

Zuguang Gu

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

11,588
citations

236925

25
h-index

315739

38
g-index

50
all docs

50
docs citations

50
times ranked

25462
citing authors

#	ARTICLE	IF	CITATIONS
1	simplifyEnrichment: A Bioconductor Package for Clustering and Visualizing Functional Enrichment Results. <i>Genomics, Proteomics and Bioinformatics</i> , 2023, 21, 190-202.	6.9	75
2	<i>spiralize</i> : an R package for visualizing data on spirals. <i>Bioinformatics</i> , 2022, 38, 1434-1436.	4.1	6
3	Improve consensus partitioning via a hierarchical procedure. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	1
4	Make Interactive Complex Heatmaps in R. <i>Bioinformatics</i> , 2022, 38, 1460-1462.	4.1	63
5	The genomic and transcriptional landscape of primary central nervous system lymphoma. <i>Nature Communications</i> , 2022, 13, 2558.	12.8	52
6	<i>pkgndep</i> : a tool for analyzing dependency heaviness of R packages. <i>Bioinformatics</i> , 2022, 38, 4248-4251.	4.1	2
7	Aggressive PDACs Show Hypomethylation of Repetitive Elements and the Execution of an Intrinsic IFN Program Linked to a Ductal Cell of Origin. <i>Cancer Discovery</i> , 2021, 11, 638-659.	9.4	65
8	Analysis of mutational signatures with yet another package for signature analysis. <i>Genes Chromosomes and Cancer</i> , 2021, 60, 314-331.	2.8	40
9	<i>cola</i> : an R/Bioconductor package for consensus partitioning through a general framework. <i>Nucleic Acids Research</i> , 2021, 49, e15-e15.	14.5	32
10	Memory-like HCV-specific CD8+ T cells retain a molecular scar after cure of chronic HCV infection. <i>Nature Immunology</i> , 2021, 22, 229-239.	14.5	95
11	IFN γ secreted by breast cancer cells undergoing chemotherapy reprograms stromal fibroblasts to support tumour growth after treatment. <i>Molecular Oncology</i> , 2021, 15, 1308-1329.	4.6	9
12	TNF α -producing macrophages determine subtype identity and prognosis via AP1 enhancer reprogramming in pancreatic cancer. <i>Nature Cancer</i> , 2021, 2, 1185-1203.	13.2	46
13	Glioblastoma epigenome profiling identifies SOX10 as a master regulator of molecular tumour subtype. <i>Nature Communications</i> , 2020, 11, 6434.	12.8	48
14	Quantitative proteomics reveals specific metabolic features of acute myeloid leukemia stem cells. <i>Blood</i> , 2020, 136, 1507-1519.	1.4	57
15	Follicular T helper cells shape the HCV-specific CD4+ T cell repertoire after virus elimination. <i>Journal of Clinical Investigation</i> , 2020, 130, 998-1009.	8.2	39
16	Pheno-seq “ linking visual features and gene expression in 3D cell culture systems. <i>Scientific Reports</i> , 2019, 9, 12367.	3.3	16
17	Mutational patterns and regulatory networks in epigenetic subgroups of meningioma. <i>Acta Neuropathologica</i> , 2019, 138, 295-308.	7.7	74
18	Evolutionary Trajectories of IDHWT Glioblastomas Reveal a Common Path of Early Tumorigenesis Instigated Years ahead of Initial Diagnosis. <i>Cancer Cell</i> , 2019, 35, 692-704.e12.	16.8	172

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19	Whole genome sequencing puts forward hypotheses on metastasis evolution and therapy in colorectal cancer. <i>Nature Communications</i> , 2018, 9, 4782.	12.8	103
20	EnrichedHeatmap: an R/Bioconductor package for comprehensive visualization of genomic signal associations. <i>BMC Genomics</i> , 2018, 19, 234.	2.8	152
21	The benzene metabolite 1,4-benzoquinone reduces regulatory T-cell function: A potential mechanism for tobacco smoke-associated atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 140, 603-605.	2.9	2
22	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017, 547, 311-317.	27.8	787
23	RAS-pathway mutation patterns define epigenetic subclasses in juvenile myelomonocytic leukemia. <i>Nature Communications</i> , 2017, 8, 2126.	12.8	91
24	Environment-induced epigenetic reprogramming in genomic regulatory elements in smoking mothers and their children. <i>Molecular Systems Biology</i> , 2016, 12, 861.	7.2	97
25	Complex heatmaps reveal patterns and correlations in multidimensional genomic data. <i>Bioinformatics</i> , 2016, 32, 2847-2849.	4.1	5,891
26	Aromatic and proteomic analyses corroborate the distinction between Mediterranean landraces and modern varieties of durum wheat. <i>Scientific Reports</i> , 2016, 6, 34619.	3.3	15
27	Prenatal maternal stress and wheeze in children: novel insights into epigenetic regulation. <i>Scientific Reports</i> , 2016, 6, 28616.	3.3	55
28	gtrellis: an R/Bioconductor package for making genome-level Trellis graphics. <i>BMC Bioinformatics</i> , 2016, 17, 169.	2.6	21
29	HilbertCurve: an R/Bioconductor package for high-resolution visualization of genomic data. <i>Bioinformatics</i> , 2016, 32, 2372-2374.	4.1	29
30	Mutations in the SIX1/2 Pathway and the DROSHA/DGCR8 miRNA Microprocessor Complex Underlie High-Risk Blastemal Type Wilms Tumors. <i>Cancer Cell</i> , 2015, 27, 298-311.	16.8	248
31	BAZ2A (TIP5) is involved in epigenetic alterations in prostate cancer and its overexpression predicts disease recurrence. <i>Nature Genetics</i> , 2015, 47, 22-30.	21.4	141
32	Abstract A61: Exploring the PDAC-subtype-associated microenvironment in PDX models and patients. , 2015, , .		0
33	<i>circize</i> implements and enhances circular visualization in R. <i>Bioinformatics</i> , 2014, 30, 2811-2812.	4.1	2,736
34	CePa: an R package for finding significant pathways weighted by multiple network centralities. <i>Bioinformatics</i> , 2013, 29, 658-660.	4.1	54
35	Gene regulation is governed by a core network in hepatocellular carcinoma. <i>BMC Systems Biology</i> , 2012, 6, 32.	3.0	13
36	Centrality-based pathway enrichment: a systematic approach for finding significant pathways dominated by key genes. <i>BMC Systems Biology</i> , 2012, 6, 56.	3.0	69

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37	MiRmat: Mature microRNA Sequence Prediction. PLoS ONE, 2012, 7, e51673.	2.5	24
38	InterMitoBase: An annotated database and analysis platform of protein-protein interactions for human mitochondria. BMC Genomics, 2011, 12, 335.	2.8	9
39	Notice of Retraction: Finding Significant Gene Sets with Weighted Distribution of Gene Expression. , 2011, , .		0
40	Hypoxia induces PGC-1 β expression and mitochondrial biogenesis in the myocardium of TOF patients. Cell Research, 2010, 20, 676-687.	12.0	89