Ashwini Kumar

List of Publications by Year in descending order

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Δεμνλινί Κιιμλα

#	Article	IF	CITATIONS
1	Implementing a Functional Precision Medicine Tumor Board for Acute Myeloid Leukemia. Cancer Discovery, 2022, 12, 388-401.	9.4	73
2	Comparison of Structural and Short Variants Detected by Linked-Read and Whole-Exome Sequencing in Multiple Myeloma. Cancers, 2021, 13, 1212.	3.7	5
3	FLT3-ITD allelic ratio and HLF expression predict FLT3 inhibitor efficacy in adult AML. Scientific Reports, 2021, 11, 23565.	3.3	6
4	KIT pathway upregulation predicts dasatinib efficacy in acute myeloid leukemia. Leukemia, 2020, 34, 2780-2784.	7.2	6
5	Mutation accumulation in cancer genes relates to nonoptimal outcome in chronic myeloid leukemia. Blood Advances, 2020, 4, 546-559.	5.2	36
6	Phenotype-based drug screening reveals association between venetoclax response and differentiation stage in acute myeloid leukemia. Haematologica, 2020, 105, 708-720.	3.5	99
7	Allelic Imbalance of Recurrently Mutated Genes in Acute Myeloid Leukaemia. Scientific Reports, 2019, 9, 11796.	3.3	9
8	Elevated expression of S100A8 and S100A9 correlates with resistance to the BCL-2 inhibitor venetoclax in AML. Leukemia, 2019, 33, 2548-2553.	7.2	25
9	Hemap: An Interactive Online Resource for Characterizing Molecular Phenotypes across Hematologic Malignancies. Cancer Research, 2019, 79, 2466-2479.	0.9	23
10	Dasatinib and navitoclax act synergistically to target NUP98-NSD1+/FLT3-ITD+ acute myeloid leukemia. Leukemia, 2019, 33, 1360-1372.	7.2	40
11	Chimeric NUP98–NSD1 transcripts from the cryptic t(5;11)(q35.2;p15.4) in adult de novo acute myeloid leukemia. Leukemia and Lymphoma, 2018, 59, 725-732.	1.3	5
12	The impact of RNA sequence library construction protocols on transcriptomic profiling of leukemia. BMC Genomics, 2017, 18, 629.	2.8	42
13	Identification and Clinical Exploration of Individualized Targeted Therapeutic Approaches in Acute Myeloid Leukemia Patients By Integrating Drug Response and Deep Molecular Profiles. Blood, 2017, 130, 854-854.	1.4	1
14	DNA Damage Repair Pathway Alterations in Multiple Myeloma Predict Poor Prognosis, but Correlate with Sensitivity to IGF1R-PI3K-mTOR and HDAC Inhibitors. Blood, 2016, 128, 198-198.	1.4	0
15	The Use of RNA Sequencing to Identify Disease-Specific Gene Expression Signatures and Critical Regulatory Networks Across Hematologic Malignancies. Blood, 2014, 124, 2203-2203.	1.4	3