulating Tumor Cells in Multiple Myeloma. <i>Blood</i> , 2015, 126, 23-23.	0.6	37
10	AMD, an Automated Motif Discovery Tool Using Stepwise Refinement of Gapped Consensuses. <i>PLoS ONE</i> , 2011, 6, e24576.	1.1	33
11	Progression signature underlies clonal evolution and dissemination of multiple myeloma. <i>Blood</i> , 2021, 137, 2360-2372.	0.6	26
12	Exome sequencing reveals recurrent germ line variants in patients with familial Waldenström macroglobulinemia. <i>Blood</i> , 2016, 127, 2598-2606.	0.6	22
13	Single-Cell RNA-seq Reveals Characteristics of Malignant Cells and Immune Microenvironment in Subcutaneous Panniculitis-Like T-Cell Lymphoma. <i>Frontiers in Oncology</i> , 2021, 11, 611580.	1.3	7
14	The DNA methylation haplotype (mHap) format and mHapTools. <i>Bioinformatics</i> , 2021, 37, 4892-4894.	1.8	6
15	In vivo genome-wide CRISPR screening in murine acute myeloid leukemia uncovers microenvironmental dependencies. <i>Blood Advances</i> , 2022, 6, 5072-5084.	2.5	6
16	Characterization of the Role of Regulatory T Cells (Tregs) in Inducing Progression of Multiple Myeloma. <i>Blood</i> , 2015, 126, 502-502.	0.6	4
17	Clonal Hematopoiesis Associated with Adverse Outcomes Following Autologous Stem Cell Transplantation for Non-Hodgkin Lymphoma. <i>Blood</i> , 2016, 128, 986-986.	0.6	3
18	Driver Mutation in Waldenström's Macroglobulinemia and Their Clonal Heterogeneity during Progression and Relapse. <i>Blood</i> , 2016, 128, 1092-1092.	0.6	2

#	ARTICLE	IF	CITATIONS
19	DNA methylation profiling to determine the primary sites of metastatic cancers using formalin-fixed paraffin-embedded tissues.. Journal of Clinical Oncology, 2022, 40, 3079-3079.	0.8	1
20	A New Model for Studying the Dissemination of Myeloma Cells throughout the Bone Marrow Using Embryonic Zebrafish. Blood, 2015, 126, 915-915.	0.6	0
21	In Vivo Analysis of Clonal Evolution of Multiple Myeloma. Blood, 2016, 128, 799-799.	0.6	0
22	Deciphering Clonal Evolution and Dissemination of Multiple Myeloma Cells In Vivo. Blood, 2018, 132, 55-55.	0.6	0