

# Ashwini Kumar

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1107699/publications.pdf>

Version: 2024-02-01

15  
papers

373  
citations

1163117

8  
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1058476

14  
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15  
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15  
docs citations

15  
times ranked

669  
citing authors

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