Tiago C Silva

List of Publications by Year
in descending order

34	6,728	471509	477307
papers	citations	17	29
		h-index	g-index

49	49	49	11962
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	MethReg: estimating the regulatory potential of DNA methylation in gene transcription. Nucleic Acids Research, 2022, 50, e51-e51.	14.5	8
2	DNA methylation-based signatures classify sporadic pituitary tumors according to clinicopathological features. Neuro-Oncology, 2021, 23, 1292-1303.	1.2	6
3	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. Cell Reports, 2021, 34, 108707.	6.4	16
4	UNIQUE GENE EXPRESSION IN GUT-DERIVED PHAGOCYTIC IMMUNE CELLS FROM IBD PATIENTS. Gastroenterology, 2021, 160, S42-S43.	1.3	0
5	Sex-specific DNA methylation differences in Alzheimer's disease pathology. Acta Neuropathologica Communications, 2021, 9, 77.	5.2	26
6	A pan-cancer analysis of CpG Island gene regulation reveals extensive plasticity within Polycomb target genes. Nature Communications, 2021, 12, 2485.	12.8	21
7	Sa524 UNIQUE GENE EXPRESSION IN GUT-DERIVED PHAGOCYTIC IMMUNE CELLS FROM IBD PATIENTS. Gastroenterology, 2021, 160, S-535-S-536.	1.3	0
8	LR Hunting: A Random Forest Based Cell–Cell Interaction Discovery Method for Single-Cell Gene Expression Data. Frontiers in Genetics, 2021, 12, 708835.	2.3	9
9	Activation of bivalent factor DLX5 cooperates with master regulator TP63 to promote squamous cell carcinoma. Nucleic Acids Research, 2021, 49, 9246-9263.	14.5	13
10	Multi-omics analysis identifies therapeutic vulnerabilities in triple-negative breast cancer subtypes. Nature Communications, 2021, 12, 6276.	12.8	89
11	Sex-specific analysis of DNA methylation changes implicates new loci in Alzheimer's disease pathology. Alzheimer's and Dementia, 2021, 17, e049363.	0.8	0
12	Estimating the regulatory potential of DNA methylation in Alzheimer's disease. Alzheimer's and Dementia, 2021, 17, e049365.	0.8	0
13	PathwayMultiomics: An R Package for Efficient Integrative Analysis of Multi-Omics Datasets With Matched or Un-matched Samples. Frontiers in Genetics, 2021, 12, 783713.	2.3	9
14	RNA-Binding Protein *ZFP36L1* Suppresses Hypoxia and Cell-Cycle Signaling. Cancer Research, 2020, 80, 219-233.	0.9	40
15	Master transcription factors form interconnected circuitry and orchestrate transcriptional networks in oesophageal adenocarcinoma. Gut, 2020, 69, 630-640.	12.1	68
16	Interpreting pathways to discover cancer driver genes with Moonlight. Nature Communications, 2020, 11, 69.	12.8	66
17	Epigenome-wide meta-analysis of DNA methylation differences in prefrontal cortex implicates the immune processes in Alzheimer's disease. Nature Communications, 2020, 11, 6114.	12.8	75
18	PathwayPCA: an R/Bioconductor Package for Pathway Based Integrative Analysis of Multi-Omics Data. Proteomics, 2020, 20, e1900409.	2.2	8

#	Article	IF	Citations
19	Lineage-Specific Epigenomic and Genomic Activation of Oncogene HNF4A Promotes Gastrointestinal Adenocarcinomas. Cancer Research, 2020, 80, 2722-2736.	0.9	37
20	Abstract 5895: Whole-genome characterization of lung adenocarcinomas lacking alterations in RTK/RAS/RAF/MAPK pathway. , 2020, , .		1
21	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons' Data. Cell Systems, 2019, 9, 24-34.e10.	6.2	103
22	GENAVi: a shiny web application for gene expression normalization, analysis and visualization. BMC Genomics, 2019, 20, 745.	2.8	40
23	New functionalities in the TCGAbiolinks package for the study and integration of cancer data from GDC and GTEx. PLoS Computational Biology, 2019, 15, e1006701.	3.2	319
24	ELMER v.2: an R/Bioconductor package to reconstruct gene regulatory networks from DNA methylation and transcriptome profiles. Bioinformatics, 2019, 35, 1974-1977.	4.1	87
25	UM171 Regulates the Hematopoietic Differentiation of Human Acquired Aplastic Anemia-Derived Induced Pluripotent Stem Cells. Blood, 2019, 134, 2500-2500.	1.4	1
26	Glioma CpG island methylator phenotype (G-CIMP): biological and clinical implications. Neuro-Oncology, 2018, 20, 608-620.	1.2	194
27	Identification of distinct mutational patterns and new driver genes in oesophageal squamous cell carcinomas and adenocarcinomas. Gut, 2018, 67, 1769-1779.	12.1	101
28	The chromatin accessibility landscape of primary human cancers. Science, 2018, 362, .	12.6	781
29	SpidermiR: An R/Bioconductor Package for Integrative Analysis with miRNA Data. International Journal of Molecular Sciences, 2017, 18, 274.	4.1	50
30	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell, 2016, 164, 550-563.	28.9	1,695
31	TCGAbiolinks: an R/Bioconductor package for integrative analysis of TCGA data. Nucleic Acids Research, 2016, 44, e71-e71.	14.5	2,519
32	TCGA Workflow: Analyze cancer genomics and epigenomics data using Bioconductor packages. F1000Research, 2016, 5, 1542.	1.6	140
33	TCGAbiolinksGUI: A graphical user interface to analyze cancer molecular and clinical data. F1000Research, 0, 7, 439.	1.6	14
34	TCGA Workflow: Analyze cancer genomics and epigenomics data using Bioconductor packages. F1000Research, 0, 5, 1542.	1.6	155