

# Tiago C Silva

## 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.

33  
papers

3,433  
citations

14  
h-index

49  
g-index

49  
ext. papers

5,379  
ext. citations

11  
avg, IF

4.5  
L-index

| #  | Paper  | IF   | Citations |
|----|--|------|-----------|
| 33 | TCGAbiolinks: an R/Bioconductor package for integrative analysis of TCGA data. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, e71   | 20.1 | 1155      |
| 32 | 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      |
| 31 | The chromatin accessibility landscape of primary human cancers. <i>Science</i> , <b>2018</b> , 362,  | 33.3 | 392       |
| 30 | 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       |
| 29 | Glioma CpG island methylator phenotype (G-CIMP): biological and clinical implications. <i>Neuro-Oncology</i> , <b>2018</b> , 20, 608-620   | 1    | 97        |
| 28 | TCGA Workflow: Analyze cancer genomics and epigenomics data using Bioconductor packages. <i>F1000Research</i> , <b>2016</b> , 5, 1542  | 3.6  | 78        |
| 27 | : Analyze cancer genomics and epigenomics data using Bioconductor packages. <i>F1000Research</i> , <b>2016</b> , 5, 1542   | 3.6  | 74        |
| 26 | Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons VData. <i>Cell Systems</i> , <b>2019</b> , 9, 24-34.e10  | 10.6 | 64        |
| 25 | 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        |
| 24 | 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        |
| 23 | 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        |
| 22 | 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        |
| 21 | Interpreting pathways to discover cancer driver genes with Moonlight. <i>Nature Communications</i> , <b>2020</b> , 11, 69  | 17.4 | 23        |
| 20 | RNA-Binding Protein Suppresses Hypoxia and Cell-Cycle Signaling. <i>Cancer Research</i> , <b>2020</b> , 80, 219-233  | 10.1 | 16        |
| 19 | 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        |
| 18 | Epigenome-wide meta-analysis of DNA methylation differences in prefrontal cortex implicates the immune processes in Alzheimer's disease. <i>Nature Communications</i> , <b>2020</b> , 11, 6114 | 17.4 | 12        |
| 17 | GENAVi: a shiny web application for gene expression normalization, analysis and visualization. <i>BMC Genomics</i> , <b>2019</b> , 20, 745   | 4.5  | 10        |

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|----|---|------|----|
| 16 | Multi-omics analysis identifies therapeutic vulnerabilities in triple-negative breast cancer subtypes. <i>Nature Communications</i> , <b>2021</b> , 12, 6276                            | 17.4 | 10 |
| 15 | TCGAbiolinksGUI: A graphical user interface to analyze cancer molecular and clinical data. <i>F1000Research</i> , <b>2021</b> , 7, 439  | 3.6  | 8  |
| 14 | Whole-genome characterization of lung adenocarcinomas lacking the RTK/RAS/RAF pathway. <i>Cell Reports</i> , <b>2021</b> , 34, 108707   | 10.6 | 7  |
| 13 | 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  |
| 12 | Moonlight: a tool for biological interpretation and driver genes discovery  |      | 5  |
| 11 | 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  |
| 10 | TCGAbiolinksGUI: A graphical user interface to analyze GDC cancer molecular and clinical data   |      | 3  |
| 9  | ELMER v.2: An R/Bioconductor package to reconstruct gene regulatory networks from DNA methylation and transcriptome profiles  |      | 3  |
| 8  | Sex-specific DNA methylation differences in Alzheimer's disease pathology. <i>Acta Neuropathologica Communications</i> , <b>2021</b> , 9, 77  | 7.3  | 2  |
| 7  | 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  |
| 6  | DNA methylation-based signatures classify sporadic pituitary tumors according to clinicopathological features. <i>Neuro-Oncology</i> , <b>2021</b> , 23, 1292-1303                      | 1    | 1  |
| 5  | 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  |
| 4  | 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  |
| 3  | 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  | 0  |
| 2  | 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  |    |
| 1  | Estimating the regulatory potential of DNA methylation in Alzheimer's disease.. <i>Alzheimer's and Dementia</i> , <b>2021</b> , 17 Suppl 3, e049365                                     | 1.2  |    |