Andrew Thrasher

List of Publications by Year
in descending order

20	768	1163117 8	1125743 13
papers	citations	h-index	g-index

22	22	22	2005
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Abstract PO-046: MethylationToActivity: A deep-learning framework that reveals promoter activity landscapes from DNA methylomes in individual tumors. , 2021, , .		0
2	Abstract 2289: Empowering point-and-click genomic analysis with large pediatric genomic reference data on St. Jude Cloud. , 2021, , .		0
3	Genomes for Kids: The Scope of Pathogenic Mutations in Pediatric Cancer Revealed by Comprehensive DNA and RNA Sequencing. Cancer Discovery, 2021, 11, 3008-3027.	9.4	88
4	Abstract 642: Genomes for Kids: Comprehensive DNA and RNA sequencing defining the scope of actionable mutations in pediatric cancer. , 2021, , .		0
5	MethylationToActivity: a deep-learning framework that reveals promoter activity landscapes from DNA methylomes in individual tumors. Genome Biology, 2021, 22, 24.	8.8	8
6	St. Jude Cloud: A Pediatric Cancer Genomic Data-Sharing Ecosystem. Cancer Discovery, 2021, 11, 1082-1099.	9.4	109
7	CICERO: a versatile method for detecting complex and diverse driver fusions using cancer RNA sequencing data. Genome Biology, 2020, 21, 126.	8.8	74
8	Genetic Risk for Subsequent Neoplasms Among Long-Term Survivors of Childhood Cancer. Journal of Clinical Oncology, 2018, 36, 2078-2087.	1.6	105
9	Clinical cancer genomic profiling by three-platform sequencing of whole genome, whole exome and transcriptome. Nature Communications, 2018, 9, 3962.	12.8	142
10	Precision Medicine for Sickle Cell Disease through Whole Genome Sequencing. Blood, 2018, 132, 3641-3641.	1.4	3
11	Abstract 3001: Germline mutations in cancer predisposition genes and risk for subsequent neoplasms among long-term survivors of childhood cancer in the St. Jude Lifetime Cohort. Cancer Research, 2017, 77, 3001-3001.	0.9	2
12	Abstract 2628: Molecular diagnosis for pediatric cancer through integrative analysis of whole-genome, whole-exome and transcriptome sequencing. , 2016, , .		0
13	Scaling up genome annotation using MAKER and work queue. International Journal of Bioinformatics Research and Applications, 2014, 10, 447.	0.2	11
14	Case Studies in Designing Elastic Applications. , 2013, , .		4
15	VectorBase: improvements to a bioinformatics resource for invertebrate vector genomics. Nucleic Acids Research, 2012, 40, D729-D734.	14.5	143
16	A Framework for Scalable Genome Assembly on Clusters, Clouds, and Grids. IEEE Transactions on Parallel and Distributed Systems, 2012, 23, 2189-2197.	5.6	14
17	Shifting the bioinformatics computing paradigm: A case study in parallelizing genome annotation using MAKER and Work Queue. , 2012, , .		3
18	Scripting distributed scientific workflows using Weaver. Concurrency Computation Practice and Experience, 2012, 24, 1685-1707.	2.2	5

#	Article	IF	Citations
19	Harnessing parallelism in multicore clusters with the All-Pairs, Wavefront, and Makeflow abstractions. Cluster Computing, 2010, 13, 243-256.	5.0	35
20	Taming complex bioinformatics workflows with weaver, makeflow, and starch. , 2010, , .		12