

# Alexander Dobin

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

15  
papers

19,233  
citations

10  
h-index

19  
g-index

19  
ext. papers

30,645  
ext. citations

12.4  
avg, IF

6.62  
L-index

#	Paper	IF	Citations
15	STAR: ultrafast universal RNA-seq aligner. <i>Bioinformatics</i> , <b>2013</b> , 29, 15-21	7.2	18121
14	Mapping RNA-seq Reads with STAR. <i>Current Protocols in Bioinformatics</i> , <b>2015</b> , 51, 11.14.1-11.14.19	24.2	446
13	Accuracy assessment of fusion transcript detection via read-mapping and de novo fusion transcript assembly-based methods. <i>Genome Biology</i> , <b>2019</b> , 20, 213	18.3	163
12	High-fidelity promoter profiling reveals widespread alternative promoter usage and transposon-driven developmental gene expression. <i>Genome Research</i> , <b>2013</b> , 23, 169-80	9.7	133
11	A benchmark for RNA-seq quantification pipelines. <i>Genome Biology</i> , <b>2016</b> , 17, 74	18.3	117
10	Optimizing RNA-Seq Mapping with STAR. <i>Methods in Molecular Biology</i> , <b>2016</b> , 1415, 245-62	1.4	90
9	Is it time to change the reference genome?. <i>Genome Biology</i> , <b>2019</b> , 20, 159	18.3	72
8	Evolution of cellular diversity in primary motor cortex of human, marmoset monkey, and mouse		33
7	STARsolo: accurate, fast and versatile mapping/quantification of single-cell and single-nucleus RNA-seq data		23
6	A limited set of transcriptional programs define major cell types. <i>Genome Research</i> , <b>2020</b> , 30, 1047-1059	9.7	15
5	The fractured landscape of RNA-seq alignment: the default in our STARs. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 5125-5138	20.1	10
4	Management, Analyses, and Distribution of the MaizeCODE Data on the Cloud. <i>Frontiers in Plant Science</i> , <b>2020</b> , 11, 289	6.2	3
3	A limited set of transcriptional programs define major cell types		3
2	A community challenge to evaluate RNA-seq, fusion detection, and isoform quantification methods for cancer discovery. <i>Cell Systems</i> , <b>2021</b> , 12, 827-838.e5	10.6	3
1	The fractured landscape of RNA-seq alignment: The default in our STARs		1