

# Henrique Cesar Santejo Silveira

## List of Publications by Citations

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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	The Immune Landscape of Cancer. <i>Immunity</i> , <b>2018</b> , 48, 812-830.e14	32.3	1754
41	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , <b>2018</b> , 173, 321-337.e10	56.2	1124
40	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , <b>2018</b> , 173, 291-304.e6	56.2	888
39	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , <b>2018</b> , 173, 371-385.e18	56.2	854
38	Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , <b>2017</b> , 543, 378-384	50.4	755
37	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , <b>2018</b> , 23, 181-193.e7	10.6	366
36	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , <b>2018</b> , 173, 355-370.e14	56.2	342
35	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , <b>2018</b> , 34, 211-224.e6	24.3	327
34	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , <b>2018</b> , 6, 271-281.e7	10.6	320
33	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. <i>Cancer Discovery</i> , <b>2018</b> , 8, 1548-1565	24.4	258
32	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , <b>2018</b> , 23, 227-238.e3	10.6	235
31	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , <b>2018</b> , 33, 721-735.e8	24.3	228
30	Analysis and functional annotation of an expressed sequence tag collection for tropical crop sugarcane. <i>Genome Research</i> , <b>2003</b> , 13, 2725-35	9.7	207
29	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , <b>2018</b> , 23, 282-296.e4	10.6	188
28	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , <b>2018</b> , 173, 305-320.e10	56.2	166
27	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. <i>Cell Systems</i> , <b>2018</b> , 6, 282-300.e2	10.6	159
26	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. <i>Cell Reports</i> , <b>2018</b> , 23, 297-312.e12	10.6	147

25	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , <b>2018</b> , 23, 194-212.e6	10.6	146
24	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , <b>2018</b> , 173, 386-399.e32	10.2	133
23	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , <b>2018</b> , 23, 270-281.e3	10.6	121
22	The pH signaling transcription factor PacC mediates the growth of <i>Trichophyton rubrum</i> on human nail in vitro. <i>Medical Mycology</i> , <b>2006</b> , 44, 641-5	3.9	68
21	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , <b>2018</b> , 23, 172-180.e3	10.6	66
20	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , <b>2018</b> , 23, 213-226.e3	10.6	56
19	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> , <b>2010</b> , 10, 39	4.5	44
18	MicroRNA expression as risk biomarker of breast cancer metastasis: a pilot retrospective case-cohort study. <i>BMC Cancer</i> , <b>2014</b> , 14, 739	4.8	37
17	Transcriptional profiling reveals genes in the human pathogen <i>Trichophyton rubrum</i> that are expressed in response to pH signaling. <i>Microbial Pathogenesis</i> , <b>2010</b> , 48, 91-6	3.8	32
16	Methylation of the hsa-miR-124, SOX1, TERT, and LMX1A genes as biomarkers for precursor lesions in cervical cancer. <i>Gynecologic Oncology</i> , <b>2018</b> , 150, 545-551	4.9	30
15	Emissions generated by sugarcane burning promote genotoxicity in rural workers: a case study in Barretos, Brazil. <i>Environmental Health</i> , <b>2013</b> , 12, 87	6	21
14	Identification of genes displaying differential expression in the nuc-2 mutant strain of the mold <i>Neurospora crassa</i> grown under phosphate starvation. <i>FEMS Microbiology Letters</i> , <b>2007</b> , 269, 196-200	2.9	15
13	Micronucleus evaluation of exfoliated buccal epithelial cells using liquid-based cytology preparation. <i>Acta Cytologica</i> , <b>2014</b> , 58, 582-8	3	12
12	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> , <b>2008</b> , 54, 803-11	3.2	12
11	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> , <b>2004</b> , 37, 785-9	2.8	12
10	Transcriptional changes in the nuc-2A mutant strain of <i>Neurospora crassa</i> cultivated under conditions of phosphate shortage. <i>Microbiological Research</i> , <b>2009</b> , 164, 658-64	5.3	10
9	Evaluation of DNA Methylation Changes and Micronuclei in Workers Exposed to a Construction Environment. <i>International Journal of Environmental Research and Public Health</i> , <b>2019</b> , 16,	4.6	8
8	Isolation of transcripts overexpressed in the human pathogen <i>Trichophyton rubrum</i> grown in lipid as carbon source. <i>Canadian Journal of Microbiology</i> , <b>2011</b> , 57, 333-8	3.2	8

7	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> , <b>2021</b> , 268, 115857	9.3	8
6	Mutational Profiling of Driver Tumor Suppressor and Oncogenic Genes in Brazilian Malignant Pleural Mesotheliomas. <i>Pathobiology</i> , <b>2020</b> , 87, 208-216	3.6	6
5	MicroRNA profiling in human breast cancer cell lines exposed to the anti-neoplastic drug cediranib. <i>Oncology Reports</i> , <b>2016</b> , 36, 3197-3206	3.5	6
4	Somatic Copy Number Alterations and Associated Genes in Clear-Cell Renal-Cell Carcinoma in Brazilian Patients. <i>International Journal of Molecular Sciences</i> , <b>2021</b> , 22,	6.3	2
3	DNA methylation changes in promoter region of gene in workers exposed in construction environment. <i>Biomarkers</i> , <b>2020</b> , 25, 594-602	2.6	0
2	Genomic instability evaluation by BMCyt and telomere length in Brazilian family farmers exposed to pesticides. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , <b>2022</b> , 878, 503479 <sup>3</sup>		0
1	Absolute telomere length in peripheral blood lymphocytes of workers exposed to construction environment.. <i>International Journal of Environmental Health Research</i> , <b>2022</b> , 1-9	3.6	