

# Andrew Thrasher

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7247506/publications.pdf>

Version: 2024-02-01

20  
papers

768  
citations

1163117

8  
h-index

1125743

13  
g-index

22  
all docs

22  
docs citations

22  
times ranked

2005  
citing authors

#	ARTICLE	IF	CITATIONS
1	VectorBase: improvements to a bioinformatics resource for invertebrate vector genomics. <i>Nucleic Acids Research</i> , 2012, 40, D729-D734.	14.5	143
2	Clinical cancer genomic profiling by three-platform sequencing of whole genome, whole exome and transcriptome. <i>Nature Communications</i> , 2018, 9, 3962.	12.8	142
3	St. Jude Cloud: A Pediatric Cancer Genomic Data-Sharing Ecosystem. <i>Cancer Discovery</i> , 2021, 11, 1082-1099.	9.4	109
4	Genetic Risk for Subsequent Neoplasms Among Long-Term Survivors of Childhood Cancer. <i>Journal of Clinical Oncology</i> , 2018, 36, 2078-2087.	1.6	105
5	Genomes for Kids: The Scope of Pathogenic Mutations in Pediatric Cancer Revealed by Comprehensive DNA and RNA Sequencing. <i>Cancer Discovery</i> , 2021, 11, 3008-3027.	9.4	88
6	CICERO: a versatile method for detecting complex and diverse driver fusions using cancer RNA sequencing data. <i>Genome Biology</i> , 2020, 21, 126.	8.8	74
7	Harnessing parallelism in multicore clusters with the All-Pairs, Wavefront, and Makeflow abstractions. <i>Cluster Computing</i> , 2010, 13, 243-256.	5.0	35
8	A Framework for Scalable Genome Assembly on Clusters, Clouds, and Grids. <i>IEEE Transactions on Parallel and Distributed Systems</i> , 2012, 23, 2189-2197.	5.6	14
9	Taming complex bioinformatics workflows with weaver, makeflow, and starch. , 2010, , .		12
10	Scaling up genome annotation using MAKER and work queue. <i>International Journal of Bioinformatics Research and Applications</i> , 2014, 10, 447.	0.2	11
11	MethylationToActivity: a deep-learning framework that reveals promoter activity landscapes from DNA methylomes in individual tumors. <i>Genome Biology</i> , 2021, 22, 24.	8.8	8
12	Scripting distributed scientific workflows using Weaver. <i>Concurrency Computation Practice and Experience</i> , 2012, 24, 1685-1707.	2.2	5
13	Case Studies in Designing Elastic Applications. , 2013, , .		4
14	Shifting the bioinformatics computing paradigm: A case study in parallelizing genome annotation using MAKER and Work Queue. , 2012, , .		3
15	Precision Medicine for Sickle Cell Disease through Whole Genome Sequencing. <i>Blood</i> , 2018, 132, 3641-3641.	1.4	3
16	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. <i>Cancer Research</i> , 2017, 77, 3001-3001.	0.9	2
17	Abstract PO-046: MethylationToActivity: A deep-learning framework that reveals promoter activity landscapes from DNA methylomes in individual tumors. , 2021, , .		0
18	Abstract 2289: Empowering point-and-click genomic analysis with large pediatric genomic reference data on St. Jude Cloud. , 2021, , .		0

#	ARTICLE	IF	CITATIONS
19	Abstract 642: Genomes for Kids: Comprehensive DNA and RNA sequencing defining the scope of actionable mutations in pediatric cancer. , 2021, , .		0
20	Abstract 2628: Molecular diagnosis for pediatric cancer through integrative analysis of whole-genome, whole-exome and transcriptome sequencing. , 2016, , .		0