Shweta S Chavan

List of Publications by Year
in descending order

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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	WEE1 inhibition enhances the antitumor immune response to PD-L1 blockade by the concomitant activation of STING and STAT1 pathways in SCLC. Cell Reports, 2022, 39, 110814.	2.9	43
2	Prevalence and Characterization of Biallelic and Monoallelic NTHL1 and MSH3 Variant Carriers From a Pan-Cancer Patient Population. JCO Precision Oncology, 2021, 5, 455-465.	1.5	10
3	Multiomic Analysis of Lung Tumors Defines Pathways Activated in Neuroendocrine Transformation. Cancer Discovery, 2021, 11, 3028-3047.	7.7	66
4	Comprehensive molecular characterization of lung tumors implicates AKT and MYC signaling in adenocarcinoma to squamous cell transdifferentiation. Journal of Hematology and Oncology, 2021, 14, 170.	6.9	26
5	MAPK pathway activation selectively inhibits ASCL1-driven small cell lung cancer. IScience, 2021, 24, 103224.	1.9	13
6	The context-specific role of germline pathogenicity in tumorigenesis. Nature Genetics, 2021, 53, 1577-1585.	9.4	44
7	First-line pembrolizumab and trastuzumab in HER2-positive oesophageal, gastric, or gastro-oesophageal junction cancer: an open-label, single-arm, phase 2 trial. Lancet Oncology, The, 2020, 21, 821-831.	5.1	243
8	Genomic Landscape of Uterine Sarcomas Defined Through Prospective Clinical Sequencing. Clinical Cancer Research, 2020, 26, 3881-3888.	3.2	59
9	Germ cell tumors and associated hematologic malignancies evolve from a common shared precursor. Journal of Clinical Investigation, 2020, 130, 6668-6676.	3.9	28
10	Tumour lineage shapes BRCA-mediated phenotypes. Nature, 2019, 571, 576-579.	13.7	295
11	Genomic Correlates of Disease Progression and Treatment Response in Prospectively Characterized Gliomas. Clinical Cancer Research, 2019, 25, 5537-5547.	3.2	107
12	Clonal selection and double-hit events involving tumor suppressor genes underlie relapse in myeloma. Blood, 2016, 128, 1735-1744.	0.6	170
13	A common genetic variant in 19q13Â·3 is associated with outcome of multiple myeloma patients treated with Total Therapy 2 and 3. British Journal of Haematology, 2016, 174, 991-993.	1.2	6
14	The Spectrum and Clinical Impact of Epigenetic Modifier Mutations in Myeloma. Clinical Cancer Research, 2016, 22, 5783-5794.	3.2	81
15	Extensive Regional Intra-Clonal Heterogeneity in Multiple Myeloma - Implications for Diagnostics, Risk Stratification and Targeted Treatment. Blood, 2016, 128, 3278-3278.	0.6	2
16	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). Blood, 2016, 128, 4412-4412.	0.6	2
17	The Clinical Impact of Macrofocal Disease in Multiple Myeloma Differs Between Presentation and Relapse. Blood, 2016, 128, 4431-4431.	0.6	8
18	A Survey of Fusion Genes in Myeloma Identifies Kinase Domain Activation Which Could be Targeted with Available Treatments. Blood, 2016, 128, 117-117.	0.6	1

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19	High Risk Myeloma Is Characterized By the Bi-Allelic Inactivation of CDKN2C and RB1. Blood, 2016, 128, 4416-4416.	0.6	1
20	The Mutational and Signaling Landscape of Multiple Myeloma Varies Dependent upon Translocation Cyclin D (TC) Subgroup. Blood, 2016, 128, 4441-4441.	0.6	0
21	High Risk Multiple Myeloma Demonstrates Marked Spatial Genomic Heterogeneity Between Focal Lesions and Random Bone Marrow; Implications for Targeted Therapy and Treatment Resistance. Blood, 2015, 126, 20-20.	0.6	7
22	Comprehensive Genomic Profiling of Multiple Myeloma in the Course of Clinical Care Identifies Targetable and Prognostically Significant Genomic Alterations. Blood, 2015, 126, 369-369.	0.6	1
23	The Impact of Combination Chemotherapy and Tandem Stem Cell Transplant on Clonal Substructure and Mutational Pattern at Relapse of MM. Blood, 2015, 126, 372-372.	0.6	1
24	Molecular Subtyping and Risk Stratification for the Classification of Myeloma. Blood, 2015, 126, 4173-4173.	0.6	0
25	Differential ICAM3 Gene Expression Correlates with Susceptibility to Natural Killer Cell-Mediated Lysis in Multiple Myeloma. Blood, 2015, 126, 2990-2990.	0.6	0
26	Genome-wide scan identifies variant in 2q12.3 associated with risk for multiple myeloma. Blood, 2014, 124, 2001-2003.	0.6	17
27	Phosphoproteomic Analyses Reveal Signaling Pathways That Facilitate Lytic Gammaherpesvirus Replication. PLoS Pathogens, 2013, 9, e1003583.	2.1	24
28	Non-Producing Multiple Myeloma (MM) Is a Distinct Subset Of Non-Secretory MM Characterized By High Cyclin D1 Expression and Decreased Progression Free Survival. Blood, 2013, 122, 1911-1911.	0.6	2
29	Amplification of JNK Signaling Is Necessary To Complete the Murine Gammaherpesvirus 68 Lytic Replication Cycle. Journal of Virology, 2012, 86, 13253-13262.	1.5	21
30	FISH and GEP Based Prediction of Chromosomal Translocation Identifies Myeloma Patients Who Do Not Benefit From Bortezomib. Blood, 2012, 120, 1814-1814.	0.6	0