

# Tiago C Silva

## List of Publications by Year in descending order

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Version: 2024-02-01

34  
papers

6,728  
citations

471509

17  
h-index

477307

29  
g-index

49  
all docs

49  
docs citations

49  
times ranked

11962  
citing authors

#	ARTICLE	IF	CITATIONS
1	TCGAbiolinks: an R/Bioconductor package for integrative analysis of TCGA data. <i>Nucleic Acids Research</i> , 2016, 44, e71-e71.	14.5	2,519
2	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016, 164, 550-563.	28.9	1,695
3	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018, 362, .	12.6	781
4	New functionalities in the TCGAbiolinks package for the study and integration of cancer data from GDC and GTEx. <i>PLoS Computational Biology</i> , 2019, 15, e1006701.	3.2	319
5	Glioma CpG island methylator phenotype (G-CIMP): biological and clinical implications. <i>Neuro-Oncology</i> , 2018, 20, 608-620.	1.2	194
6	TCGA Workflow: Analyze cancer genomics and epigenomics data using Bioconductor packages. <i>F1000Research</i> , 0, 5, 1542.	1.6	155
7	TCGA Workflow: Analyze cancer genomics and epigenomics data using Bioconductor packages. <i>F1000Research</i> , 2016, 5, 1542.	1.6	140
8	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons™ Data. <i>Cell Systems</i> , 2019, 9, 24-34.e10.	6.2	103
9	Identification of distinct mutational patterns and new driver genes in oesophageal squamous cell carcinomas and adenocarcinomas. <i>Gut</i> , 2018, 67, 1769-1779.	12.1	101
10	Multi-omics analysis identifies therapeutic vulnerabilities in triple-negative breast cancer subtypes. <i>Nature Communications</i> , 2021, 12, 6276.	12.8	89
11	ELMER v.2: an R/Bioconductor package to reconstruct gene regulatory networks from DNA methylation and transcriptome profiles. <i>Bioinformatics</i> , 2019, 35, 1974-1977.	4.1	87
12	Epigenome-wide meta-analysis of DNA methylation differences in prefrontal cortex implicates the immune processes in Alzheimer's disease. <i>Nature Communications</i> , 2020, 11, 6114.	12.8	75
13	Master transcription factors form interconnected circuitry and orchestrate transcriptional networks in oesophageal adenocarcinoma. <i>Gut</i> , 2020, 69, 630-640.	12.1	68
14	Interpreting pathways to discover cancer driver genes with Moonlight. <i>Nature Communications</i> , 2020, 11, 69.	12.8	66
15	SpidermiR: An R/Bioconductor Package for Integrative Analysis with miRNA Data. <i>International Journal of Molecular Sciences</i> , 2017, 18, 274.	4.1	50
16	GENAVI: a shiny web application for gene expression normalization, analysis and visualization. <i>BMC Genomics</i> , 2019, 20, 745.	2.8	40
17	RNA-Binding Protein <i>ZFP36L1</i> Suppresses Hypoxia and Cell-Cycle Signaling. <i>Cancer Research</i> , 2020, 80, 219-233.	0.9	40
18	Lineage-Specific Epigenomic and Genomic Activation of Oncogene HNF4A Promotes Gastrointestinal Adenocarcinomas. <i>Cancer Research</i> , 2020, 80, 2722-2736.	0.9	37

#	ARTICLE	IF	CITATIONS
19	Sex-specific DNA methylation differences in Alzheimer's disease pathology. <i>Acta Neuropathologica Communications</i> , 2021, 9, 77.	5.2	26
20	A pan-cancer analysis of CpG Island gene regulation reveals extensive plasticity within Polycomb target genes. <i>Nature Communications</i> , 2021, 12, 2485.	12.8	21
21	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. <i>Cell Reports</i> , 2021, 34, 108707.	6.4	16
22	TCGAbiolinksGUI: A graphical user interface to analyze cancer molecular and clinical data. <i>F1000Research</i> , 0, 7, 439.	1.6	14
23	Activation of bivalent factor DLX5 cooperates with master regulator TP63 to promote squamous cell carcinoma. <i>Nucleic Acids Research</i> , 2021, 49, 9246-9263.	14.5	13
24	LR Hunting: A Random Forest Based Cell-Cell Interaction Discovery Method for Single-Cell Gene Expression Data. <i>Frontiers in Genetics</i> , 2021, 12, 708835.	2.3	9
25	PathwayMultiomics: An R Package for Efficient Integrative Analysis of Multi-Omics Datasets With Matched or Un-matched Samples. <i>Frontiers in Genetics</i> , 2021, 12, 783713.	2.3	9
26	PathwayPCA: an R/Bioconductor Package for Pathway Based Integrative Analysis of Multi-Omics Data. <i>Proteomics</i> , 2020, 20, e1900409.	2.2	8
27	MethReg: estimating the regulatory potential of DNA methylation in gene transcription. <i>Nucleic Acids Research</i> , 2022, 50, e51-e51.	14.5	8
28	DNA methylation-based signatures classify sporadic pituitary tumors according to clinicopathological features. <i>Neuro-Oncology</i> , 2021, 23, 1292-1303.	1.2	6
29	UM171 Regulates the Hematopoietic Differentiation of Human Acquired Aplastic Anemia-Derived Induced Pluripotent Stem Cells. <i>Blood</i> , 2019, 134, 2500-2500.	1.4	1
30	Abstract 5895: Whole-genome characterization of lung adenocarcinomas lacking alterations in RTK/RAS/RAF/MAPK pathway. , 2020, , .		1
31	UNIQUE GENE EXPRESSION IN GUT-DERIVED PHAGOCYtic IMMUNE CELLS FROM IBD PATIENTS. <i>Gastroenterology</i> , 2021, 160, S42-S43.	1.3	0
32	Sa524 UNIQUE GENE EXPRESSION IN GUT-DERIVED PHAGOCYtic IMMUNE CELLS FROM IBD PATIENTS. <i>Gastroenterology</i> , 2021, 160, S-535-S-536.	1.3	0
33	Sex-specific analysis of DNA methylation changes implicates new loci in Alzheimer's disease pathology. <i>Alzheimer's and Dementia</i> , 2021, 17, e049363.	0.8	0
34	Estimating the regulatory potential of DNA methylation in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2021, 17, e049365.	0.8	0