# Tathiane M Malta

List of Publications by Year
in descending order



| 63 | 12,898 | 393982 19 | 360668 35 |
|---|---|---|---|
| papers | citations | h-index | g-index |

| 72 | 72 | 72 | 20016 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14. | 6.6 | 3,706 |
| 2 | TCGAbiolinks: an R/Bioconductor package for integrative analysis of TCGA data. Nucleic Acids Research, 2016, 44, e71-e71. | 6.5 | 2,519 |
| 3 | Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6. | 13.5 | 1,718 |
| 4 | Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell, 2016, 164, 550-563. | 13.5 | 1,695 |
| 5 | Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15. | 13.5 | 1,417 |
| 6 | Longitudinal molecular trajectories of diffuse glioma in adults. Nature, 2019, 576, 112-120. | 13.7 | 320 |
| 7 | Glioma CpG island methylator phenotype (G-CIMP): biological and clinical implications. Neuro-Oncology, 2018, 20, 608-620. | 0.6 | 194 |
| 8 | DNA methylation profiling to predict recurrence risk in meningioma: development and validation of a nomogram to optimize clinical management. Neuro-Oncology, 2019, 21, 901-910. | 0.6 | 184 |
| 9 | A global metagenomic map of urban microbiomes and antimicrobial resistance. Cell, 2021, 184, 3376-3393.e17. | 13.5 | 164 |
| 10 | A Distinct DNA Methylation Shift in a Subset of Glioma CpG Island Methylator Phenotypes during Tumor Recurrence. Cell Reports, 2018, 23, 637-651. | 2.9 | 137 |
| 11 | Patient-derived organoids and orthotopic xenografts of primary and recurrent gliomas represent relevant patient avatars for precision oncology. Acta Neuropathologica, 2020, 140, 919-949. | 3.9 | 72 |
| 12 | A serum-based DNA methylation assay provides accurate detection of glioma. Neuro-Oncology, 2021, 23, 1494-1508. | 0.6 | 53 |
| 13 | Mutated CEACAMs Disrupt Transforming Growth Factor Beta Signaling and Alter the Intestinal Microbiome to Promote Colorectal Carcinogenesis. Gastroenterology, 2020, 158, 238-252. | 0.6 | 46 |
| 14 | Cultured Human Adipose Tissue Pericytes and Mesenchymal Stromal Cells Display a Very Similar Gene Expression Profile. Stem Cells and Development, 2015, 24, 2822-2840. | 1.1 | 44 |
| 15 | HTLV-1/2 seroprevalence and coinfection rate in Brazilian first-time blood donors: an 11-year follow-up. Revista Do Instituto De Medicina Tropical De Sao Paulo, 2012, 54, 123-130. | 0.5 | 35 |
| 16 | Metabolic reprogramming associated with aggressiveness occurs in the G-CIMP-high molecular subtypes of IDH1mut lower grade gliomas. Neuro-Oncology, 2020, 22, 480-492. | 0.6 | 31 |
| 17 | Predicting master transcription factors from pan-cancer expression data. Science Advances, 2021, 7, eabf6123. | 4.7 | 30 |
| 18 | Transcriptomic comparisons between cultured human adipose tissue-derived pericytes and mesenchymal stromal cells. Genomics Data, 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. Neuro-Oncology Advances, 2019, 1, vdz015. | 0.4 | 22 |
| 20 | Generation of induced pluripotent stem cells from large domestic animals. Stem Cell Research and Therapy, 2020, 11, 247. | 2.4 | 21 |
| 21 | Molecular landscape of IDH-mutant primary astrocytoma Grade IV/glioblastomas. Modern Pathology, 2021, 34, 1245-1260. | 2.9 | 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. AIDS Research and Human Retroviruses, 2014, 30, 610-622. | 0.5 | 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. Experimental Cell Research, 2016, 349, 239-254. | 1.2 | 19 |
| 24 | Targeting the E3 Ubiquitin Ligase PJA1 Enhances Tumor-Suppressing TGFÎ² Signaling. Cancer Research, 2020, 80, 1819-1832. | 0.4 | 17 |
| 25 | TCGAbiolinksGUI: A graphical user interface to analyze cancer molecular and clinical data. F1000Research, 0, 7, 439. | 0.8 | 14 |
| 26 | Short Communication Forced expression of OCT4 influences the expression of pluripotent genes in human mesenchymal stem cells and fibroblasts. Genetics and Molecular Research, 2013, 12, 1054-1060. | 0.3 | 13 |
| 27 | Leukotrienes Are Upregulated and Associated with Human T-Lymphotropic Virus Type 1 (HTLV-1)-Associated Neuroinflammatory Disease. PLoS ONE, 2012, 7, e51873. | 1.1 | 10 |
| 28 | Detection of tumor-specific DNA methylation markers in the blood of patients with pituitary neuroendocrine tumors. Neuro-Oncology, 2022, 24, 1126-1139. | 0.6 | 9 |
| 29 | Molecular landscape of <scp>IDH</scp>â€wild type, <scp>pTERT</scp>â€wild type adult glioblastomas. Brain Pathology, 2022, 32, . | 2.1 | 9 |
| 30 | Functional and bioinformatics analyses reveal conservation of cisâ€regulatory elements between sciaridae and drosophilidae. Genesis, 2008, 46, 43-51. | 0.8 | 6 |
| 31 | T cell receptor signaling pathway is overexpressed in CD4+ T cells from HAM/TSP individuals. Brazilian Journal of Infectious Diseases, 2015, 19, 578-584. | 0.3 | 6 |
| 32 | DNA methylation-based signatures classify sporadic pituitary tumors according to clinicopathological features. Neuro-Oncology, 2021, 23, 1292-1303. | 0.6 | 6 |
| 33 | Altered Expression of Degranulation-Related Genes in CD8+T Cells in Human T Lymphotropic Virus Type I Infection. AIDS Research and Human Retroviruses, 2013, 29, 826-836. | 0.5 | 4 |
| 34 | Genes related to antiviral activity are differentially expressed in CD4+ T cell in HAM/TSP patients. Retrovirology, 2014, 11, . | 0.9 | 1 |
| 35 | GENE-61. METHYLATION-BASED LIQUID BIOPSY OF MENINGIOMA PRIMARY AND RECURRENT SAMPLES. Neuro-Oncology, 2019, 21, vi111-vi111. | 0.6 | 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. | 0.4 | 0 |
| 38 | Novel polymorphisms in the promoter region of the perforin gene among distinct <scp>B</scp>razilian populations and their functional impact. International Journal of Immunogenetics, 2014, 41, 198-205. | 0.8 | 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. | 0.6 | 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. | 0.6 | 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. | 0.6 | 0 |
| 42 | GENT-33. EPIGENETIC ALTERATIONS AT INTERGENIC REGIONS ASSOCIATED WITH PROGRESSION IN AÂSUBSET OF IDH MUTANT GLIOMAS. Neuro-Oncology, 2016, 18, vi81-vi81. | 0.6 | 0 |
| 43 | GENT-34. EPIGENOMIC STEMNESS SIGNATURE ASSOCIATED WITH GLIOMA MOLECULAR SUBTYPES. Neuro-Oncology, 2016, 18, vi81-vi81. | 0.6 | 0 |
| 44 | IMMU-60. PD-L1 EXPRESSION ASSOCIATED WITH GLIOMA MOLECULAR SUBTYPES: CLINICAL IMPLICATIONS. Neuro-Oncology, 2017, 19, vi126-vi126. | 0.6 | 0 |
| 45 | GENE-52. EPIGENOMIC GLIOMA SUBTYPE EVALUATION ACROSS 31 TUMOR TYPES. Neuro-Oncology, 2017, 19, vi103-vi104. | 0.6 | 0 |
| 46 | GENE-09. FUNCTIONAL GENOMIC ELEMENTS DEFINED BY DNA METHYLATION CAN DISTINGUISH MENINGIOMA SUBGROUPS. Neuro-Oncology, 2018, 20, vi104-vi104. | 0.6 | 0 |
| 47 | GENE-07. GENOMIC ENHANCER METHYLATION IS ASSOCIATED WITH BIOLOGICAL AND CLINICAL FEATURES IN PITUITARY TUMORS. Neuro-Oncology, 2018, 20, vi104-vi104. | 0.6 | 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. | 0.6 | 0 |
| 49 | Combined epigenetic signature and gene copy number variations in IDH-mutant glioblastomas showed varied risk stratification. Neuro-Oncology, 2019, 21, iv2-iv2. | 0.6 | 0 |
| 50 | Detection of Glioma and Prognostic Subtypes by Noninvasive Circulating Cell-Free DNA Methylation Markers. Neurosurgery, 2019, 66, 310-630. | 0.6 | 0 |
| 51 | Candidate Regulatory Elements in Coding and Noncoding Regions are Associated With Invasive Behavior in Pituitary Tumors. Neurosurgery, 2019, 66, . | 0.6 | 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. | 0.6 | 0 |
| 53 | GENE-58. ACTIVE TRANSCRIPTION START SITES OF MENINGIOMA SAMPLES ASSOCIATED WITH RISK OF RECURRENCE. Neuro-Oncology, 2019, 21, vi110-vi110. | 0.6 | 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. | 0.8 | 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, . | 0.1 | 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 |