Elisa N Ferreira

List of Publications by Year
in descending order

29	636	758635 12	580395 25
papers	citations	h-index	g-index

29	29	29	1530
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Mutational Portrait of Lung Adenocarcinoma in Brazilian Patients: Past, Present, and Future of Molecular Profiling in the Clinic. Frontiers in Oncology, 2020, 10, 1068.	1.3	11
2	A comparison between SOLiD 5500XLand Ion Torrent PGM-derived miRNA expression profiles in two breast cell lines. Genetics and Molecular Biology, 2020, 43, e20180351.	0.6	1
3	Influence of BRCA1 Germline Mutations in the Somatic Mutational Burden of Triple-Negative Breast Cancer. Translational Oncology, 2019, 12, 1453-1460.	1.7	6
4	Effects of tumor biobank storage on polysome stability. Applied Cancer Research, 2019, 39, .	1.0	1
5	A transcriptome-based signature of pathological angiogenesis predicts breast cancer patient survival. PLoS Genetics, 2019, 15, e1008482.	1.5	12
6	Contribution of the GSTP1 c.313A>G variant to hearing loss risk in patients exposed to platin chemotherapy during childhood. Clinical and Translational Oncology, 2019, 21, 630-635.	1.2	14
7	BRCA1 deficiency is a recurrent event in early-onset triple-negative breast cancer: a comprehensive analysis of germline mutations and somatic promoter methylation. Breast Cancer Research and Treatment, 2018, 167, 803-814.	1.1	36
8	Complex Landscape of Germline Variants in Brazilian Patients With Hereditary and Early Onset Breast Cancer. Frontiers in Genetics, 2018, 9, 161.	1.1	21
9	Case report: Chondrosarcoma of the head and neck. Human Pathology: Case Reports, 2017, 7, 4-7.	0.2	7
10	A genomic case study of desmoplastic small round cell tumor: comprehensive analysis reveals insights into potential therapeutic targets and development of a monitoring tool for a rare and aggressive disease. Human Genomics, 2016, 10, 36.	1.4	28
11	Genomic imbalances pinpoint potential oncogenes and tumor suppressors in Wilms tumors. Molecular Cytogenetics, 2016, 9, 20.	0.4	36
12	Epithelial cells captured from ductal carcinoma in situ reveal a gene expression signature associated with progression to invasive breast cancer. Oncotarget, 2016, 7, 75672-75684.	0.8	5
13	Abstract A32: Urine as a potential liquid biopsy for detecting tumor DNA in Wilms tumor patient: Detection of somatic mutations in urine opens perspectives of monitoring chemotherapy response in WT patients. , 2016, , .		0
14	Linear mRNA amplification approach for RNAseq from limited amount of RNA. Gene, 2015, 564, 220-227.	1.0	2
15	Intratumoral heterogeneity of ADAM23 promotes tumor growth and metastasis through LGI4 and nitric oxide signals. Oncogene, 2015, 34, 1270-1279.	2.6	20
16	Gene expression patterns through oral squamous cell carcinoma development: PD-L1 expression in primary tumor and circulating tumor cells. Oncotarget, 2015, 6, 20902-20920.	0.8	96
17	Upregulated genes at 2q24 gains as candidate oncogenes in hepatoblastomas. Future Oncology, 2014, 10, 2449-2457.	1.1	29
18	Recurrent somatic mutation in DROSHA induces microRNA profile changes in Wilms tumour. Nature Communications, 2014, 5, 4039.	5.8	159

#	Article	IF	Citations
19	Abstract 452: Comprehensive gene expression analysis identifies molecular markers involved with the progression of ductal carcinoma in situ of the breast. , 2014, , .		0
20	TGIF1 splicing variant 8 is overexpressed in oral squamous cell carcinoma and is related to pathologic and clinical behavior. Oral Surgery, Oral Medicine, Oral Pathology and Oral Radiology, 2013, 116, 614-625.	0.2	14
21	Down-regulation of ANAPC13 and CLTCL1: Early Events in the Progression of Preinvasive Ductal Carcinoma of the Breast. Translational Oncology, 2012, 5, 113-IN8.	1.7	13
22	Poly (A)+ Transcriptome Assessment of ERBB2-Induced Alterations in Breast Cell Lines. PLoS ONE, 2011, 6, e21022.	1.1	17
23	Alternative splicing enriched cDNA libraries identify breast cancer-associated transcripts. BMC Genomics, 2010, 11, S4.	1.2	10
24	Evaluation of Quantitative RT-PCR Using Nonamplified and Amplified RNA. Diagnostic Molecular Pathology, 2010, 19, 45-53.	2.1	9
25	Reciprocal changes in gene expression profiles of cocultured breast epithelial cells and primary fibroblasts. International Journal of Cancer, 2009, 125, 2767-2777.	2.3	52
26	Heteroduplex formation and S1 digestion for mapping alternative splicing sites. Genetics and Molecular Research, 2008, 7, 958-969.	0.3	2
27	Alternative splicing: a bioinformatics perspective. Molecular BioSystems, 2007, 3, 473.	2.9	13
28	A Transcript Finishing Initiative for Closing Gaps in the Human Transcriptome. Genome Research, 2004, 14, 1413-1423.	2.4	22
29	Identification and complete sequencing of novel human transcripts through the use of mouse orthologs and testis cDNA sequences. Genetics and Molecular Research, 2004, 3, 493-511.	0.3	0