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	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
2	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
3	Triple-Negative Breast Cancer circRNAome Reveals Hsa_circ_0072309 as a Potential Risk Biomarker. Cancers, 2022, 14, 3280.	3.7	3
4	Impact of BRCA1/2 Mutations on the Efficacy of Secondary Cytoreductive Surgery. Annals of Surgical Oncology, 2021, 28, 3637-3645.	1.5	8
5	DNA methylation as a key epigenetic player for hepatoblastoma characterization. Clinics and Research in Hepatology and Gastroenterology, 2021, 45, 101684.	1.5	3
6	The mutational repertoire of uterine sarcomas and carcinosarcomas in a Brazilian cohort: A preliminary study. Clinics, 2021, 76, e2324.	1.5	6
7	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
8	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
9	Hepatoblastomas exhibit markedNNMTdownregulation driven by promoter DNA hypermethylation. Tumor Biology, 2020, 42, 101042832097712.	1.8	11
10	Deep Learning Predicts Underlying Features on Pathology Images with Therapeutic Relevance for Breast and Gastric Cancer. Cancers, 2020, 12, 3687.	3.7	34
11	Insights Into the Somatic Mutation Burden of Hepatoblastomas From Brazilian Patients. Frontiers in Oncology, 2020, 10, 556.	2.8	12
12	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
13	Assessment of somatic mutations in urine and plasma of Wilms tumor patients. Cancer Medicine, 2020, 9, 5948-5959.	2.8	10
14	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
15	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
16	Influence of BRCA1 Germline Mutations in the Somatic Mutational Burden of Triple-Negative Breast Cancer. Translational Oncology, 2019, 12, 1453-1460.	3.7	6
17	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
18	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

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19	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
20	TET Upregulation Leads to 5-Hydroxymethylation Enrichment in Hepatoblastoma. Frontiers in Genetics, 2019, 10, 553.	2.3	17
21	NDRG4 promoter hypermethylation is a mechanistic biomarker associated with metastatic progression in breast cancer patients. Npj Breast Cancer, 2019, 5, 11.	5.2	7
22	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
23	Clinical Potential of Sputum in Detecting Driver Mutations in Patients with Non-Small Cell Lung Cancer: A Preliminary Study. , 2019, , .		0
24	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
25	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
26	Abstract 2213: Investigation of treatment resistance with DNA-damage agents in patients with triple negative breast cancer by ctDNA. , 2019, , .		0
27	Biomolecular analysis of matrix proteoglycans as biomarkers in non small cell lung cancer. Glycoconjugate Journal, 2018, 35, 233-242.	2.7	20
28	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
29	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
30	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
31	Complex Landscape of Germline Variants in Brazilian Patients With Hereditary and Early Onset Breast Cancer. Frontiers in Genetics, 2018, 9, 161.	2.3	21
32	The germline mutational landscape of BRCA1 and BRCA2 in Brazil. Scientific Reports, 2018, 8, 9188.	3.3	61
33	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
34	Abstract 2072: Genomic studies of Brazilian patients with hepatoblastoma: Insight into somatic mutations using whole-exome sequencing. , 2018, , .		0
35	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
36	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

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37	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
38	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
39	Biobanking and cytopathology: Challenges and opportunities from a Brazilian perspective. Cancer Cytopathology, 2017, 125, 373-377.	2.4	1
40	Tumor banking for health research in Brazil and Latin America: time to leave the cradle. Applied Cancer Research, 2017, 37, .	1.0	2
41	Tissue alkalosis in cold-ischemia time. Scientific Reports, 2017, 7, 10867.	3.3	5
42	DNA repair genes PAXIP1 and TP53BP1 expression is associated with breast cancer prognosis. Cancer Biology and Therapy, 2017, 18, 439-449.	3.4	21
43	Increasing evidence for the presence of alternative proteins in human tissues and cell lines. Applied Cancer Research, 2017, 37, .	1.0	1
44	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
45	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
46	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
47	Germline mutations in BRCA1 and BRCA2 in epithelial ovarian cancer patients in Brazil. BMC Cancer, 2016, 16, 934.	2.6	50
48	LINE-1 hypomethylation and mutational status in cutaneous melanomas. Journal of Investigative Medicine, 2016, 64, 899-904.	1.6	10
49	Role of rare germline copy number variation in melanoma-prone patients. Future Oncology, 2016, 12, 1345-1357.	2.4	8
50	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
51	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
52	Genomic imbalances pinpoint potential oncogenes and tumor suppressors in Wilms tumors. Molecular Cytogenetics, 2016, 9, 20.	0.9	36
53	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
54	ROBO1 deletion as a novel germline alteration in breast and colorectal cancer patients. Tumor Biology, 2016, 37, 3145-3153.	1.8	9

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55	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
56	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
57	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
58	Phosphodiesterase sequence variants may predispose to prostate cancer. Endocrine-Related Cancer, 2015, 22, 519-530.	3.1	13
59	Co-expression network of neural-differentiation genes shows specific pattern in schizophrenia. BMC Medical Genomics, 2015, 8, 23.	1.5	45
60	Innate immune response is differentially dysregulated between bipolar disease and schizophrenia. Schizophrenia Research, 2015, 161, 215-221.	2.0	58
61	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
62	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
63	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
64	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
65	LINE-1 hypermethylation in peripheral blood of cutaneous melanoma patients is associated with metastasis. Melanoma Research, 2015, 25, 173-177.	1.2	20
66	Linear mRNA amplification approach for RNAseq from limited amount of RNA. Gene, 2015, 564, 220-227.	2.2	2
67	Intratumoral heterogeneity of ADAM23 promotes tumor growth and metastasis through LGI4 and nitric oxide signals. Oncogene, 2015, 34, 1270-1279.	5.9	20
68	Clinical and Molecular Characterization of Brazilian Patients Suspected to Have Lynch Syndrome. PLoS ONE, 2015, 10, e0139753.	2.5	25
69	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
70	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
71	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
72	S-Score: A Scoring System for the Identification and Prioritization of Predicted Cancer Genes. PLoS ONE, 2014, 9, e94147.	2.5	8

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73	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
74	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
75	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
76	Upregulated genes at 2q24 gains as candidate oncogenes in hepatoblastomas. Future Oncology, 2014, 10, 2449-2457.	2.4	29
77	Recurrent somatic mutation in DROSHA induces microRNA profile changes in Wilms tumour. Nature Communications, 2014, 5, 4039.	12.8	159
78	Biobanking Practice: RNA Storage at Low Concentration Affects Integrity. Biopreservation and Biobanking, 2014, 12, 46-52.	1.0	52
79	Ductal carcinoma in situ of the breast: morphological and molecular features implicated in progression. Bioscience Reports, 2014, 34, .	2.4	43
80	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
81	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
82	Germline CDKN2A mutations in Brazilian patients of hereditary cutaneous melanoma. Familial Cancer, 2014, 13, 645-649.	1.9	18
83	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
84	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
85	KRAS insertions in colorectal cancer: What do we know about unusual KRAS mutations?. Experimental and Molecular Pathology, 2014, 96, 257-260.	2.1	10
86	Training in molecular pathology during residency: the experience of a Brazilian hospital. Journal of Clinical Pathology, 2014, 67, 647-648.	2.0	2
87	Association of melanoma with intraepithelial neoplasia of the pancreas in three patients. Experimental and Molecular Pathology, 2014, 97, 144-147.	2.1	1
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	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
90	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

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91	MicroRNAs Discriminate Familial from Sporadic Non-BRCA1/2 Breast Carcinoma Arising in Patients â‰¤35 Years. PLoS ONE, 2014, 9, e101656.	2.5	10
92	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
93	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
94	The Human Cell Surfaceome of Breast Tumors. BioMed Research International, 2013, 2013, 1-11.	1.9	6
95	Mutation spectrum in South American Lynch syndrome families. Hereditary Cancer in Clinical Practice, 2013, 11, 18.	1.5	26
96	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
97	Germline BAX Deletion in a Patient With Melanoma and Gastrointestinal Stromal Tumor. American Journal of Gastroenterology, 2013, 108, 1372-1375.	0.4	3
98	P53 and Expression of Immunological Markers May Identify Early Stage Thyroid Tumors. Clinical and Developmental Immunology, 2013, 2013, 1-9.	3.3	16
99	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
100	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
101	Gene expression of peripheral blood lymphocytes may discriminate patients with schizophrenia from controls. Psychiatry Research, 2012, 200, 1018-1021.	3.3	15
102	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
103	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
104	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
105	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
106	Li-Fraumeni-like syndrome associated with a large BRCA1 intragenic deletion. BMC Cancer, 2012, 12, 237.	2.6	25
107	Primary Cutaneous Melanoma Arising in Agminated Melanocytic Nevi: CDKN2A and CDK4 Mutation Screening. Acta Dermato-Venereologica, 2012, 92, 98-99.	1.3	8
108	Amyloid-Î² Oligomers Induce Differential Gene Expression in Adult Human Brain Slices. Journal of Biological Chemistry, 2012, 287, 7436-7445.	3.4	80

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109	Predictive models for mutations in mismatch repair genes: implication for genetic counseling in developing countries. BMC Cancer, 2012, 12, 64.	2.6	11
110	Germline DNA copy number variation in familial and early-onset breast cancer. Breast Cancer Research, 2012, 14, R24.	5.0	76
111	Transcriptional Alterations Related to Neuropathology and Clinical Manifestation of Alzheimerâ€™s Disease. PLoS ONE, 2012, 7, e48751.	2.5	39
112	Differentially expressed genes and lincRNAs throughout oral squamous cell carcinoma development. FASEB Journal, 2012, 26, lb461.	0.5	0
113	Evaluation of MLH1 I219V polymorphism in unrelated South American individuals suspected of having Lynch syndrome. Anticancer Research, 2012, 32, 4347-51.	1.1	7
114	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
115	Evaluation of O6-methylguanine-DNA methyltransferase by immunohistochemistry: Best clinical and research practices. Pathology Research and Practice, 2011, 207, 492-497.	2.3	6
116	Poly (A)+ Transcriptome Assessment of ERBB2-Induced Alterations in Breast Cell Lines. PLoS ONE, 2011, 6, e21022.	2.5	17
117	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
118	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
119	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
120	Influence of the interaction between nodal fibroblast and breast cancer cells on gene expression. Tumor Biology, 2011, 32, 145-157.	1.8	21
121	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
122	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
123	Phosphodiesterase 11A (PDE11A) Genetic Variants May Increase Susceptibility to Prostatic Cancer. Journal of Clinical Endocrinology and Metabolism, 2011, 96, E135-E140.	3.6	41
124	Abstract 3765: APC and MUTYH mutation spectrum in Brazil: First genotype characterization of brazilian FAP and AFAP patients identifies 6 novel mutations. , 2011, , .		0
125	Alternative splicing enriched cDNA libraries identify breast cancer-associated transcripts. BMC Genomics, 2010, 11, S4.	2.8	10
126	Evaluation of Quantitative RT-PCR Using Nonamplified and Amplified RNA. Diagnostic Molecular Pathology, 2010, 19, 45-53.	2.1	9

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127	No-match ORESTES explored as tumor markers. Nucleic Acids Research, 2009, 37, 2607-2617.	14.5	9
128	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
129	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
130	Epigenetic Silencing of CRABP2 and MX1 in Head and Neck Tumors. Neoplasia, 2009, 11, 1329-IN9.	5.3	70
131	Gene expression profile of residual breast cancer after doxorubicin and cyclophosphamide neoadjuvant chemotherapy. Oncology Reports, 2009, 22, 805-13.	2.6	29
132	Mismatch repair genes in Lynch syndrome: a review. Sao Paulo Medical Journal, 2009, 127, 46-51.	0.9	56
133	Two new MLH1 germline mutations in Brazilian lynch syndrome families. International Journal of Colorectal Disease, 2008, 23, 1263-1264.	2.2	3
134	A genome survey of Moniliophthora perniciosa gives new insights into Witches' Broom Disease of cacao. BMC Genomics, 2008, 9, 548.	2.8	120
135	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
136	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
137	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
138	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
139	Heteroduplex formation and S1 digestion for mapping alternative splicing sites. Genetics and Molecular Research, 2008, 7, 958-969.	0.2	2
140	Alternative splicing: a bioinformatics perspective. Molecular BioSystems, 2007, 3, 473.	2.9	13
141	Gene stage-specific expression in the microenvironment of pediatric myelodysplastic syndromes. Leukemia Research, 2007, 31, 579-589.	0.8	31
142	From Tissue Samples to Tumor Markers. , 2007, , 17-28.		0
143	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
144	Gene expression arrays in cancer research: methods and applications. Critical Reviews in Oncology/Hematology, 2005, 54, 95-105.	4.4	72

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145	Gene Expression Profile Associated with Response to Doxorubicin-Based Therapy in Breast Cancer. Clinical Cancer Research, 2005, 11, 7434-7443.	7.0	168
146	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
147	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
148	A Transcript Finishing Initiative for Closing Gaps in the Human Transcriptome. Genome Research, 2004, 14, 1413-1423.	5.5	22
149	Generation of longer 3' cDNA fragments from massively parallel signature sequencing tags. Nucleic Acids Research, 2004, 32, e94-e94.	14.5	12
150	The Genome Sequence of the Gram-Positive Sugarcane Pathogen Leifsonia xyli subsp. xyli. Molecular Plant-Microbe Interactions, 2004, 17, 827-836.	2.6	119
151	Structural features and transcript-editing analysis of sugarcane (Saccharum officinarum L.) chloroplast genome. Current Genetics, 2004, 46, 366-373.	1.7	76
152	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
153	Analysis and Functional Annotation of an Expressed Sequence Tag Collection for Tropical Crop Sugarcane. Genome Research, 2003, 13, 2725-2735.	5.5	254
154	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
155	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
156	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
157	PCR-Assisted Contig Extension: Stepwise Strategy for Bacterial Genome Closure. BioTechniques, 2003, 34, 626-632.	1.8	11
158	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
159	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
160	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
161	The genome sequence of the plant pathogen Xylella fastidiosa. Nature, 2000, 406, 151-157.	27.8	827
162	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

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163	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