

Sherri Z Millis

List of Publications by Year in descending order

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Version: 2024-02-01

38
papers

660
citations

623734

14
h-index

580821

25
g-index

39
all docs

39
docs citations

39
times ranked

1330
citing authors

#	ARTICLE	IF	CITATIONS
1	Drivers of genomic loss of heterozygosity in leiomyosarcoma are distinct from carcinomas. <i>Npj Precision Oncology</i> , 2022, 6, 29.	5.4	6
2	Clinical genomic profiling in the management of patients with soft tissue and bone sarcoma. <i>Nature Communications</i> , 2022, 13, .	12.8	51
3	Cyclin Pathway Genomic Alterations Across 190,247 Solid Tumors: Leveraging Large-Scale Data to Inform Therapeutic Directions. <i>Oncologist</i> , 2021, 26, e78-e89.	3.7	18
4	Landscape of Cyclin Pathway Genomic Alterations Across 5,356 Prostate Cancers: Implications for Targeted Therapeutics. <i>Oncologist</i> , 2021, 26, e715-e718.	3.7	5
5	Multiscale-omic assessment of EWSR1-NFATc2 fusion positive sarcomas identifies the mTOR pathway as a potential therapeutic target. <i>Npj Precision Oncology</i> , 2021, 5, 43.	5.4	14
6	Genomic alterations and associated pathway abnormalities in Ewing sarcoma.. <i>Journal of Clinical Oncology</i> , 2021, 39, 11532-11532.	1.6	0
7	Prevalence of Homologous Recombination Pathway Gene Mutations in Melanoma: Rationale for a New Targeted Therapeutic Approach. <i>Journal of Investigative Dermatology</i> , 2021, 141, 2028-2036.e2.	0.7	17
8	The Panâ€Cancer Landscape of Coamplification of the Tyrosine Kinases KIT, KDR, and PDGFRA. <i>Oncologist</i> , 2020, 25, e39-e47.	3.7	13
9	Recurrent secondary genomic alterations in desmoplastic small round cell tumors. <i>BMC Medical Genetics</i> , 2020, 21, 101.	2.1	10
10	Identifying Opportunities and Challenges for Patients With Sarcoma as a Result of Comprehensive Genomic Profiling of Sarcoma Specimens. <i>JCO Precision Oncology</i> , 2020, 4, 176-182.	3.0	9
11	Multiscale omic assessment of EWSR1-NFATc2 fusion positive sarcomas to identify conserved fusion breakpoint and activation of the mTOR pathway.. <i>Journal of Clinical Oncology</i> , 2020, 38, e23536-e23536.	1.6	0
12	Cyclin pathway genomic alterations across 5,356 prostate cancers.. <i>Journal of Clinical Oncology</i> , 2020, 38, 179-179.	1.6	0
13	Landscape of cyclin pathway genomic alterations across 7,207 non-prostate genitourinary tumors.. <i>Journal of Clinical Oncology</i> , 2020, 38, 549-549.	1.6	0
14	Prevalence of established and emerging biomarkers of immune checkpoint inhibitor response in advanced hepatocellular carcinoma. <i>Oncotarget</i> , 2019, 10, 4018-4025.	1.8	118
15	Common Secondary Genomic Variants Associated With Advanced Epithelioid Hemangioendothelioma. <i>JAMA Network Open</i> , 2019, 2, e1912416.	5.9	19
16	<i>BRCA1/2</i> Functional Loss Defines a Targetable Subset in Leiomyosarcoma. <i>Oncologist</i> , 2019, 24, 973-979.	3.7	49
17	Clinical, pathological, and genomic features ofâ€EWSR1-PATZ1 fusion sarcoma. <i>Modern Pathology</i> , 2019, 32, 1593-1604.	5.5	74
18	Prospective Comprehensive Genomic Profiling of Primary and Metastatic Prostate Tumors. <i>JCO Precision Oncology</i> , 2019, 3, 1-23.	3.0	63

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19	Genomic Features for Therapeutic Insights of Chemotherapy-Resistant, Primary Mediastinal Nonseminomatous Germ Cell Tumors and Comparison with Gonadal Counterpart. <i>Oncologist</i> , 2019, 24, e142-e145.	3.7	22
20	Degree of <i>MDM2</i> Amplification Affects Clinical Outcomes in Dedifferentiated Liposarcoma. <i>Oncologist</i> , 2019, 24, 989-996.	3.7	23
21	Phosphatidylinositol 3-kinase pathway genomic alterations in 60,991 diverse solid tumors informs targeted therapy opportunities. <i>Cancer</i> , 2019, 125, 1185-1199.	4.1	36
22	Ductal and acinar carcinomas of the prostate: A comparative comprehensive genomic profiling study.. <i>Journal of Clinical Oncology</i> , 2019, 37, 271-271.	1.6	0
23	Genomic findings in adenocarcinoma of the urinary bladder.. <i>Journal of Clinical Oncology</i> , 2019, 37, 132-132.	1.6	0
24	Histone H3 modifying genes may serve as a predictive marker for metastasis in synovial sarcoma.. <i>Journal of Clinical Oncology</i> , 2019, 37, 11058-11058.	1.6	0
25	Secondary genomic alterations in Ewing sarcoma.. <i>Journal of Clinical Oncology</i> , 2019, 37, 11024-11024.	1.6	0
26	Determinants of secondary alterations in <i>WWTR1-CAMTA1</i> fusion epithelioid hemangioendothelioma.. <i>Journal of Clinical Oncology</i> , 2019, 37, 11045-11045.	1.6	0
27	<i>BRAF</i> in Lung Cancers: Analysis of Patient Cases Reveals Recurrent <i>BRAF</i> Mutations, Fusions, Kinase Duplications, and Concurrent Alterations. <i>JCO Precision Oncology</i> , 2018, 2, 1-15.	3.0	24
28	Genomic Landscape of Appendiceal Neoplasms. <i>JCO Precision Oncology</i> , 2018, 2, 1-18.	3.0	23
29	Comprehensive genomic characterization of chemotherapy-resistant testicular germ cell tumors (TGCT).. <i>Journal of Clinical Oncology</i> , 2018, 36, 4555-4555.	1.6	1
30	Refractory testicular pure seminoma (PS) and non-seminomatous(NS) germ cell tumors (GCT): A comprehensive genomic profiling (CGP) study.. <i>Journal of Clinical Oncology</i> , 2018, 36, 565-565.	1.6	1
31	<i>FGFR3</i> Driven Metastatic Urothelial Carcinoma of the Urinary Bladder (mUCB): A Comprehensive Genomic Profiling Study.. <i>Journal of Clinical Oncology</i> , 2018, 36, 4531-4531.	1.6	0
32	Genomic subtypes of angiosarcoma: A comprehensive genomic profiling (CGP) study.. <i>Journal of Clinical Oncology</i> , 2018, 36, 11576-11576.	1.6	1
33	Next-Generation Sequencing in the Clinical Setting Clarifies Patient Characteristics and Potential Actionability. <i>Cancer Research</i> , 2017, 77, 6313-6320.	0.9	22
34	Clinical Benefit from Trametinib in a Patient with Appendiceal Adenocarcinoma with a GNAS R201H Mutation. <i>Case Reports in Oncology</i> , 2017, 10, 548-552.	0.7	9
35	Impact of next-generation sequencing (NGS) on diagnostic and therapeutic options in soft-tissue and bone sarcoma.. <i>Journal of Clinical Oncology</i> , 2017, 35, 11001-11001.	1.6	26
36	Identification of novel fumarate hydratase gene alterations in prostate cancer.. <i>Journal of Clinical Oncology</i> , 2017, 35, 11585-11585.	1.6	3

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37	Comprehensive genomic sequencing of appendiceal cancer tumors to identify different genomic alterations by subtype, novel treatment opportunities, and improved outcomes.. Journal of Clinical Oncology, 2017, 35, 599-599.	1.6	0
38	Frequency of genetic homologous recombination (HR) alterations in metastatic cutaneous melanoma.. Journal of Clinical Oncology, 2017, 35, e21033-e21033.	1.6	3