

Shweta S Chavan

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

1,284
citations

623188

14
h-index

525886

27
g-index

32
all docs

32
docs citations

32
times ranked

2622
citing authors

#	ARTICLE	IF	CITATIONS
1	Tumour lineage shapes BRCA-mediated phenotypes. <i>Nature</i> , 2019, 571, 576-579.	13.7	295
2	First-line pembrolizumab and trastuzumab in HER2-positive oesophageal, gastric, or gastro-oesophageal junction cancer: an open-label, single-arm, phase 2 trial. <i>Lancet Oncology</i> , The, 2020, 21, 821-831.	5.1	243
3	Clonal selection and double-hit events involving tumor suppressor genes underlie relapse in myeloma. <i>Blood</i> , 2016, 128, 1735-1744.	0.6	170
4	Genomic Correlates of Disease Progression and Treatment Response in Prospectively Characterized Gliomas. <i>Clinical Cancer Research</i> , 2019, 25, 5537-5547.	3.2	107
5	The Spectrum and Clinical Impact of Epigenetic Modifier Mutations in Myeloma. <i>Clinical Cancer Research</i> , 2016, 22, 5783-5794.	3.2	81
6	Multioomic Analysis of Lung Tumors Defines Pathways Activated in Neuroendocrine Transformation. <i>Cancer Discovery</i> , 2021, 11, 3028-3047.	7.7	66
7	Genomic Landscape of Uterine Sarcomas Defined Through Prospective Clinical Sequencing. <i>Clinical Cancer Research</i> , 2020, 26, 3881-3888.	3.2	59
8	The context-specific role of germline pathogenicity in tumorigenesis. <i>Nature Genetics</i> , 2021, 53, 1577-1585.	9.4	44
9	WEE1 inhibition enhances the antitumor immune response to PD-L1 blockade by the concomitant activation of STING and STAT1 pathways in SCLC. <i>Cell Reports</i> , 2022, 39, 110814.	2.9	43
10	Germ cell tumors and associated hematologic malignancies evolve from a common shared precursor. <i>Journal of Clinical Investigation</i> , 2020, 130, 6668-6676.	3.9	28
11	Comprehensive molecular characterization of lung tumors implicates AKT and MYC signaling in adenocarcinoma to squamous cell transdifferentiation. <i>Journal of Hematology and Oncology</i> , 2021, 14, 170.	6.9	26
12	Phosphoproteomic Analyses Reveal Signaling Pathways That Facilitate Lytic Gammaherpesvirus Replication. <i>PLoS Pathogens</i> , 2013, 9, e1003583.	2.1	24
13	Amplification of JNK Signaling Is Necessary To Complete the Murine Gammaherpesvirus 68 Lytic Replication Cycle. <i>Journal of Virology</i> , 2012, 86, 13253-13262.	1.5	21
14	Genome-wide scan identifies variant in 2q12.3 associated with risk for multiple myeloma. <i>Blood</i> , 2014, 124, 2001-2003.	0.6	17
15	MAPK pathway activation selectively inhibits ASCL1-driven small cell lung cancer. <i>IScience</i> , 2021, 24, 103224.	1.9	13
16	Prevalence and Characterization of Biallelic and Monoallelic <i>NTHL1</i> and <i>MSH3</i> Variant Carriers From a Pan-Cancer Patient Population. <i>JCO Precision Oncology</i> , 2021, 5, 455-465.	1.5	10
17	The Clinical Impact of Macrofocal Disease in Multiple Myeloma Differs Between Presentation and Relapse. <i>Blood</i> , 2016, 128, 4431-4431.	0.6	8
18	High Risk Multiple Myeloma Demonstrates Marked Spatial Genomic Heterogeneity Between Focal Lesions and Random Bone Marrow; Implications for Targeted Therapy and Treatment Resistance. <i>Blood</i> , 2015, 126, 20-20.	0.6	7

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19	A common genetic variant in 19q13.3 is associated with outcome of multiple myeloma patients treated with Total Therapy 2 and 3. <i>British Journal of Haematology</i> , 2016, 174, 991-993.	1.2	6
20	Extensive Regional Intra-Clonal Heterogeneity in Multiple Myeloma - Implications for Diagnostics, Risk Stratification and Targeted Treatment. <i>Blood</i> , 2016, 128, 3278-3278.	0.6	2
21	The Impact of Maintenance Lenalidomide on the Mutational Status of the Myeloma Clone at Relapse in the NCRI Myeloma XI Trial for Newly Diagnosed Multiple Myeloma Patients (NDMM). <i>Blood</i> , 2016, 128, 4412-4412.	0.6	2
22	Non-Producing Multiple Myeloma (MM) Is a Distinct Subset Of Non-Secretory MM Characterized By High Cyclin D1 Expression and Decreased Progression Free Survival. <i>Blood</i> , 2013, 122, 1911-1911.	0.6	2
23	Comprehensive Genomic Profiling of Multiple Myeloma in the Course of Clinical Care Identifies Targetable and Prognostically Significant Genomic Alterations. <i>Blood</i> , 2015, 126, 369-369.	0.6	1
24	The Impact of Combination Chemotherapy and Tandem Stem Cell Transplant on Clonal Substructure and Mutational Pattern at Relapse of MM. <i>Blood</i> , 2015, 126, 372-372.	0.6	1
25	A Survey of Fusion Genes in Myeloma Identifies Kinase Domain Activation Which Could be Targeted with Available Treatments. <i>Blood</i> , 2016, 128, 117-117.	0.6	1
26	High Risk Myeloma Is Characterized By the Bi-Allelic Inactivation of CDKN2C and RB1. <i>Blood</i> , 2016, 128, 4416-4416.	0.6	1
27	FISH and GEP Based Prediction of Chromosomal Translocation Identifies Myeloma Patients Who Do Not Benefit From Bortezomib. <i>Blood</i> , 2012, 120, 1814-1814.	0.6	0
28	Molecular Subtyping and Risk Stratification for the Classification of Myeloma. <i>Blood</i> , 2015, 126, 4173-4173.	0.6	0
29	Differential ICAM3 Gene Expression Correlates with Susceptibility to Natural Killer Cell-Mediated Lysis in Multiple Myeloma. <i>Blood</i> , 2015, 126, 2990-2990.	0.6	0
30	The Mutational and Signaling Landscape of Multiple Myeloma Varies Dependent upon Translocation Cyclin D (TC) Subgroup. <i>Blood</i> , 2016, 128, 4441-4441.	0.6	0