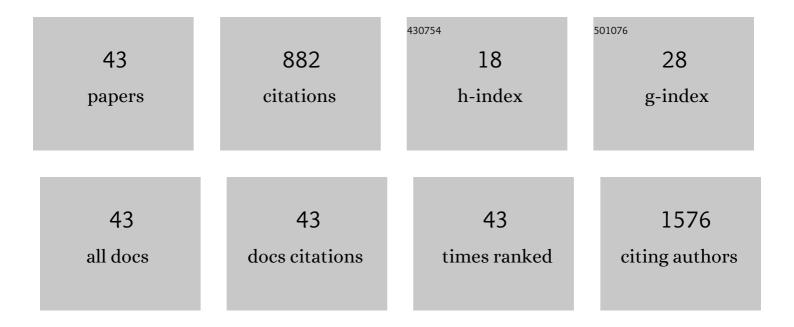
Mateus C Barros-Filho

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9045134/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Characterization of BRAF mutation in patients older than 45 years with well-differentiated thyroid carcinoma. Brazilian Journal of Otorhinolaryngology, 2022, 88, 523-528.	0.4	4
2	Genetic and Epigenetic Mechanisms Deregulate the CRL2pVHL Complex in Hepatocellular Carcinoma. Frontiers in Genetics, 2022, 13, .	1.1	1
3	Circulating let-7e-5p, miR-106a-5p, miR-28-3p, and miR-542-5p as a Promising microRNA Signature for the Detection of Colorectal Cancer. Cancers, 2021, 13, 1493.	1.7	29
4	Reactivation of Multiple Fetal miRNAs in Lung Adenocarcinoma. Cancers, 2021, 13, 2686.	1.7	0
5	Multi-analytical test based on serum miRNAs and proteins quantification for ovarian cancer early detection. PLoS ONE, 2021, 16, e0255804.	1.1	11
6	miR-22 and miR-205 Drive Tumor Aggressiveness of Mucoepidermoid Carcinomas of Salivary Glands. Frontiers in Oncology, 2021, 11, 786150.	1.3	6
7	Circulating mRNA signature as a marker for high-risk prostate cancer. Carcinogenesis, 2020, 41, 139-145.	1.3	12
8	Comprehensive Analysis of DNA Methylation and Prediction of Response to NeoadjuvantTherapy in Locally Advanced Rectal Cancer. Cancers, 2020, 12, 3079.	1.7	13
9	GADD45B Transcript Is a Prognostic Marker in Papillary Thyroid Carcinoma Patients Treated With Total Thyroidectomy and Radioiodine Therapy. Frontiers in Endocrinology, 2020, 11, 269.	1.5	15
10	Janus or Hydra: The Many Faces of T Helper Cells in the Human Tumour Microenvironment. Advances in Experimental Medicine and Biology, 2020, 1224, 35-51.	0.8	10
11	DNA Methylation-Based Method to Differentiate Malignant from Benign Thyroid Lesions. Thyroid, 2019, 29, 1244-1254.	2.4	19
12	Locally advanced rectal cancer transcriptomic-based secretome analysis reveals novel biomarkers useful to identify patients according to neoadjuvant chemoradiotherapy response. Scientific Reports, 2019, 9, 8702.	1.6	14
13	Integrated miRNA and mRNA expression analysis uncovers drug targets in laryngeal squamous cell carcinoma patients. Oral Oncology, 2019, 93, 76-84.	0.8	25
14	PFKFB2 Promoter Hypomethylation as Recurrence Predictive Marker in Well-Differentiated Thyroid Carcinomas. International Journal of Molecular Sciences, 2019, 20, 1334.	1.8	15
15	Previously undescribed thyroid-specific miRNA sequences in papillary thyroid carcinoma. Journal of Human Genetics, 2019, 64, 505-508.	1.1	13
16	Small Noncoding RNA Expression in Cancer. , 2019, , .		1
17	Upgrading the Repertoire of miRNAs in Gastric Adenocarcinoma to Provide a New Resource for Biomarker Discovery. International Journal of Molecular Sciences, 2019, 20, 5697.	1.8	6
18	Expanding the Transcriptome of Head and Neck Squamous Cell Carcinoma Through Novel MicroRNA Discovery. Frontiers in Oncology, 2019, 9, 1305.	1.3	15

#	Article	IF	CITATIONS
19	Loss of DNA methylation is related to increased expression of miR-21 and miR-146b in papillary thyroid carcinoma. Clinical Epigenetics, 2018, 10, 144.	1.8	27
20	Downregulation of <scp>AGR</scp> 2, p21, and cyclin D and alterations in p53 function were associated with tumor progression and chemotherapy resistance in epithelial ovarian carcinoma. Cancer Medicine, 2018, 7, 3188-3199.	1.3	16
21	Nuclear loss and cytoplasmic expression of androgen receptor in penile carcinomas: role as a driver event and as a prognosis factor. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2018, 473, 607-614.	1.4	7
22	MicroRNAs involved in the <i>HMGA2</i> deregulation and its co-occurrence with <i>MED12</i> mutation in uterine leiomyoma. Molecular Human Reproduction, 2018, 24, 556-563.	1.3	14
23	Oncogenic drivers in 11q13 associated with prognosis and response to therapy in advanced oropharyngeal carcinomas. Oral Oncology, 2018, 83, 81-90.	0.8	20
24	Integrated data analysis reveals potential drivers and pathways disrupted by DNA methylation in papillary thyroid carcinomas. Clinical Epigenetics, 2017, 9, 45.	1.8	68
25	Multidimensional integrative analysis uncovers driver candidates and biomarkers in penile carcinoma. Scientific Reports, 2017, 7, 6707.	1.6	35
26	Prognostic Classifier Based on Genome-Wide DNA Methylation Profiling in Well-Differentiated Thyroid Tumors. Journal of Clinical Endocrinology and Metabolism, 2017, 102, 4089-4099.	1.8	45
27	Circulating mRNAs and miRNAs as candidate markers for the diagnosis and prognosis of prostate cancer. PLoS ONE, 2017, 12, e0184094.	1.1	95
28	Oestrogen receptor beta isoform expression in sporadic colorectal cancer, familial adenomatous polyposis and progressive stages of colorectal cancer. BMC Cancer, 2017, 17, 754.	1.1	7
29	Integrative miRNA and mRNA analysis in penile carcinomas reveals markers and pathways with potential clinical impact. Oncotarget, 2017, 8, 15294-15306.	0.8	39
30	<i>PHF21B</i> as a candidate tumor suppressor gene in head and neck squamous cell carcinomas. Molecular Oncology, 2015, 9, 450-462.	2.1	18
31	Genome-wide methylation and transcriptome analysis in penile carcinoma: uncovering new molecular markers. Clinical Epigenetics, 2015, 7, 46.	1.8	48
32	High Diagnostic Accuracy Based on <i>CLDN10</i> , <i>HMGA2</i> , and <i>LAMB3</i> Transcripts in Papillary Thyroid Carcinoma. Journal of Clinical Endocrinology and Metabolism, 2015, 100, E890-E899.	1.8	49
33	Down-Regulation of <i>SLC8A1</i> as a Putative Apoptosis Evasion Mechanism by Modulation of Calcium Levels in Penile Carcinoma. Journal of Urology, 2015, 194, 245-251.	0.2	36
34	Abstract 3828: Genomic, transcriptome and epigenomic analysis reveal new genetic pathways in penile carcinoma. , 2015, , .		0
35	Abstract 3829: DNA methylation profile in papillary thyroid cancer according to BRAF (V600E) mutation. , 2015, , .		0
36	Effect of <scp>UGT1A1</scp> , <scp>UGT1A3</scp> , <scp>DIO1</scp> and <scp>DIO2</scp> polymorphisms on <scp>L</scp> â€thyroxine doses required for <scp>TSH</scp> suppression in patients with differentiated thyroid cancer. British Journal of Clinical Pharmacology, 2014, 78, 1067-1075.	1.1	26

MATEUS C BARROS-FILHO

#	Article	IF	CITATIONS
37	Gene Expression Profiling in Leiomyosarcomas and Undifferentiated Pleomorphic Sarcomas: SRC as a New Diagnostic Marker. PLoS ONE, 2014, 9, e102281.	1.1	28
38	Abstract 2242: Comprehensive genome methylation and whole genome expression analysis in penile carcinoma: Uncovering new molecular markers. , 2014, , .		0
39	Genomic Signatures Predict Poor Outcome in Undifferentiated Pleomorphic Sarcomas and Leiomyosarcomas. PLoS ONE, 2013, 8, e67643.	1.1	24
40	An Integrative Genomic and Transcriptomic Analysis Reveals Potential Targets Associated with Cell Proliferation in Uterine Leiomyomas. PLoS ONE, 2013, 8, e57901.	1.1	22
41	Cene trio signatures as molecular markers to predict response to doxorubicin cyclophosphamide neoadjuvant chemotherapy in breast cancerpatients. Brazilian Journal of Medical and Biological Research, 2010, 43, 1225-1231.	0.7	19
42	Gene expression profile of residual breast cancer after doxorubicin and cyclophosphamide neoadjuvant chemotherapy. Oncology Reports, 2009, 22, 805-13.	1.2	29
43	Tumour Suppressor Genes with Oncogenic Roles in Lung Cancer. , 0, , .		1