Dirce Maria Carraro

List of Publications by Year
in descending order

163	6,187	87888 38	85541 71
papers	citations	h-index	g-index

166	166	166	10093
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The genome sequence of the plant pathogen Xylella fastidiosa. Nature, 2000, 406, 151-157.	27.8	827
2	Comparative Analyses of the Complete Genome Sequences of Pierce's Disease and Citrus Variegated Chlorosis Strains of Xylella fastidiosa. Journal of Bacteriology, 2003, 185, 1018-1026.	2.2	307
3	Swine and Poultry Pathogens: the Complete Genome Sequences of Two Strains ofMycoplasma hyopneumoniaeand a Strain ofMycoplasma synoviae. Journal of Bacteriology, 2005, 187, 5568-5577.	2.2	289
4	Analysis and Functional Annotation of an Expressed Sequence Tag Collection for Tropical Crop Sugarcane. Genome Research, 2003, 13, 2725-2735.	5.5	254
5	PRUNE2 is a human prostate cancer suppressor regulated by the intronic long noncoding RNA PCA3. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 8403-8408.	7.1	226
6	Gene Expression Profile Associated with Response to Doxorubicin-Based Therapy in Breast Cancer. Clinical Cancer Research, 2005, 11, 7434-7443.	7.0	168
7	Recurrent somatic mutation in DROSHA induces microRNA profile changes in Wilms tumour. Nature Communications, 2014, 5, 4039.	12.8	159
8	The contribution of 700,000 ORF sequence tags to the definition of the human transcriptome. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 12103-12108.	7.1	123
9	Evidence that molecular changes in cells occur before morphological alterations during the progression of breast ductal carcinoma. Breast Cancer Research, 2008, 10, R87.	5.0	122
10	A genome survey of Moniliophthora perniciosa gives new insights into Witches' Broom Disease of cacao. BMC Genomics, 2008, 9, 548.	2.8	120
11	The Genome Sequence of the Gram-Positive Sugarcane Pathogen Leifsonia xyli subsp. xyli. Molecular Plant-Microbe Interactions, 2004, 17, 827-836.	2.6	119
12	The generation and utilization of a cancer-oriented representation of the human transcriptome by using expressed sequence tags. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 13418-13423.	7.1	105
13	Gene expression patterns through oral squamous cell carcinoma development: PD-L1 expression in primary tumor and circulating tumor cells. Oncotarget, 2015, 6, 20902-20920.	1.8	96
14	The mitochondrial genome of the phytopathogenic basidiomycete Moniliophthora perniciosa is 109kb in size and contains a stable integrated plasmid. Mycological Research, 2008, 112, 1136-1152.	2.5	87
15	Amyloid-Î² Oligomers Induce Differential Gene Expression in Adult Human Brain Slices. Journal of Biological Chemistry, 2012, 287, 7436-7445.	3.4	80
16	Repair of Oxidative DNA Damage, Cell-Cycle Regulation and Neuronal Death May Influence the Clinical Manifestation of Alzheimerâ€™s Disease. PLoS ONE, 2014, 9, e99897.	2.5	78
17	Structural features and transcript-editing analysis of sugarcane (Saccharum officinarum L.) chloroplast genome. Current Genetics, 2004, 46, 366-373.	1.7	76
18	Germline DNA copy number variation in familial and early-onset breast cancer. Breast Cancer Research, 2012, 14, R24.	5.0	76

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19	Gene expression arrays in cancer research: methods and applications. Critical Reviews in Oncology/Hematology, 2005, 54, 95-105.	4.4	72
20	Identification of human chromosome 22 transcribed sequences with ORF expressed sequence tags. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 12690-12693.	7.1	70
21	Epigenetic Silencing of CRABP2 and MX1 in Head and Neck Tumors. Neoplasia, 2009, 11, 1329-IN9.	5.3	70
22	Comprehensive Analysis of BRCA1, BRCA2 and TP53 Germline Mutation and Tumor Characterization: A Portrait of Early-Onset Breast Cancer in Brazil. PLoS ONE, 2013, 8, e57581.	2.5	70
23	Identification of Astyanax altiparanae (Teleostei, Characidae) in the IguaÃ§u River, Brazil, based on mitochondrial DNA and RAPD markers. Genetics and Molecular Biology, 2002, 25, 421-430.	1.3	61
24	The germline mutational landscape of BRCA1 and BRCA2 in Brazil. Scientific Reports, 2018, 8, 9188.	3.3	61
25	Innate immune response is differentially dysregulated between bipolar disease and schizophrenia. Schizophrenia Research, 2015, 161, 215-221.	2.0	58
26	Hereditary breast and ovarian cancer: assessment of point mutations and copy number variations in Brazilian patients. BMC Medical Genetics, 2014, 15, 55.	2.1	57
27	Mismatch repair genes in Lynch syndrome: a review. Sao Paulo Medical Journal, 2009, 127, 46-51.	0.9	56
28	Polybromoâ€1 (<scp>PBRM</scp>1), a <scp>SWI</scp>/<scp>SNF</scp> complex subunit is a prognostic marker in clear cell renal cell carcinoma. BJU International, 2014, 113, E157-63.	2.5	54
29	Reciprocal changes in gene expression profiles of cocultured breast epithelial cells and primary fibroblasts. International Journal of Cancer, 2009, 125, 2767-2777.	5.1	52
30	Biobanking Practice: RNA Storage at Low Concentration Affects Integrity. Biopreservation and Biobanking, 2014, 12, 46-52.	1.0	52
31	TWIST1 is a molecular marker for a poor prognosis in oral cancer and represents a potential therapeutic target. Cancer, 2014, 120, 352-362.	4.1	52
32	Clinicopathological significance of ubiquitin-specific protease 2a (USP2a), fatty acid synthase (FASN), and ErbB2 expression in oral squamous cell carcinomas. Oral Oncology, 2009, 45, e134-e139.	1.5	51
33	Differential Gene Expression Between the Biotrophic-Like and Saprotrophic Mycelia of the Witches' Broom Pathogen Moniliophthora perniciosa. Molecular Plant-Microbe Interactions, 2008, 21, 891-908.	2.6	50
34	Germline mutations in BRCA1 and BRCA2 in epithelial ovarian cancer patients in Brazil. BMC Cancer, 2016, 16, 934.	2.6	50
35	Expression of putative pathogenicity-related genes inXylella fastidiosagrown at low and high cell density conditions in vitro. FEMS Microbiology Letters, 2003, 222, 83-92.	1.8	49
36	Co-expression network of neural-differentiation genes shows specific pattern in schizophrenia. BMC Medical Genomics, 2015, 8, 23.	1.5	45

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37	Ductal carcinoma in situ of the breast: morphological and molecular features implicated in progression. Bioscience Reports, 2014, 34, .	2.4	43
38	Phosphodiesterase 11A (PDE11A) Genetic Variants May Increase Susceptibility to Prostatic Cancer. Journal of Clinical Endocrinology and Metabolism, 2011, 96, E135-E140.	3.6	41
39	Transcriptional Alterations Related to Neuropathology and Clinical Manifestation of Alzheimerâ€™s Disease. PLoS ONE, 2012, 7, e48751.	2.5	39
40	Infections with multiple highâ€risk HPV types are associated with highâ€grade and persistent lowâ€grade intraepithelial lesions of the cervix. Cancer Cytopathology, 2017, 125, 138-143.	2.4	38
41	Genomic imbalances pinpoint potential oncogenes and tumor suppressors in Wilms tumors. Molecular Cytogenetics, 2016, 9, 20.	0.9	36
42	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.	2.5	36
43	Mutational spectrum of the APC and MUTYH genes and genotypeâ€“phenotype correlations in Brazilian FAP, AFAP, and MAP patients. Orphanet Journal of Rare Diseases, 2013, 8, 54.	2.7	35
44	Deep Learning Predicts Underlying Features on Pathology Images with Therapeutic Relevance for Breast and Gastric Cancer. Cancers, 2020, 12, 3687.	3.7	34
45	Molecular Profiling of Isolated Histological Components of Wilms Tumor Implicates a Common Role for the Wnt Signaling Pathway in Kidney and Tumor Development. Oncology, 2008, 75, 81-91.	1.9	33
46	Germline variants in DNA repair genes associated with hereditary breast and ovarian cancer syndrome: analysis of a 21 gene panel in the Brazilian population. BMC Medical Genomics, 2020, 13, 21.	1.5	32
47	DNA methylation landscape of hepatoblastomas reveals arrest at early stages of liver differentiation and cancer-related alterations. Oncotarget, 2017, 8, 97871-97889.	1.8	32
48	Gene stage-specific expression in the microenvironment of pediatric myelodysplastic syndromes. Leukemia Research, 2007, 31, 579-589.	0.8	31
49	Multiple mutations in the Kras gene in colorectal cancer: review of the literature with two case reports. International Journal of Colorectal Disease, 2011, 26, 1241-1248.	2.2	31
50	Characterization of individuals at high risk of developing melanoma in Latin America: bases for genetic counseling in melanoma. Genetics in Medicine, 2016, 18, 727-736.	2.4	31
51	The Value of a Tumor Bank in the Development of Cancer Research in Brazil: 13 Years of Experience at the A C Camargo Hospital. Biopreservation and Biobanking, 2012, 10, 168-173.	1.0	30
52	Enhanced type I interferon gene signature in primary antiphospholipid syndrome: Association with earlier disease onset and preeclampsia. Autoimmunity Reviews, 2019, 18, 393-398.	5.8	30
53	Gene expression profile of residual breast cancer after doxorubicin and cyclophosphamide neoadjuvant chemotherapy. Oncology Reports, 2009, 22, 805-13.	2.6	29
54	Transcriptional profile of fibroblasts obtained from the primary site, lymph node and bone marrow of breast cancer patients. Genetics and Molecular Biology, 2014, 37, 480-489.	1.3	29

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55	Upregulated genes at 2q24 gains as candidate oncogenes in hepatoblastomas. Future Oncology, 2014, 10, 2449-2457.	2.4	29
56	Gene expression analysis of blastemal component reveals genes associated with relapse mechanism in Wilms tumour. European Journal of Cancer, 2011, 47, 2715-2722.	2.8	28
57	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.	2.9	28
58	International distribution and age estimation of the Portuguese BRCA2 c.156_157insAlu founder mutation. Breast Cancer Research and Treatment, 2011, 127, 671-679.	2.5	27
59	Early Gene Expression Changes in Skeletal Muscle from SOD1G93A Amyotrophic Lateral Sclerosis Animal Model. Cellular and Molecular Neurobiology, 2014, 34, 451-462.	3.3	27
60	Mutation spectrum in South American Lynch syndrome families. Hereditary Cancer in Clinical Practice, 2013, 11, 18.	1.5	26
61	Characterization of germline mutations of MLH1 and MSH2 in unrelated south American suspected Lynch syndrome individuals. Familial Cancer, 2011, 10, 641-647.	1.9	25
62	Li-Fraumeni-like syndrome associated with a large BRCA1 intragenic deletion. BMC Cancer, 2012, 12, 237.	2.6	25
63	Clinical and Molecular Characterization of Brazilian Patients Suspected to Have Lynch Syndrome. PLoS ONE, 2015, 10, e0139753.	2.5	25
64	Temporal blastemal cell gene expression analysis in the kidney reveals new Wnt and related signaling pathway genes to be essential for Wilms' tumor onset. Cell Death and Disease, 2011, 2, e224-e224.	6.3	23
65	A Transcript Finishing Initiative for Closing Gaps in the Human Transcriptome. Genome Research, 2004, 14, 1413-1423.	5.5	22
66	Gene expression profiling of clinical stages II and III breast cancer. Brazilian Journal of Medical and Biological Research, 2006, 39, 1101-1113.	1.5	22
67	Influence of the interaction between nodal fibroblast and breast cancer cells on gene expression. Tumor Biology, 2011, 32, 145-157.	1.8	21
68	A clinical, pathologic, and molecular study of p53 and murine double minute 2 in penile carcinogenesis and its relation to prognosis. Human Pathology, 2012, 43, 481-488.	2.0	21
69	Tissue hyaluronan expression, as reflected in the sputum of lung cancer patients, is an indicator of malignancy. Brazilian Journal of Medical and Biological Research, 2015, 48, 557-567.	1.5	21
70	Lymphovascular invasion and histologic grade are associated with specific genomic profiles in invasive carcinomas of the breast. Tumor Biology, 2015, 36, 1835-1848.	1.8	21
71	Mutational Profile and New IASLC/ATS/ERS Classification Provide Additional Prognostic Information about Lung Adenocarcinoma: A Study of 125 Patients from Brazil. Oncology, 2015, 89, 175-186.	1.9	21
72	Contribution of rare germline copy number variations and common susceptibility loci in Lynch syndrome patients negative for mutations in the mismatch repair genes. International Journal of Cancer, 2016, 138, 1928-1935.	5.1	21

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73	DNA repair genes PAXIP1 and TP53BP1 expression is associated with breast cancer prognosis. Cancer Biology and Therapy, 2017, 18, 439-449.	3.4	21
74	Complex Landscape of Germline Variants in Brazilian Patients With Hereditary and Early Onset Breast Cancer. Frontiers in Genetics, 2018, 9, 161.	2.3	21
75	LINE-1 hypermethylation in peripheral blood of cutaneous melanoma patients is associated with metastasis. Melanoma Research, 2015, 25, 173-177.	1.2	20
76	Intratumoral heterogeneity of ADAM23 promotes tumor growth and metastasis through LGI4 and nitric oxide signals. Oncogene, 2015, 34, 1270-1279.	5.9	20
77	Biomolecular analysis of matrix proteoglycans as biomarkers in non small cell lung cancer. Glycoconjugate Journal, 2018, 35, 233-242.	2.7	20
78	RAS mutations vary between lesions in synchronous primary Colorectal Cancer: Testing only one lesion is not sufficient to guide anti-EGFR treatment decisions.. Oncoscience, 2015, 2, 125-130.	2.2	20
79	Breakpoint characterization of a novel large intragenic deletion of MUTYH detected in a MAP patient: Case report. BMC Medical Genetics, 2011, 12, 128.	2.1	18
80	Germline CDKN2A mutations in Brazilian patients of hereditary cutaneous melanoma. Familial Cancer, 2014, 13, 645-649.	1.9	18
81	Poly (A)+ Transcriptome Assessment of ERBB2-Induced Alterations in Breast Cell Lines. PLoS ONE, 2011, 6, e21022.	2.5	17
82	DNA Methylation Levels of Melanoma Risk Genes Are Associated with Clinical Characteristics of Melanoma Patients. BioMed Research International, 2015, 2015, 1-8.	1.9	17
83	Prevalence of BRCA1 and BRCA2 pathogenic and likely pathogenic variants in non-selected ovarian carcinoma patients in Brazil. BMC Cancer, 2019, 19, 4.	2.6	17
84	TET Upregulation Leads to 5-Hydroxymethylation Enrichment in Hepatoblastoma. Frontiers in Genetics, 2019, 10, 553.	2.3	17
85	P53 and Expression of Immunological Markers May Identify Early Stage Thyroid Tumors. Clinical and Developmental Immunology, 2013, 2013, 1-9.	3.3	16
86	Gene expression of peripheral blood lymphocytes may discriminate patients with schizophrenia from controls. Psychiatry Research, 2012, 200, 1018-1021.	3.3	15
87	Hyaluronidase splice variants are associated with histology and outcome in adenocarcinoma and squamous cell carcinoma of the lung. Human Pathology, 2012, 43, 675-683.	2.0	15
88	Mutational status of VHL gene and its clinical importance in renal clear cell carcinoma. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2014, 465, 321-330.	2.8	15
89	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.	0.4	14
90	Epidermal growth factor receptor as an adverse survival predictor in squamous cell carcinoma of the penis. Human Pathology, 2017, 61, 97-104.	2.0	14

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91	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.	2.4	14
92	From colorectal cancer pattern to the characterization of individuals at risk: Picture for genetic research in Latin America. International Journal of Cancer, 2019, 145, 318-326.	5.1	14
93	Clinical and Molecular Assessment of Patients with Lynch Syndrome and Sarcomas Underpinning the Association with MSH2 Germline Pathogenic Variants. Cancers, 2020, 12, 1848.	3.7	14
94	Alternative splicing: a bioinformatics perspective. Molecular BioSystems, 2007, 3, 473.	2.9	13
95	Down-regulation of ANAPC13 and CLTCL1: Early Events in the Progression of Preinvasive Ductal Carcinoma of the Breast. Translational Oncology, 2012, 5, 113-IN8.	3.7	13
96	Phosphodiesterase sequence variants may predispose to prostate cancer. Endocrine-Related Cancer, 2015, 22, 519-530.	3.1	13
97	Association of Folate and Vitamins Involved in the 1-Carbon Cycle with Polymorphisms in the Methylenetetrahydrofolate Reductase Gene (MTHFR) and Global DNA Methylation in Patients with Colorectal Cancer. Nutrients, 2019, 11, 1368.	4.1	13
98	Generation of longer 3' cDNA fragments from massively parallel signature sequencing tags. Nucleic Acids Research, 2004, 32, e94-e94.	14.5	12
99	A novel SYBR-based duplex qPCR for the detection of gene dosage: detection of an APC large deletion in a familial adenomatous polyposis patient with an unusual phenotype. BMC Medical Genetics, 2012, 13, 55.	2.1	12
100	Insights Into the Somatic Mutation Burden of Hepatoblastomas From Brazilian Patients. Frontiers in Oncology, 2020, 10, 556.	2.8	12
101	PCR-Assisted Contig Extension: Stepwise Strategy for Bacterial Genome Closure. BioTechniques, 2003, 34, 626-632.	1.8	11
102	Predictive models for mutations in mismatch repair genes: implication for genetic counseling in developing countries. BMC Cancer, 2012, 12, 64.	2.6	11
103	Estrogen-Responsive Genes Overlap with Triiodothyronine-Responsive Genes in a Breast Carcinoma Cell Line. Scientific World Journal, The, 2014, 2014, 1-7.	2.1	11
104	Pitfalls in genetic testing: a case of a <scp>SNP</scp> in primerâ€annealing region leading to allele dropout in <scp>BRCA</scp>1. Molecular Genetics & Genomic Medicine, 2017, 5, 443-447.	1.2	11
105	Hepatoblastomas exhibit markedNNMTdownregulation driven by promoter DNA hypermethylation. Tumor Biology, 2020, 42, 101042832097712.	1.8	11
106	Mutational Portrait of Lung Adenocarcinoma in Brazilian Patients: Past, Present, and Future of Molecular Profiling in the Clinic. Frontiers in Oncology, 2020, 10, 1068.	2.8	11
107	Alternative splicing enriched cDNA libraries identify breast cancer-associated transcripts. BMC Genomics, 2010, 11, S4.	2.8	10
108	KRAS insertions in colorectal cancer: What do we know about unusual KRAS mutations?. Experimental and Molecular Pathology, 2014, 96, 257-260.	2.1	10

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109	LINE-1 hypomethylation and mutational status in cutaneous melanomas. Journal of Investigative Medicine, 2016, 64, 899-904.	1.6	10
110	Assessment of somatic mutations in urine and plasma of Wilms tumor patients. Cancer Medicine, 2020, 9, 5948-5959.	2.8	10
111	MicroRNAs Discriminate Familial from Sporadic Non-BRCA1/2 Breast Carcinoma Arising in Patients â‰¤35 Years. PLoS ONE, 2014, 9, e101656.	2.5	10
112	No-match ORESTES explored as tumor markers. Nucleic Acids Research, 2009, 37, 2607-2617.	14.5	9
113	Evaluation of Quantitative RT-PCR Using Nonamplified and Amplified RNA. Diagnostic Molecular Pathology, 2010, 19, 45-53.	2.1	9
114	ROBO1 deletion as a novel germline alteration in breast and colorectal cancer patients. Tumor Biology, 2016, 37, 3145-3153.	1.8	9
115	Mutation Detection in Tumor-Derived Cell Free DNA Anticipates Progression in a Patient With Metastatic Colorectal Cancer. Frontiers in Oncology, 2018, 8, 306.	2.8	9
116	The transcription factor Snf1p is involved in a Tup1p-independent manner in the glucose regulation of the major methanol metabolism genes of Hansenula polymorpha. Genetics and Molecular Biology, 2003, 26, 521-528.	1.3	8
117	Primary Cutaneous Melanoma Arising in Agminated Melanocytic Nevi: CDKN2A and CDK4 Mutation Screening. Acta Dermato-Venereologica, 2012, 92, 98-99.	1.3	8
118	S-Score: A Scoring System for the Identification and Prioritization of Predicted Cancer Genes. PLoS ONE, 2014, 9, e94147.	2.5	8
119	Role of rare germline copy number variation in melanoma-prone patients. Future Oncology, 2016, 12, 1345-1357.	2.4	8
120	Rare germline alterations in cancer-related genes associated with the risk of multiple primary tumor development. Journal of Molecular Medicine, 2017, 95, 523-533.	3.9	8
121	BAP1 tumor predisposition syndrome case report: pathological and clinical aspects of BAP1-inactivated melanocytic tumors (BIMTs), including dermoscopy and confocal microscopy. BMC Cancer, 2019, 19, 1077.	2.6	8
122	Impact of BRCA1/2 Mutations on the Efficacy of Secondary Cytoreductive Surgery. Annals of Surgical Oncology, 2021, 28, 3637-3645.	1.5	8
123	NDRG4 promoter hypermethylation is a mechanistic biomarker associated with metastatic progression in breast cancer patients. Npj Breast Cancer, 2019, 5, 11.	5.2	7
124	Evaluation of MLH1 I219V polymorphism in unrelated South American individuals suspected of having Lynch syndrome. Anticancer Research, 2012, 32, 4347-51.	1.1	7
125	A Region of the Cellobiohydrolase I Promoter from the Filamentous FungusTrichoderma reeseiMediates Glucose Repression inSaccharomyces cerevisiae,Dependent on Mitochondrial Activity. Biochemical and Biophysical Research Communications, 1998, 253, 407-414.	2.1	6
126	In silico characterization and expression analyses of sugarcane putative sucrose non-fermenting-1 (SNF1) related kinases. Genetics and Molecular Biology, 2001, 24, 35-41.	1.3	6

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127	Evaluation of O6-methylguanine-DNA methyltransferase by immunohistochemistry: Best clinical and research practices. Pathology Research and Practice, 2011, 207, 492-497.	2.3	6
128	The Human Cell Surfaceome of Breast Tumors. BioMed Research International, 2013, 2013, 1-11.	1.9	6
129	Germline Mutations in MLH1 Leading to Isolated Loss of PMS2 Expression in Lynch Syndrome: Implications for Diagnostics in the Clinic. American Journal of Surgical Pathology, 2017, 41, 861-864.	3.7	6
130	Influence of BRCA1 Germline Mutations in the Somatic Mutational Burden of Triple-Negative Breast Cancer. Translational Oncology, 2019, 12, 1453-1460.	3.7	6
131	The mutational repertoire of uterine sarcomas and carcinosarcomas in a Brazilian cohort: A preliminary study. Clinics, 2021, 76, e2324.	1.5	6
132	Proficiency of DNA repair genes and microsatellite instability in operated colorectal cancer patients with clinical suspicion of lynch syndrome. Journal of Gastrointestinal Oncology, 2015, 6, 628-37.	1.4	6
133	Analysis of FOXP3 Gene and Protein Expressions in Renal Allograft Biopsies and Their Association with Graft Outcomes. Renal Failure, 2013, 35, 521-530.	2.1	5
134	Genome-wide DNA methylation profile of leukocytes from melanoma patients with and without CDKN2A mutations. Experimental and Molecular Pathology, 2014, 97, 425-432.	2.1	5
135	Tissue alkalosis in cold-ischemia time. Scientific Reports, 2017, 7, 10867.	3.3	5
136	MLH1 intronic variants mapping toâ€‰+â€‰5 position of splice donor sites lead to deleterious effects on RNA splicing. Familial Cancer, 2020, 19, 323-336.	1.9	5
137	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.	1.8	5
138	Family-based whole-exome sequencing identifies rare variants potentially related to cutaneous melanoma predisposition in Brazilian melanoma-prone families. PLoS ONE, 2022, 17, e0262419.	2.5	5
139	Copy Number Alterations in Hepatoblastoma: Literature Review and a Brazilian Cohort Analysis Highlight New Biological Pathways. Frontiers in Oncology, 2021, 11, 741526.	2.8	5
140	Does germ-line deletion of the PIP gene constitute a widespread risk for cancer?. European Journal of Human Genetics, 2014, 22, 307-309.	2.8	4
141	KRAS gene mutation in a series of unselected colorectal carcinoma patients with prognostic morphological correlations: A pyrosequencing method improved by nested PCR. Experimental and Molecular Pathology, 2015, 98, 563-567.	2.1	4
142	Expanding morphological and clinical aspects of hereditary leiomyomatosis and renal cell carcinoma (HLRCC): a case report in a patient with unusual morphology and clinical presentation. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2018, 473, 775-779.	2.8	4
143	Genetic and epigenetic characterization of the BRCA1 gene in Brazilian women at-risk for hereditary breast cancer. Oncotarget, 2017, 8, 2850-2862.	1.8	4
144	Two new MLH1 germline mutations in Brazilian lynch syndrome families. International Journal of Colorectal Disease, 2008, 23, 1263-1264.	2.2	3

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145	Germline BAX Deletion in a Patient With Melanoma and Gastrointestinal Stromal Tumor. American Journal of Gastroenterology, 2013, 108, 1372-1375.	0.4	3
146	DNA methylation as a key epigenetic player for hepatoblastoma characterization. Clinics and Research in Hepatology and Gastroenterology, 2021, 45, 101684.	1.5	3
147	Triple-Negative Breast Cancer circRNAome Reveals Hsa_circ_0072309 as a Potential Risk Biomarker. Cancers, 2022, 14, 3280.	3.7	3
148	Training in molecular pathology during residency: the experience of a Brazilian hospital. Journal of Clinical Pathology, 2014, 67, 647-648.	2.0	2
149	Linear mRNA amplification approach for RNAseq from limited amount of RNA. Gene, 2015, 564, 220-227.	2.2	2
150	Tumor banking for health research in Brazil and Latin America: time to leave the cradle. Applied Cancer Research, 2017, 37, .	1.0	2
151	Heteroduplex formation and S1 digestion for mapping alternative splicing sites. Genetics and Molecular Research, 2008, 7, 958-969.	0.2	2
152	Association of melanoma with intraepithelial neoplasia of the pancreas in three patients. Experimental and Molecular Pathology, 2014, 97, 144-147.	2.1	1
153	Biobanking and cytopathology: Challenges and opportunities from a Brazilian perspective. Cancer Cytopathology, 2017, 125, 373-377.	2.4	1
154	Increasing evidence for the presence of alternative proteins in human tissues and cell lines. Applied Cancer Research, 2017, 37, .	1.0	1
155	Cloning and sequence analysis of tomato cpDNA fragments: towards developing homologous chloroplast transformation vectors. Brazilian Journal of Plant Physiology, 2005, 17, 239-246.	0.5	1
156	Clinical Potential of Sputum in Detecting Driver Mutations in Patients with Non-Small Cell Lung Cancer: A Preliminary Study. , 2019, , .		0
157	Abstract 3765: APC and MUTYH mutation spectrum in Brazil: First genotype characterization of brazilian FAP and AFAP patients identifies 6 novel mutations. , 2011, , .		0
158	Differentially expressed genes and lincRNAs throughout oral squamous cell carcinoma development. FASEB Journal, 2012, 26, lb461.	0.5	0
159	PROX: Primary resistance to oxaliplatin containing regimen in the first line treatment of metastatic colorectal carcinomaâ€"Retrospective analysis.. Journal of Clinical Oncology, 2018, 36, 855-855.	1.6	0
160	Abstract 2072: Genomic studies of Brazilian patients with hepatoblastoma: Insight into somatic mutations using whole-exome sequencing. , 2018, , .		0
161	Abstract 2213: Investigation of treatment resistance with DNA-damage agents in patients with triple negative breast cancer by ctDNA. , 2019, , .		0
162	From Tissue Samples to Tumor Markers. , 2007, , 17-28.		0

#	Article	IF	Citations
163	Monitoring non-small cell lung cancer progression and treatment response through hyaluronic acid in sputum. Brazilian Journal of Medical and Biological Research, 2022, 55, e11513.	1.5	0