

Martin Morgan

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

5,282
citations

623734

14
h-index

752698

20
g-index

31
all docs

31
docs citations

31
times ranked

13170
citing authors

#	ARTICLE	IF	CITATIONS
1	Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space. <i>Cell Genomics</i> , 2022, 2, 100085.	6.5	59
2	Toward a gold standard for benchmarking gene set enrichment analysis. <i>Briefings in Bioinformatics</i> , 2021, 22, 545-556.	6.5	83
3	<i>Bioconductor</i> toolchain for reproducible bioinformatics pipelines using <i>Rcwl</i> and <i>RcwlPipelines</i> . <i>Bioinformatics</i> , 2021, 37, 3351-3352.	4.1	3
4	Open-source Software Sustainability Models: Initial White Paper From the Informatics Technology for Cancer Research Sustainability and Industry Partnership Working Group. <i>Journal of Medical Internet Research</i> , 2021, 23, e20028.	4.3	2
5	Orchestrating single-cell analysis with Bioconductor. <i>Nature Methods</i> , 2020, 17, 137-145.	19.0	488
6	Multiomic Analysis of Subtype Evolution and Heterogeneity in High-Grade Serous Ovarian Carcinoma. <i>Cancer Research</i> , 2020, 80, 4335-4345.	0.9	57
7	Multiomic Integration of Public Oncology Databases in Bioconductor. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 958-971.	2.1	42
8	Cancer Moonshot Immuno-Oncology Translational Network (IOTN): accelerating the clinical translation of basic discoveries for improving immunotherapy and immunoprevention of cancer. , 2020, 8, e000796.		7
9	Global Alliance for Genomics and Health Meets Bioconductor: Toward Reproducible and Agile Cancer Genomics at Cloud Scale. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 472-479.	2.1	4
10	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. <i>PLoS Computational Biology</i> , 2020, 16, e1007664.	3.2	165
11	Reliable Analysis of Clinical Tumor-Only Whole-Exome Sequencing Data. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 321-335.	2.1	20
12	restfulSE: A semantically rich interface for cloud-scale genomics with Bioconductor. <i>F1000Research</i> , 2019, 8, 21.	1.6	0
13	Accessible, curated metagenomic data through ExperimentHub. <i>Nature Methods</i> , 2017, 14, 1023-1024.	19.0	292
14	Software for the Integration of Multiomics Experiments in Bioconductor. <i>Cancer Research</i> , 2017, 77, e39-e42.	0.9	80
15	Genomic Annotation Resources in R/Bioconductor. <i>Methods in Molecular Biology</i> , 2016, 1418, 67-90.	0.9	27
16	Public data and open source tools for multi-assay genomic investigation of disease. <i>Briefings in Bioinformatics</i> , 2016, 17, 603-615.	6.5	46
17	Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , 2015, 12, 115-121.	19.0	3,070
18	The Bioconductor channel in F1000Research. <i>F1000Research</i> , 2015, 4, 217.	1.6	6

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19	The Bioconductor channel in F1000Research. F1000Research, 2015, 4, 217.	1.6	4
20	<code>VariantAnnotation</code> : a <code>Bioconductor</code> package for exploration and annotation of genetic variants. Bioinformatics, 2014, 30, 2076-2078.	4.1	293
21	Scalable Genomics with R and Bioconductor. Statistical Science, 2014, 29, 214-226.	2.8	8
22	ShortRead: a bioconductor package for input, quality assessment and exploration of high-throughput sequence data. Bioinformatics, 2009, 25, 2607-2608.	4.1	481