

Jiantao Shi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2413470/publications.pdf>

Version: 2024-02-01

22
papers

1,233
citations

758635

12
h-index

839053

18
g-index

22
all docs

22
docs citations

22
times ranked

3082
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	In vivo genome-wide CRISPR screening in murine acute myeloid leukemia uncovers microenvironmental dependencies. Blood Advances, 2022, 6, 5072-5084.	2.5	6
3	Progression signature underlies clonal evolution and dissemination of multiple myeloma. Blood, 2021, 137, 2360-2372.	0.6	26
4	Single-Cell RNA-seq Reveals Characteristics of Malignant Cells and Immune Microenvironment in Subcutaneous Panniculitis-Like T-Cell Lymphoma. Frontiers in Oncology, 2021, 11, 611580.	1.3	7
5	The DNA methylation haplotype (mHap) format and mHapTools. Bioinformatics, 2021, 37, 4892-4894.	1.8	6
6	Blocking IFNAR1 inhibits multiple myeloma-driven Treg expansion and immunosuppression. Journal of Clinical Investigation, 2018, 128, 2487-2499.	3.9	80
7	Deciphering Clonal Evolution and Dissemination of Multiple Myeloma Cells In Vivo. Blood, 2018, 132, 55-55.	0.6	0
8	Clonal Hematopoiesis Associated With Adverse Outcomes After Autologous Stem-Cell Transplantation for Lymphoma. Journal of Clinical Oncology, 2017, 35, 1598-1605.	0.8	339
9	Prognostic role of circulating exosomal miRNAs in multiple myeloma. Blood, 2017, 129, 2429-2436.	0.6	214
10	Inhibiting the oncogenic translation program is an effective therapeutic strategy in multiple myeloma. Science Translational Medicine, 2017, 9, .	5.8	53
11	The Mutational Landscape of Circulating Tumor Cells in Multiple Myeloma. Cell Reports, 2017, 19, 218-224.	2.9	92
12	Epigenetic restriction of extraembryonic lineages mirrors the somatic transition to cancer. Nature, 2017, 549, 543-547.	13.7	146
13	Exome sequencing reveals recurrent germ line variants in patients with familial Waldenström macroglobulinemia. Blood, 2016, 127, 2598-2606.	0.6	22
14	Cancer Cell Dissemination and Homing to the Bone Marrow in a Zebrafish Model. Cancer Research, 2016, 76, 463-471.	0.4	39
15	Driver Mutation in Waldenstrom's Macroglobulinemia and Their Clonal Heterogeneity during Progression and Relapse. Blood, 2016, 128, 1092-1092.	0.6	2
16	Clonal Hematopoiesis Associated with Adverse Outcomes Following Autologous Stem Cell Transplantation for Non-Hodgkin Lymphoma. Blood, 2016, 128, 986-986.	0.6	3
17	In Vivo Analysis of Clonal Evolution of Multiple Myeloma. Blood, 2016, 128, 799-799.	0.6	0
18	CXCR4 Regulates Extra-Medullary Myeloma through Epithelial-Mesenchymal-Transition-like Transcriptional Activation. Cell Reports, 2015, 12, 622-635.	2.9	123

#	ARTICLE	IF	CITATIONS
19	Mutational Profile and Prognostic Relevance of Circulating Tumor Cells in Multiple Myeloma. <i>Blood</i> , 2015, 126, 23-23.	0.6	37
20	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
21	A New Model for Studying the Dissemination of Myeloma Cells throughout the Bone Marrow Using Embryonic Zebrafish. <i>Blood</i> , 2015, 126, 915-915.	0.6	0
22	AMD, an Automated Motif Discovery Tool Using Stepwise Refinement of Gapped Consensuses. <i>PLoS ONE</i> , 2011, 6, e24576.	1.1	33