

Henrique Cesar Santejo Silveira

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

42
papers

9,302
citations

28
h-index

45
g-index

45
ext. papers

13,785
ext. citations

15.9
avg, IF

3.8
L-index

#	Paper	IF	Citations
42	Genomic instability evaluation by BMCyt and telomere length in Brazilian family farmers exposed to pesticides. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2022 , 878, 503479	3	0
41	Absolute telomere length in peripheral blood lymphocytes of workers exposed to construction environment.. <i>International Journal of Environmental Health Research</i> , 2022 , 1-9	3.6	
40	Detection of anti-cancer drugs and metabolites in the effluents from a large Brazilian cancer hospital and an evaluation of ecotoxicology. <i>Environmental Pollution</i> , 2021 , 268, 115857	9.3	8
39	Somatic Copy Number Alterations and Associated Genes in Clear-Cell Renal-Cell Carcinoma in Brazilian Patients. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	2
38	Mutational Profiling of Driver Tumor Suppressor and Oncogenic Genes in Brazilian Malignant Pleural Mesotheliomas. <i>Pathobiology</i> , 2020 , 87, 208-216	3.6	6
37	DNA methylation changes in promoter region of gene in workers exposed in construction environment. <i>Biomarkers</i> , 2020 , 25, 594-602	2.6	0
36	Evaluation of DNA Methylation Changes and Micronuclei in Workers Exposed to a Construction Environment. <i>International Journal of Environmental Research and Public Health</i> , 2019 , 16,	4.6	8
35	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018 , 173, 371-385.e18	56.2	854
34	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018 , 173, 291-304.e6	56.2	888
33	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018 , 173, 386-399.e12	56.2	133
32	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018 , 173, 305-320.e10	56.2	166
31	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018 , 173, 321-337.e10	56.2	1124
30	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018 , 173, 355-370.e14	56.2	342
29	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018 , 23, 282-296.e4	10.6	188
28	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018 , 23, 227-238.e3	10.6	235
27	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018 , 23, 194-212.e6	10.6	146
26	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. <i>Cell Reports</i> , 2018 , 23, 297-312.e12	10.6	147

25	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018 , 23, 181-193.e7	10.6	366
24	The Immune Landscape of Cancer. <i>Immunity</i> , 2018 , 48, 812-830.e14	32.3	1754
23	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 172-180.e3	10.6	66
22	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018 , 23, 213-226.e3	26.3	56
21	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018 , 23, 270-281.e3	10.6	121
20	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018 , 6, 271-281.e7	10.6	320
19	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. <i>Cell Systems</i> , 2018 , 6, 282-300.e2	10.6	159
18	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018 , 33, 721-735.e8	24.3	228
17	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018 , 34, 211-224.e6	24.3	327
16	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. <i>Cancer Discovery</i> , 2018 , 8, 1548-1565	24.4	258
15	Methylation of the hsa-miR-124, SOX1, TERT, and LMX1A genes as biomarkers for precursor lesions in cervical cancer. <i>Gynecologic Oncology</i> , 2018 , 150, 545-551	4.9	30
14	Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , 2017 , 543, 378-384	50.4	755
13	MicroRNA profiling in human breast cancer cell lines exposed to the anti-neoplastic drug cediranib. <i>Oncology Reports</i> , 2016 , 36, 3197-3206	3.5	6
12	Micronucleus evaluation of exfoliated buccal epithelial cells using liquid-based cytology preparation. <i>Acta Cytologica</i> , 2014 , 58, 582-8	3	12
11	MicroRNA expression as risk biomarker of breast cancer metastasis: a pilot retrospective case-cohort study. <i>BMC Cancer</i> , 2014 , 14, 739	4.8	37
10	Emissions generated by sugarcane burning promote genotoxicity in rural workers: a case study in Barretos, Brazil. <i>Environmental Health</i> , 2013 , 12, 87	6	21
9	Isolation of transcripts overexpressed in the human pathogen <i>Trichophyton rubrum</i> grown in lipid as carbon source. <i>Canadian Journal of Microbiology</i> , 2011 , 57, 333-8	3.2	8
8	Transcriptional profiling reveals genes in the human pathogen <i>Trichophyton rubrum</i> that are expressed in response to pH signaling. <i>Microbial Pathogenesis</i> , 2010 , 48, 91-6	3.8	32

7	Transcriptional profiling reveals the expression of novel genes in response to various stimuli in the human dermatophyte <i>Trichophyton rubrum</i> . <i>BMC Microbiology</i> , 2010 , 10, 39	4.5	44
6	Transcriptional changes in the <i>nuc-2A</i> mutant strain of <i>Neurospora crassa</i> cultivated under conditions of phosphate shortage. <i>Microbiological Research</i> , 2009 , 164, 658-64	5.3	10
5	Identification of genes differentially expressed in a strain of the mold <i>Aspergillus nidulans</i> carrying a loss-of-function mutation in the <i>palA</i> gene. <i>Canadian Journal of Microbiology</i> , 2008 , 54, 803-11	3.2	12
4	Identification of genes displaying differential expression in the <i>nuc-2</i> mutant strain of the mold <i>Neurospora crassa</i> grown under phosphate starvation. <i>FEMS Microbiology Letters</i> , 2007 , 269, 196-200	2.9	15
3	The pH signaling transcription factor PacC mediates the growth of <i>Trichophyton rubrum</i> on human nail in vitro. <i>Medical Mycology</i> , 2006 , 44, 641-5	3.9	68
2	A calcineurin inhibitory protein overexpressed in Downæ syndrome interacts with the product of a ubiquitously expressed transcript. <i>Brazilian Journal of Medical and Biological Research</i> , 2004 , 37, 785-9	2.8	12
1	Analysis and functional annotation of an expressed sequence tag collection for tropical crop sugarcane. <i>Genome Research</i> , 2003 , 13, 2725-35	9.7	207