

Diego M Marzese

List of Publications by Year in descending order

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66
papers

1,685
citations

304743

22
h-index

302126

39
g-index

69
all docs

69
docs citations

69
times ranked

3181
citing authors

#	ARTICLE	IF	CITATIONS
1	ASO Author Reflections: Establishing Novel Molecular Subtypes of Appendiceal Cancer. <i>Annals of Surgical Oncology</i> , 2022, 29, 2126-2127.	1.5	0
2	ASO Visual Abstract: Establishing Novel Molecular Subtypes of Appendiceal Cancer. <i>Annals of Surgical Oncology</i> , 2022, 29, 2128-2128.	1.5	0
3	Establishing Novel Molecular Subtypes of Appendiceal Cancer. <i>Annals of Surgical Oncology</i> , 2022, 29, 2118-2125.	1.5	6
4	ASO Author Reflections: Entering the Era of Biomarker-Driven Management of the Axilla. <i>Annals of Surgical Oncology</i> , 2022, , .	1.5	0
5	Glioblastoma Embryonic-like Stem Cells Exhibit Immune-Evasive Phenotype. <i>Cancers</i> , 2022, 14, 2070.	3.7	4
6	Epigenetic Signatures Predict Pathologic Nodal Stage in Breast Cancer Patients with Estrogen Receptor-Positive, Clinically Node-Positive Disease. <i>Annals of Surgical Oncology</i> , 2022, 29, 4716-4724.	1.5	5
7	Machine Learning-Based Epigenetic Classifiers for Axillary Staging of Patients with ER-Positive Early-Stage Breast Cancer. <i>Annals of Surgical Oncology</i> , 2022, 29, 6407-6414.	1.5	5
8	A Microcosm of Disparities in Breast Cancer: Comparison Between a Private Hospital and a Safety-Net County Hospital Within Los Angeles County. <i>American Surgeon</i> , 2021, , 000313482199866.	0.8	0
9	Familial Psychosis Associated With a Missense Mutation at MACF1 Gene Combined With the Rare Duplications DUP3p26.3 and DUP16q23.3, Affecting the CNTN6 and CDH13 Genes. <i>Frontiers in Genetics</i> , 2021, 12, 622886.	2.3	3
10	A Systems Approach to Brain Tumor Treatment. <i>Cancers</i> , 2021, 13, 3152.	3.7	21
11	Current Triple-Negative Breast Cancer Subtypes: Dissecting the Most Aggressive Form of Breast Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 681476.	2.8	71
12	Is the 21-Gene Recurrence Score on Core Needle Biopsy Equivalent to Surgical Specimen in Early-Stage Breast Cancer? A Comparison of Gene Expression Between Paired Core Needle Biopsy and Surgical Specimens. <i>Annals of Surgical Oncology</i> , 2021, 28, 5588-5596.	1.5	10
13	Chromatin insulation dynamics in glioblastoma: challenges and future perspectives of precision oncology. <i>Clinical Epigenetics</i> , 2021, 13, 150.	4.1	9
14	Epigenetic Regulation of Immunotherapy Response in Triple-Negative Breast Cancer. <i>Cancers</i> , 2021, 13, 4139.	3.7	10
15	iGlioSub: an integrative transcriptomic and epigenomic classifier for glioblastoma molecular subtypes. <i>BioData Mining</i> , 2021, 14, 42.	4.0	7
16	ASO Visual Abstract: Is the 21-Gene Recurrence Score on Core Needle Biopsy Equivalent to Surgical Specimen in Early-Stage Breast Cancer?. <i>Annals of Surgical Oncology</i> , 2021, 28, 643-644.	1.5	2
17	Abstract P5-05-12: Small molecule targeting regulated cell death pathways in treating triple negative breast cancer. , 2020, , .		0
18	The metastatic microenvironment: Melanomaâ€™microglia cross-talk promotes the malignant phenotype of melanoma cells. <i>International Journal of Cancer</i> , 2019, 144, 802-817.	5.1	34

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19	Clinicopathological Features of Triple-Negative Breast Cancer Epigenetic Subtypes. <i>Annals of Surgical Oncology</i> , 2019, 26, 3344-3353.	1.5	15
20	Clinical Implications of Transcriptomic Changes After Neoadjuvant Chemotherapy in Patients with Triple-Negative Breast Cancer. <i>Annals of Surgical Oncology</i> , 2019, 26, 3185-3193.	1.5	4
21	Demethylation by low-dose 5-aza-2- β -deoxycytidine impairs 3D melanoma invasion partially through miR-199a-3p expression revealing the role of this miR in melanoma. <i>Clinical Epigenetics</i> , 2019, 11, 9.	4.1	12
22	Mitochondrial stress triggers a pro-survival response through epigenetic modifications of nuclear DNA. <i>Cellular and Molecular Life Sciences</i> , 2019, 76, 1397-1417.	5.4	7
23	Commonly integrated epigenetic modifications of differentially expressed genes lead to adaptive resistance in cancer. <i>Epigenomics</i> , 2019, 11, 732-737.	2.1	11
24	B7H3 regulates differentiation and serves as a potential biomarker and theranostic target for human glioblastoma. <i>Laboratory Investigation</i> , 2019, 99, 1117-1129.	3.7	29
25	Epigenetic Classifiers for Precision Diagnosis of Brain Tumors. <i>Epigenetics Insights</i> , 2019, 12, 251686571984028.	2.0	11
26	Cancer Epigenomics on Precision Medicine and Immunotherapy. , 2019, , 483-503.		0
27	Multiplex Gene Profiling of Cell-Free DNA in Patients With Metastatic Melanoma for Monitoring Disease. <i>JCO Precision Oncology</i> , 2018, 2, 1-30.	3.0	13
28	Epigenetic profiling for the molecular classification of metastatic brain tumors. <i>Nature Communications</i> , 2018, 9, 4627.	12.8	79
29	Alternative splicing and cancer metastasis: prognostic and therapeutic applications. <i>Clinical and Experimental Metastasis</i> , 2018, 35, 393-402.	3.3	38
30	The Epigenomic Landscape of Pituitary Adenomas Reveals Specific Alterations and Differentiates Among Acromegaly, Cushing's Disease and Endocrine-Inactive Subtypes. <i>Clinical Cancer Research</i> , 2018, 24, 4126-4136.	7.0	105
31	Epigenomic and Transcriptomic Characterization of Secondary Breast Cancers. <i>Annals of Surgical Oncology</i> , 2018, 25, 3082-3087.	1.5	4
32	KDM6B Counteracts EZH2-Mediated Suppression of <i>IGFBP5</i> to Confer Resistance to PI3K/AKT Inhibitor Treatment in Breast Cancer. <i>Molecular Cancer Therapeutics</i> , 2018, 17, 1973-1983.	4.1	35
33	Brain metastasis DNA methylomes, a novel resource for the identification of biological and clinical features. <i>Scientific Data</i> , 2018, 5, 180245.	5.3	18
34	TP73 DNA methylation and upregulation of β -Np73 are associated with an adverse prognosis in breast cancer. <i>Journal of Clinical Pathology</i> , 2018, 71, 52-58.	2.0	10
35	Abstract 3541: Epigenetic regulation of KPC1 ubiquitin ligase has a regulatory role on the NF- κ B pathway in metastatic melanoma. <i>Cancer Research</i> , 2018, 78, 3541-3541.	0.9	1
36	Distinct histone modifications denote early stress-induced drug tolerance in cancer. <i>Oncotarget</i> , 2018, 9, 8206-8222.	1.8	54

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37	Mechanisms of immune evasion in triple-negative breast cancer patients.. Journal of Clinical Oncology, 2018, 36, 1096-1096.	1.6	21
38	Genome-wide chromatin accessibility, DNA methylation and gene expression analysis of histone deacetylase inhibition in triple-negative breast cancer. Genomics Data, 2017, 12, 14-16.	1.3	17
39	Epigenetic Regulation of KPC1 Ubiquitin Ligase Affects the NF- κ B Pathway in Melanoma. Clinical Cancer Research, 2017, 23, 4831-4842.	7.0	33
40	MiR-200a Regulates CDK4/6 Inhibitor Effect by Targeting CDK6 in Metastatic Melanoma. Journal of Investigative Dermatology, 2017, 137, 1955-1964.	0.7	32
41	Hypomethylation of CNTFR β is associated with proliferation and poor prognosis in lower grade gliomas. Scientific Reports, 2017, 7, 7079.	3.3	18
42	The RhoJ-BAD signaling network: An Achilles' heel for BRAF mutant melanomas. PLoS Genetics, 2017, 13, e1006913.	3.5	20
43	CCR4 is a determinant of melanoma brain metastasis. Oncotarget, 2017, 8, 31079-31091.	1.8	65
44	ANGPTL4 promotes the progression of cutaneous melanoma to brain metastasis. Oncotarget, 2017, 8, 75778-75796.	1.8	23
45	Cancer Epigenomics on Precision Medicine and Immunotherapy. , 2017, , 1-21.		0
46	Genome-Wide Hypomethylation and Specific Tumor-Related Gene Hypermethylation are Associated with Esophageal Squamous Cell Carcinoma Outcome. Journal of Thoracic Oncology, 2015, 10, 509-517.	1.1	35
47	The CASC15 Long Intergenic Noncoding RNA Locus Is Involved in Melanoma Progression and Phenotype Switching. Journal of Investigative Dermatology, 2015, 135, 2464-2474.	0.7	90
48	Epigenomic landscape of melanoma progression to brain metastasis: unexplored therapeutic alternatives. Epigenomics, 2015, 7, 1303-1311.	2.1	18
49	In Situ Sodium Bisulfite Modification of Genomic DNA from Microdissected Melanoma Paraffin-Embedded Archival Tissues. Methods in Molecular Biology, 2015, , 1.	0.9	1
50	Epigenetic variations in breast cancer progression to lymph node metastasis. Clinical and Experimental Metastasis, 2015, 32, 99-110.	3.3	19
51	Emerging technologies for studying DNA methylation for the molecular diagnosis of cancer. Expert Review of Molecular Diagnostics, 2015, 15, 647-664.	3.1	40
52	Epigenetic Changes of EGFR Have an Important Role in BRAF Inhibitor-Resistant Cutaneous Melanomas. Journal of Investigative Dermatology, 2015, 135, 532-541.	0.7	79
53	Brain metastasis is predetermined in early stages of cutaneous melanoma by CD44v6 expression through epigenetic regulation of the spliceosome. Pigment Cell and Melanoma Research, 2015, 28, 82-93.	3.3	50
54	Abstract A10: Higher incidence of epigenomic alterations on BRAF and NRAS wild type melanoma brain metastases. , 2015, , .		0

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55	Multi-platform genome-wide analysis of melanoma progression to brain metastasis. <i>Genomics Data</i> , 2014, 2, 150-152.	1.3	16
56	Epigenome-wide DNA methylation landscape of melanoma progression to brain metastasis reveals aberrations on homeobox D cluster associated with prognosis. <i>Human Molecular Genetics</i> , 2014, 23, 226-238.	2.9	96
57	DNA methylation and gene deletion analysis of brain metastases in melanoma patients identifies mutually exclusive molecular alterations. <i>Neuro-Oncology</i> , 2014, 16, 1499-1509.	1.2	65
58	RASAL2 activates RAC1 to promote triple-negative breast cancer progression. <i>Journal of Clinical Investigation</i> , 2014, 124, 5291-5304.	8.2	72
59	Diagnostic and prognostic value of circulating tumor-related DNA in cancer patients. <i>Expert Review of Molecular Diagnostics</i> , 2013, 13, 827-844.	3.1	103
60	Epigenetic regulation of <i>REG1A</i> and chemosensitivity of cutaneous melanoma. <i>Epigenetics</i> , 2013, 8, 1043-1052.	2.7	14
61	DNA Methylation Index and Methylation Profile of Invasive Ductal Breast Tumors. <i>Journal of Molecular Diagnostics</i> , 2012, 14, 613-622.	2.8	35
62	Aberrant DNA methylation of cancer-related genes in giant breast fibroadenoma: a case report. <i>Journal of Medical Case Reports</i> , 2011, 5, 516.	0.8	7
63	Simultaneous analysis of the methylation profile of 26 cancer related regions in invasive breast carcinomas by MS-MLPA and drMS-MLPA. <i>Molecular and Cellular Probes</i> , 2010, 24, 271-280.	2.1	20
64	Asymptomatic Becker muscular dystrophy in a family with a multiexon deletion. <i>Muscle and Nerve</i> , 2009, 39, 239-243.	2.2	51
65	MLPA mutation detection in Argentine HNPCC and FAP families. <i>Familial Cancer</i> , 2009, 8, 67-73.	1.9	5
66	Development of a Premature Stop Codon-detection method based on a bacterial two-hybrid system. <i>BMC Biotechnology</i> , 2006, 6, 38.	3.3	6