

Tathiane M Malta

List of Publications by Year in descending order

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63
papers

12,898
citations

394421

19
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361022

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72
all docs

72
docs citations

72
times ranked

20016
citing authors

#	ARTICLE	IF	CITATIONS
1	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	14.3	3,706
2	TCGAbiolinks: an R/Bioconductor package for integrative analysis of TCGA data. <i>Nucleic Acids Research</i> , 2016, 44, e71-e71.	14.5	2,519
3	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018, 173, 291-304.e6.	28.9	1,718
4	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016, 164, 550-563.	28.9	1,695
5	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	28.9	1,417
6	Longitudinal molecular trajectories of diffuse glioma in adults. <i>Nature</i> , 2019, 576, 112-120.	27.8	320
7	Glioma CpG island methylator phenotype (G-CIMP): biological and clinical implications. <i>Neuro-Oncology</i> , 2018, 20, 608-620.	1.2	194
8	DNA methylation profiling to predict recurrence risk in meningioma: development and validation of a nomogram to optimize clinical management. <i>Neuro-Oncology</i> , 2019, 21, 901-910.	1.2	184
9	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021, 184, 3376-3393.e17.	28.9	164
10	A Distinct DNA Methylation Shift in a Subset of Glioma CpG Island Methylator Phenotypes during Tumor Recurrence. <i>Cell Reports</i> , 2018, 23, 637-651.	6.4	137
11	Patient-derived organoids and orthotopic xenografts of primary and recurrent gliomas represent relevant patient avatars for precision oncology. <i>Acta Neuropathologica</i> , 2020, 140, 919-949.	7.7	72
12	A serum-based DNA methylation assay provides accurate detection of glioma. <i>Neuro-Oncology</i> , 2021, 23, 1494-1508.	1.2	53
13	Mutated CEACAMs Disrupt Transforming Growth Factor Beta Signaling and Alter the Intestinal Microbiome to Promote Colorectal Carcinogenesis. <i>Gastroenterology</i> , 2020, 158, 238-252.	1.3	46
14	Cultured Human Adipose Tissue Pericytes and Mesenchymal Stromal Cells Display a Very Similar Gene Expression Profile. <i>Stem Cells and Development</i> , 2015, 24, 2822-2840.	2.1	44
15	HTLV-1/2 seroprevalence and coinfection rate in Brazilian first-time blood donors: an 11-year follow-up. <i>Revista Do Instituto De Medicina Tropical De Sao Paulo</i> , 2012, 54, 123-130.	1.1	35
16	Metabolic reprogramming associated with aggressiveness occurs in the G-CIMP-high molecular subtypes of IDH1mut lower grade gliomas. <i>Neuro-Oncology</i> , 2020, 22, 480-492.	1.2	31
17	Predicting master transcription factors from pan-cancer expression data. <i>Science Advances</i> , 2021, 7, eabf6123.	10.3	30
18	Transcriptomic comparisons between cultured human adipose tissue-derived pericytes and mesenchymal stromal cells. <i>Genomics Data</i> , 2016, 7, 20-25.	1.3	25

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19	Identification of subsets of IDH-mutant glioblastomas with distinct epigenetic and copy number alterations and stratified clinical risks. <i>Neuro-Oncology Advances</i> , 2019, 1, vdz015.	0.7	22
20	Generation of induced pluripotent stem cells from large domestic animals. <i>Stem Cell Research and Therapy</i> , 2020, 11, 247.	5.5	21
21	Molecular landscape of IDH-mutant primary astrocytoma Grade IV/glioblastomas. <i>Modern Pathology</i> , 2021, 34, 1245-1260.	5.5	21
22	Genes Related to Antiviral Activity, Cell Migration, and Lysis Are Differentially Expressed in CD4+T Cells in Human T Cell Leukemia Virus Type 1-Associated Myelopathy/Tropical Spastic Paraparesis Patients. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, 610-622.	1.1	20
23	The gene expression profile of non-cultured, highly purified human adipose tissue pericytes: Transcriptomic evidence that pericytes are stem cells in human adipose tissue. <i>Experimental Cell Research</i> , 2016, 349, 239-254.	2.6	19
24	Targeting the E3 Ubiquitin Ligase PJA1 Enhances Tumor-Suppressing TGF β ² Signaling. <i>Cancer Research</i> , 2020, 80, 1819-1832.	0.9	17
25	TCGAbiolinksGUI: A graphical user interface to analyze cancer molecular and clinical data. <i>F1000Research</i> , 0, 7, 439.	1.6	14
26	Short Communication Forced expression of OCT4 influences the expression of pluripotent genes in human mesenchymal stem cells and fibroblasts. <i>Genetics and Molecular Research</i> , 2013, 12, 1054-1060.	0.2	13
27	Leukotrienes Are Upregulated and Associated with Human T-Lymphotropic Virus Type 1 (HTLV-1)-Associated Neuroinflammatory Disease. <i>PLoS ONE</i> , 2012, 7, e51873.	2.5	10
28	Detection of tumor-specific DNA methylation markers in the blood of patients with pituitary neuroendocrine tumors. <i>Neuro-Oncology</i> , 2022, 24, 1126-1139.	1.2	9
29	Molecular landscape of IDH-wild type, TERT-wild type adult glioblastomas. <i>Brain Pathology</i> , 2022, 32, .	4.1	9
30	Functional and bioinformatics analyses reveal conservation of cis-regulatory elements between sciaridae and drosophilidae. <i>Genesis</i> , 2008, 46, 43-51.	1.6	6
31	T cell receptor signaling pathway is overexpressed in CD4+ T cells from HAM/TSP individuals. <i>Brazilian Journal of Infectious Diseases</i> , 2015, 19, 578-584.	0.6	6
32	DNA methylation-based signatures classify sporadic pituitary tumors according to clinicopathological features. <i>Neuro-Oncology</i> , 2021, 23, 1292-1303.	1.2	6
33	Altered Expression of Degranulation-Related Genes in CD8+T Cells in Human T Lymphotropic Virus Type I Infection. <i>AIDS Research and Human Retroviruses</i> , 2013, 29, 826-836.	1.1	4
34	Genes related to antiviral activity are differentially expressed in CD4+ T cell in HAM/TSP patients. <i>Retrovirology</i> , 2014, 11, .	2.0	1
35	GENE-61. METHYLATION-BASED LIQUID BIOPSY OF MENINGIOMA PRIMARY AND RECURRENT SAMPLES. <i>Neuro-Oncology</i> , 2019, 21, vi111-vi111.	1.2	1
36	Abstract LB-373: Comprehensive analysis of cancer stemness. , 2018, , .		1

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37	Distribution of QPY and RAH haplotypes of granzyme B gene in distinct Brazilian populations. Revista Da Sociedade Brasileira De Medicina Tropical, 2012, 45, 496-499.	0.9	0
38	Novel polymorphisms in the promoter region of the perforin gene among distinct Brazilian populations and their functional impact. International Journal of Immunogenetics, 2014, 41, 198-205.	1.8	0
39	EPIG-14EPIGENOMIC (DNA METHYLATION AND EXPRESSION) SIGNATURES DEFINE SUBSETS OF BOTH IDHmut AND IDHwt GLIOMA WITH DISTINCT CLINICAL OUTCOMES. Neuro-Oncology, 2015, 17, v89.2-v89.	1.2	0
40	EPIG-16MOST DIFFERENTIAL DNA METHYLATION CHANGES OCCUR AT CANDIDATE ENHANCER ELEMENTS FOR RECURRENT LOWER GRADE GLIOMA AND GLIOBLASTOMA. Neuro-Oncology, 2015, 17, v89.4-v90.	1.2	0
41	GENO-06A PAN-GLIOMA CHARACTERIZATION OF GENOMIC, EPIGENOMIC AND TRANSCRIPTOMIC ACTIVITIES REVEALS NOVEL RELATIONSHIPS BETWEEN HISTOLOGICAL SUBTYPES AND MOLECULAR SIGNATURES. Neuro-Oncology, 2015, 17, v92.2-v92.	1.2	0
42	GENT-33. EPIGENETIC ALTERATIONS AT INTERGENIC REGIONS ASSOCIATED WITH PROGRESSION IN A SUBSET OF IDH MUTANT GLIOMAS. Neuro-Oncology, 2016, 18, vi81-vi81.	1.2	0
43	GENT-34. EPIGENOMIC STEMNESS SIGNATURE ASSOCIATED WITH GLIOMA MOLECULAR SUBTYPES. Neuro-Oncology, 2016, 18, vi81-vi81.	1.2	0
44	IMMU-60. PD-L1 EXPRESSION ASSOCIATED WITH GLIOMA MOLECULAR SUBTYPES: CLINICAL IMPLICATIONS. Neuro-Oncology, 2017, 19, vi126-vi126.	1.2	0
45	GENE-52. EPIGENOMIC GLIOMA SUBTYPE EVALUATION ACROSS 31 TUMOR TYPES. Neuro-Oncology, 2017, 19, vi103-vi104.	1.2	0
46	GENE-09. FUNCTIONAL GENOMIC ELEMENTS DEFINED BY DNA METHYLATION CAN DISTINGUISH MENINGIOMA SUBGROUPS. Neuro-Oncology, 2018, 20, vi104-vi104.	1.2	0
47	GENE-07. GENOMIC ENHANCER METHYLATION IS ASSOCIATED WITH BIOLOGICAL AND CLINICAL FEATURES IN PITUITARY TUMORS. Neuro-Oncology, 2018, 20, vi104-vi104.	1.2	0
48	CBMT-42. LOSS OF PROMOTER METHYLATION IN GLYCOLYTIC GENES IS ASSOCIATED WITH AGGRESSIVENESS IN IDH1-MUTANT LOWER GRADE GLIOMAS. Neuro-Oncology, 2018, 20, vi41-vi42.	1.2	0
49	Combined epigenetic signature and gene copy number variations in IDH-mutant glioblastomas showed varied risk stratification. Neuro-Oncology, 2019, 21, iv2-iv2.	1.2	0
50	Detection of Glioma and Prognostic Subtypes by Noninvasive Circulating Cell-Free DNA Methylation Markers. Neurosurgery, 2019, 66, 310-630.	1.1	0
51	Candidate Regulatory Elements in Coding and Noncoding Regions are Associated With Invasive Behavior in Pituitary Tumors. Neurosurgery, 2019, 66, .	1.1	0
52	GENE-24. DNA METHYLATION SIGNATURES DETECTED IN A SERUM-BASED LIQUID BIOPSY DISTINGUISH FUNCTIONAL AND INVASIVENESS FEATURES IN PITUITARY ADENOMAS. Neuro-Oncology, 2019, 21, vi102-vi102.	1.2	0
53	GENE-58. ACTIVE TRANSCRIPTION START SITES OF MENINGIOMA SAMPLES ASSOCIATED WITH RISK OF RECURRENCE. Neuro-Oncology, 2019, 21, vi110-vi110.	1.2	0
54	Abstract LB-004: Molecular hallmarks of cancer: Stemness. , 2017, , .		0

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55	Distinct Epigenetic Shift in a Subset of Glioma CpG Island Methylator Phenotype (G-CIMP) During Tumor Recurrence. SSRN Electronic Journal, 0, , .	0.4	0
56	IDO1 expression in glioma molecular subtypes.. Journal of Clinical Oncology, 2018, 36, e14029-e14029.	1.6	0
57	OR24-5 Aberrant DNA Methylation in Regulatory Genomic Elements Are Associated with Invasive Behavior of Pituitary Macroadenomas: An Integrative Analysis of Epigenome-Wide Studies. Journal of the Endocrine Society, 2019, 3, .	0.2	0
58	Abstract 1939: Non-invasive prediction of glioma tumor stemness using multimodal MRI. , 2019, , .		0
59	Abstract 1640: Deep learning classification of neuro-oncology medical documents. , 2019, , .		0
60	Abstract LB-234: Pre-surgical identification of diagnostic, prognostic and predictive DNA methylation-based markers in serum (liquid biopsy) of patients harboring gliomas. , 2019, , .		0
61	Abstract A11: Serum cell-free DNA methylome-based signatures distinguish pituitary tumor from other neoplasias and by clinicopathologic features. , 2020, , .		0
62	Abstract A10: Glioma cell-free DNA methylation marker for diagnosis and monitoring. , 2020, , .		0
63	Abstract 841: Meningioma subgroups associated with functional genomic elements defined by DNA methylation. , 2019, , .		0