## Tiago C Silva

## 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.

3,433 14 49 33 h-index g-index citations papers 11 49 5,379 4.5 L-index ext. citations ext. papers avg, IF

#	Paper	IF	Citations
33	Multi-omics analysis identifies therapeutic vulnerabilities in triple-negative breast cancer subtypes.  Nature Communications, <b>2021</b> , 12, 6276	17.4	10
32	Sex-specific DNA methylation differences in Alzheimer disease pathology. <i>Acta Neuropathologica Communications</i> , <b>2021</b> , 9, 77	7.3	2
31	A pan-cancer analysis of CpG Island gene regulation reveals extensive plasticity within Polycomb target genes. <i>Nature Communications</i> , <b>2021</b> , 12, 2485	17.4	6
30	DNA methylation-based signatures classify sporadic pituitary tumors according to clinicopathological features. <i>Neuro-Oncology</i> , <b>2021</b> , 23, 1292-1303	1	1
29	Whole-genome characterization of lung adenocarcinomas lacking the RTK/RAS/RAF pathway. <i>Cell Reports</i> , <b>2021</b> , 34, 108707	10.6	7
28	LR Hunting: A Random Forest Based Cell-Cell Interaction Discovery Method for Single-Cell Gene Expression Data. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 708835	4.5	1
27	Activation of bivalent factor DLX5 cooperates with master regulator TP63 to promote squamous cell carcinoma. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, 9246-9263	20.1	1
26	Sex-specific analysis of DNA methylation changes implicates new loci in Alzheimer\s disease pathology <i>Alzheimer\s and Dementia</i> , <b>2021</b> , 17 Suppl 3, e049363	1.2	
25	Estimating the regulatory potential of DNA methylation in Alzheimer disease <i>Alzheimer and Dementia</i> , <b>2021</b> , 17 Suppl 3, e049365	1.2	
24	PathwayMultiomics: An R Package for Efficient Integrative Analysis of Multi-Omics Datasets With Matched or Un-matched Samples <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 783713	4.5	О
23	PathwayPCA: an R/Bioconductor Package for Pathway Based Integrative Analysis of Multi-Omics Data. <i>Proteomics</i> , <b>2020</b> , 20, e1900409	4.8	4
22	Lineage-Specific Epigenomic and Genomic Activation of Oncogene HNF4A Promotes Gastrointestinal Adenocarcinomas. <i>Cancer Research</i> , <b>2020</b> , 80, 2722-2736	10.1	14
21	Interpreting pathways to discover cancer driver genes with Moonlight. <i>Nature Communications</i> , <b>2020</b> , 11, 69	17.4	23
20	Epigenome-wide meta-analysis of DNA methylation differences in prefrontal cortex implicates the immune processes in Alzheimer disease. <i>Nature Communications</i> , <b>2020</b> , 11, 6114	17.4	12
19	RNA-Binding Protein Suppresses Hypoxia and Cell-Cycle Signaling. <i>Cancer Research</i> , <b>2020</b> , 80, 219-233	10.1	16
18	Master transcription factors form interconnected circuitry and orchestrate transcriptional networks in oesophageal adenocarcinoma. <i>Gut</i> , <b>2020</b> , 69, 630-640	19.2	27
17	New functionalities in the TCGAbiolinks package for the study and integration of cancer data from GDC and GTEx. <i>PLoS Computational Biology</i> , <b>2019</b> , 15, e1006701	5	143

## LIST OF PUBLICATIONS

16	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data CommonsVData. <i>Cell Systems</i> , <b>2019</b> , 9, 24-34.e10	10.6	64
15	GENAVi: a shiny web application for gene expression normalization, analysis and visualization. <i>BMC Genomics</i> , <b>2019</b> , 20, 745	4.5	10
14	UM171 Regulates the Hematopoietic Differentiation of Human Acquired Aplastic Anemia-Derived Induced Pluripotent Stem Cells. <i>Blood</i> , <b>2019</b> , 134, 2500-2500	2.2	1
13	ELMER v.2: an R/Bioconductor package to reconstruct gene regulatory networks from DNA methylation and transcriptome profiles. <i>Bioinformatics</i> , <b>2019</b> , 35, 1974-1977	7.2	35
12	Glioma CpG island methylator phenotype (G-CIMP): biological and clinical implications. <i>Neuro-Oncology</i> , <b>2018</b> , 20, 608-620	1	97
11	Identification of distinct mutational patterns and new driver genes in oesophageal squamous cell carcinomas and adenocarcinomas. <i>Gut</i> , <b>2018</b> , 67, 1769-1779	19.2	62
10	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , <b>2018</b> , 362,	33.3	392
9	SpidermiR: An R/Bioconductor Package for Integrative Analysis with miRNA Data. <i>International Journal of Molecular Sciences</i> , <b>2017</b> , 18,	6.3	35
8	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , <b>2016</b> , 164, 550-63	56.2	1140
7	TCGAbiolinks: an R/Bioconductor package for integrative analysis of TCGA data. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, e71	20.1	1155
6	: Analyze cancer genomics and epigenomics data using Bioconductor packages. <i>F1000Research</i> , <b>2016</b> , 5, 1542	3.6	74
5	TCGAbiolinksGUI: A graphical user interface to analyze cancer molecular and clinical data. <i>F1000Research</i> ,7, 439	3.6	8
4	TCGA Workflow: Analyze cancer genomics and epigenomics data using Bioconductor packages. <i>F1000Research</i> ,5, 1542	3.6	78
3	TCGAbiolinksGUI: A graphical user interface to analyze GDC cancer molecular and clinical data		3
2	ELMER v.2: An R/Bioconductor package to reconstruct gene regulatory networks from DNA methylation and transcriptome profiles		3
1	Moonlight: a tool for biological interpretation and driver genes discovery		5