

Alexander Dobin

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4366447/publications.pdf>

Version: 2024-02-01

12
papers

37,545
citations

933264

10
h-index

1199470

12
g-index

19
all docs

19
docs citations

19
times ranked

79673
citing authors

#	ARTICLE	IF	CITATIONS
1	STAR: ultrafast universal RNA-seq aligner. <i>Bioinformatics</i> , 2013, 29, 15-21.	1.8	35,376
2	Mapping RNA-seq Reads with STAR. <i>Current Protocols in Bioinformatics</i> , 2015, 51, 11.14.1-11.14.19.	25.8	858
3	Accuracy assessment of fusion transcript detection via read-mapping and de novo fusion transcript assembly-based methods. <i>Genome Biology</i> , 2019, 20, 213.	3.8	379
4	Optimizing RNA-Seq Mapping with STAR. <i>Methods in Molecular Biology</i> , 2016, 1415, 245-262.	0.4	178
5	High-fidelity promoter profiling reveals widespread alternative promoter usage and transposon-driven developmental gene expression. <i>Genome Research</i> , 2013, 23, 169-180.	2.4	176
6	A benchmark for RNA-seq quantification pipelines. <i>Genome Biology</i> , 2016, 17, 74.	3.8	160
7	Is it time to change the reference genome?. <i>Genome Biology</i> , 2019, 20, 159.	3.8	134
8	A limited set of transcriptional programs define major cell types. <i>Genome Research</i> , 2020, 30, 1047-1059.	2.4	32
9	The fractured landscape of RNA-seq alignment: the default in our STARs. <i>Nucleic Acids Research</i> , 2018, 46, 5125-5138.	6.5	17
10	A community challenge to evaluate RNA-seq, fusion detection, and isoform quantification methods for cancer discovery. <i>Cell Systems</i> , 2021, 12, 827-838.e5.	2.9	15
11	Pan-human consensus genome significantly improves the accuracy of RNA-seq analyses. <i>Genome Research</i> , 2022, 32, 738-749.	2.4	6
12	Management, Analyses, and Distribution of the MaizeCODE Data on the Cloud. <i>Frontiers in Plant Science</i> , 2020, 11, 289.	1.7	4